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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:01:00 2000; MasPar time 3.40 Seconds 215.791 Million cell updates/sec

labular output not generated.

>US-19-142-524A.4 (1-31) from TSC9142524A.pep 225 Intle: Description: Perfect Score:

FAM 150 Gap 11 Scoring table:

1 IFSKNINIKINMFLYIAGNKRRFIKRVSNVI 31 ecquence:

188963 seqs, 23686106 residues Scarched:

Minimum Match 0% Listing first 45 summaries Post-processing:

argeneseq35 ligeneseqp Database:

Mean 23.433; Variance 89.397; scale 0.262 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

Result	:				:		
02	Socie	Karc:	.ength	g :	3	Description	Pred. No.
. 1	225	100.0	3.5	٦	W27372	Multi-epitope peptide	4.18e-14
7	C 17 (20	-	W42130	T-cell epitope peptide	. 27
~	143	63.6	354	. 1	W04344	Chamaecyparis obtusa p	9.27e-
4	1.43	63.6	354	,-1	W42121	Japanese cypress polle	9.27
'n	143	63.5	(۳)	- 1	W04345	Chamaecyparis obtusa p	9.27e
φ	123		3	-	R45577		. 28e
7	:23	77	m	~	R45578	Jun v I.	8.28e-04
ന	11.8	52.4		7	W27371	Multi-epitope peptide	.50e-
σ	118	∧		, -1	R75388	Japanese cedar pollen	.50e-
10	118	52.4	353	٠,	R81587	len a	
1.1	8::	(4	374	~	R31937	Cry ji.	
12	118	52.4	374	٠,	260166	Japanese cedar pollen	.50e-
13	118	52.4	374	•4	882490	Cry j I Japanese Cedar	.50e-
7.	113	52.4	374	-	R45541	١٦	2.50e-03
U 1	m • 1	50.2	20	٠ ١	R45549	I polien	•
40	£	50.2	20	-	R82498	н	7.48e-03
<i>:</i> :	7:3	50.2	3.0	-	W44682	T.	7.48e-03
18	87	38.3	105	~	W27370	i-epitope p	1.88e+00
19	92	36.4	31	-	W27373		5.23e+00
2.0	G G G	W. CO	38	-1	M27369	Multi-epitope peptide	7.84e+C0
21	ι. Q	35.1	1018	٠,	WC6485	Rat contactin ligand f	9.59e+00
22	3.4	32.9	20	-1	W42131	top	2.59e+01
23	7.	32.9	637	. 1	W52294		2.59e+01

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3.15e+01	نت	, £66+	· 65e+	5.65e-01	, ac.,	. 55e -	1)	6.85e-01	6.85e-03	4900	850	£ 85e+01	8.50e+01	8.30e+01	8 e-0.	8.40e+01	1.01e+02	1.016+02	1.010-02	1.0le-02
Human thoracic aorta G Human thoracic aorta G	mostable enzyme (Tomato IGETR1 ethylene	QETR ethylene response	A. thaliana ethylene r	Racillus subtilis teic	Racillus subtilis teic	T-cell epitope peptide	Tomato ethylene respon	Tomato ethylene respon	Nr (never ripe) torato	Tomate ethylene respen	Home sapiens DE185_1 c	class	Human SR-BI class B Sc	Human contactin (EMBL	Human contactin.	Ethylene response (EIR	response (ET	Ethylene response (ETR	A. thallana ethylene r
4755 4727	O	R74630	R74532	W73122	W34454	W34455	W42129	W 3124	W 3125	1.1633	:629	1961	558.	006.	98C- X	E. 32	S)	R69852	98	W73119
. 4	۰, ۱	٦	~	-	۲,	-4	٠.	7	-	~	-1	٠,	٠.4	~	~	٦	~		٠,	٠,
2.58	963	615	613	613	721	746	20	635	535	635	635	1028	503	509	1018	1018	738	738	738	738
32.4	, N		31.1	31.1	31.1	31.1	3C.7	30.7	30.7	30.7	30.7	30.7	30.2	30.2	30.2	30.2				
73	72	71	70	0	70	20	69	69	69	69	69	59	99	89	98	69 69	67	67	67	29
24	26	27	28	58	30	31	32	33	34	s) E	36	3.7	38	36	O 7	4.1	42	43	7	4.5

AL IGNMENTS

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16-JUN-1998 (first entry)
7-cell epitope peptide 10 from Japanese cypress pollen antigen Chaol.
Japanese cypress pollen; antigen: T-cell epitope: Chaol; Chaol;
diagnosis: allergy: spring tree pollen disease; pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gars
                                                                                         24-MAR-1998 (first entry)
Multi-epitope peptide used as immunotherapeutic agent #4.
Multi-epitope peptide: immunotherapeutic agent; allergic disease:
T-cell epitope region: allergen: lymphocyte: immunoglobulin E.
Synthetic.
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H42130 standard: peptide; 20 AA.
T 1 W27372 standard: peptide: 31 AA
                                                                                                                                                                                                                                                                                               12-SEP-1997.
10-MAR-1997; JG6740.
10-MAR-1996; JP-C80702.
                                                                                                                                                                                                                                                              W09732600-A1.
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375 AA;
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ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a Treell epitope peptide from Japanese oppress pollen antigen Chaol The present invention describes peptides which correspond to the Treel opitope sites on Japanese Oppress pollen autigens Chaol and Chaol. The peptides can be used as a readent for the diagnosis of allergy to Japanese cypress pollen, and as an antigen in the treatment and prevention of spring tree pollen disease in which the Sequence 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                 18-DEC-1997.
14-JUN-19997. J727-01.
14-JUN-19997. J727-01.
14-JUN-19997. J727-02.
14-JUN-19997. J727-02.
14-JUN-19997. J727-02.
14-JUN-199-1997. J727-02.
Dairiki K. Kino K.
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Claim 2 Pages 10-11, Topi Japanese.

The present sequence is the C obtuss pollen altergen tha o I, the Troeil epitopes of which tan be used in the development of a preventive and treating agent for C obtuss pollen pollinosis.

C obtuss pollen (2.4 kg) was deeptessed with district electric and dried at room temp. Overnight that of was septial from it and purified. RNA was extracted from C obtuss pollen, and mRNA and mRNA and mRNA was extracted from C obtuss pollen, and mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1996 (first outry)
Chamaecyparis oblusa pollen alleraen Cha o f (A).
Pollen alleraen: Cha o I: T-cell epitope: prevention: treatment:
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Japanese cypress pollen antiyen Chabi.
Japanese cypress pollen: antiqen; T-cell epitope; Chabi: Chab2;
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Pred. No. 9.27e-06:
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W42121:
16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pollen disease
Claim 1: Page 22 71pp: Japanese.
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Chamaevyparis obcusa.
Chamaevyparis obcusa.
Chart. 1946.
21-DEC-1944. 335689.
21-DEC-1944. 335689.
Chert. 5-3882. NRIUT MICK PROD ON UNIVERSED.
WPL. 55-3882.5/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IFSKNINIKLNMPLYIAGNK 20
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Rest Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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      Chamaeyparis obtisa W09747648-AI.
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Example 1; Page 14-15: 71pp: Japanese.

Example 1; Page 14-15: 71pp: Japanese cypress pollen antigen chaul. The present invention describes pertides which correspond to the Treal: epitope sites on Japanese cypress pollen antigens Chaol and Chauz The peptides can be used as a reagent for the diagnosts of allergy to Japanese cypress pollen, and as an antigen in the treatment and prevention of spring tree poller disease in which the pollingsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding changerypass of the superior alternance; not the analtering agent for Contrast policy prollings; provided the analtering agent for Contrast policy prollings; claim 8: pages 11-22; TAPPS Japanese.

The present sequence is the Conbtasa policy and refer cell epicopes of which can be used in the development of a preventive and treating agent for Conbtasa policy politinosis. Contrast policy of was agereased with diethyl ether, and afried at room temp, overnight. Chao I was sepd, from it and purified. NA was extracted from Coubtusa policy, and mRNA and conved.
                                                                                                                                                                                                                                                                                             The I epitope peptide portion of Lapanese cypress pollen antianns Chaol and Chaol and Chaol used for diagnosis and treatment of spring tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1996 (first entry)
Chamaecyparis obtusa pollen allergen Cha o I cENA (b).
Pollen allergen: Cha o I: I-cell epitope: prevention: treatment.
pollinosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 63.6%; Score 143: 06.1: Length 354: Local Similarity 100.0%; Prod. No. 9.27e-96: es 20: Conservative (: Mismatches 0: Indels es
diagnosis: allergy: spring tree pollen disease: pollinosis
Chamaeyparis obtusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W04345 standard, Protein; 375 Av. W04345;
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R4557 standard; Protein; 367 AA.
R45577;
13-0U-1994 (first entry)
Jun s I.
                                                                                          18-DEC-1997;
12-JUN-1997; J02031.
12-JUN-1996; JPT-153527.
(MEIP.) MELJI MILK PROD CG LITC.
Dairiki K, Kino K;
WPI; 98-052242/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chamaecyparis obtusa.
08176192-A.
09-JUC-1994.
21-DEC-1994. 335089.
(MEIP.) MEIT. MILK PROD FO CIT
WEIF.) WEIT. MILK PROD FO CIT
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PP 12-SEP-1997.

PR 10-MAR-1997. J00740.

PR 10-MAR-1996. JP-080702.

PR 10-MAR-1996. JP-080702.

PR 10-MAR-1996. JP-080702.

PR 10-MAR-1996. JP-080702.

PD Dairiki K, Iwama A, Kino K. Kume A, Sone I;

Dairiki K, Iwama A, Kino K. Kume A, Sone I;

Dairiki K, Iwama A, Kino K. Kume A, Sone I;

Dairiki K, Iwama A, Kino K. Kume A, Sone I;

Dairiki K, Iwama A, Kino K. Kume A, Sone I;

Dairiki K, Iwama A, Kino K. Kume A, Sone I;

PP Contains multi-epitope peptide containing I cell epitope regions from S Calum 6; Page 32; SRpp; Japanese.

C a new immunotherapeutic agent. It comprises I cell epitope regions from 2 Contains from 2 Contains and arginize or lysine Contains. J. Where the I cell epitope regions: have a positivity index Containers, where the I cell epitope regions: have a positivity index Contains from Faregen; have at least 70% reactivity with lymphocytes from patients contained and argent and are not reactive with immunodichilin E Contained to the allergen: and are not reactive with immunodichilin E Contained and treat a wide variety of allergen. Contained and treat a wide variety of allergen. Contained and treat a wide variety of allergen are reduced. De desensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1996 (first entry)
Japanese cedar polien allerden Cry) I.
Japanese cedar: polien allergen: Cry; I: T-cell epitope: peptides:
prevention; treatment: cryptomeria poliinosis.
Cryptomeria japonica.
                                                                                                                     24-MAR-1998 (first entry)
Hulti-epitope peptide used as immunotherapeutic agent #3.
Multi-epitope peptide; immunotherapeutic agent; allergic disease;
T-cell epitope region; allergen: lymphocyte; immunoglobulin E.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             >core 118: DB 3: Length 134;
>red. No. 2.50e-03;
5: Mismatches 6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="T-cell epitope peptide"
106. 120
/note="T-cell epitope peptide"
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/note= "T-ce.l epitope peptide"
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                                                                                                  W27371 standard; peptide; 134 AA.
W27371;
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20-001-1993: 265626.
20-001-1993: JP-265626.
(MEIP.) MEDJI MILK PROD CO LTD.
WPI: 95-203834/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              875388 stundard: protein, 753
875888,
12:888-1996 (first entry)
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Best Local Similarity 60.0%;
Matches 18; Conservative
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      105
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                                                                                                                                                                                                                                                                                                                                                                            alleray Discussive, Fig 16, 137pp, English. The sequence is that of Jun s., a homologue of the Japanese cedar pollon allergen Cry j. Antigenic peptides derived from it can be used for the treatment and diagnosis of allergies associated Sequence 157 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Discipsure: Fig 17: 137pp: English.
The sequence is that of Jun v 1, a homologue of the Japanese cedar pollen allergen Cry 1. Antiqenic peptides derived from it can be used for the treatment and diagnosis of allergies associated
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Antigens derived from Japanese cedar pollen allergen Cry ) I -
contain at least two I cell epitope(s), used to treat or diagnose
                                                                                                                                                                                                                                                                                                                                       Antiques derived from Japanese cedar pollen allergen Cry {\bf j} I contain a' least two T cell epitope(s), used to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japanese cedar: pollen allergen; allergy: treatment; diagnosis;
[ cell epitope: sensitivity: detection:
    treatment; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-1994: UCGI39.
15-JAN-1997: UCGI39.
01-SEP-1992: WS-938990.
(IMMU-) IMMULNGIC PHARM CCRP.
Bond UF, Garman RD, Griffith IC. Kto M. Pollock J:
WPI: 94-035066/04.
                                                                                                                                                                            20-JAN-1994.
15-JAN-1993: UC0139.
10-JUL-1992: UC-U05661.
C1-SEP-1992: US-938990.
(IMM-) IMMULOGIC PHARM CORP.
ROND JF, GARMON RD, Griffith IJ, Kuo M, Pollock J:
NPR: 94-C35066/C4.
Japanese cedar; pollen allergen; allergy
T cell epitope; sensitivity; detection.
Juniperus sabinoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note: "signal pertide"
22. .370
                                                                                                                                            /note= "mature peptide"
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                                                                                                    /note= "signal peptide'
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                                                               Location/Qualifiers
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R45578:
13-JUL-1994 (lirst entry)
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Best Local Similarity 75.0%;
Matches 15; Conservative
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Sequence: 37m AA;
                                                                                                                     22. 367
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/cote=
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Judiperus virazolana.
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16.8EP-1995; 3062921.

14.010-1995; 306296.

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18.40
New cryptomeria pollen allergen Incell epitope peptide - used for prevention, treatment and investigation of Japanese cedar pollenosis Disclosure, Figs 1-2, 8pp. Japanese. R7538 is the Japanese cedar pollen allergen Cry) I. from which the Incell epitope peptides R89289-R89295 were derived. The peptides can be used for the prevention and treatment of cryptomeria pollenosis, and also for the investigation of pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cedar poller allergen B.
Cedar poller allergen B.
Cedar: poller allergen: immunoqlobulin E: IgE: Treell epitope:
antibody; pollinosis: thorapy: immunotherapy.
Cryptome:ia laponica.
IS-MAC-77.
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/note=_"signal peptide"
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Sest Local Similarity 60.0%;
Matches 18; Conservative
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10-JUL-1992: U05661.
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                                                                                                        Nucleic acid sequence encoding tryptomeria japonica allerne. For the diagnosis treatment and prevention of allergic reactions for the diagnosis treatment and prevention of allergic reactions of Japonese cedar pollen collected from staminate cone samples were collected from a simple fresh pollen and staminate cone samples were collected from a simple Cryptomeria japonica (Japanese cedar) tree. RNA was preped and issert to synthesise CDNA. The CDNA was subjected to successive require por to yield a full length CTY j. clone. CTY j. I or an antiquence fragment of it may be used for detecting, treating and preventing an allergic response to Japanese cedar police allerged. It is capable of modifying both the B and T cell response to CTY j. and T cell response to a CTY j. and T cell response to CTY j. and T cell response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugi (Japanese Geda:) pollen autimen Cig): is usviul for diagnosis. Ireatment and prevention of sugi pollinosis. Claim 2: Page 5-7; gpp: Japanese. The coding sequence for the Japanese cedar ("sigi") pollen alimiten Cryl was isolated from a cDNA library prepared from polyA meNA. All or part of the Cryl: protein can be used for diagnosis, treatment sequence. 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sales
Contract
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Cry j I Japanese Cedar pollen allergen.
Cry j I: japanese cedar pollen allergen: modified; drug production:
allergy: Crytpomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R60166 standard; Protein; 374 AA.
R60166;
24-MAR-1995 (first entry)
Japanese cedar pollen antiqes: Cry)I.
Japanese edar; pollen antiqes; allerges: Cry)I: suqu: pollenosus
Cryptomer: a japonica.
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52.4%: Shore 118: 78 1; Length 334:
Best Local Similarity 56.0%: Fed. No. 2.50e-63.
Matches 18: Conservative i: Mismatches 7: Indels
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22. 374
/label- mature_cryji
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12-JUL-1991; US-729134.

15-JUL-1991; US-730452.

(IMMU-) IMMULDGIC PHARM CCRP.

BOND JF, GRIffith IJ, Pollock J;

WPI; 93-045434/0S.

N-PSUB; Q35304.
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R82490;
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07-JAN-1993: D01116.
07-JAN-1993: JP-L01116.
(MEJJ) MELL: SETKA KATSHA.
WPT: 94-268680/KK.
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WPIN 95-3659147.

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WPIN 95-3659147.

Modified Cryptomeria japonica (Cry ;) ; peptide(s) - useful for treating alleray to japanose cedar pollen allerayen or immunologically cross reactive allerayens

Solschosure, Figure 1: 60pp English.

Novel peptides of cry ; thave been modified as a part of a preformulation scheme to develop an optimised drug product for therapeutic treatment of humans suffering from alleray to Japanese cedar pollen alleragen valed is immunologically cross reactive with Japanese cedar pollen alleragen which is immunologically cross cedive with Japanese cedar pollen alleragen which is immunologically cross cedive with Japanese cedar pollen alleragen which render them particularly suitable for drug product formulation. Peptide fragments of Cry ; it modified and unmodified are given in R82491-R8255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiques derived from Japanese cedar pollen allergen Cry j I contain at least two I cell epitope(s), used to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure: Fig 4: 137pp: English.

The sequence is that of the Japanese cedar pollen allergen cry ; which contains at least two I cell epitopes. Peptide antiques derived from it can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen. The poptides have enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.4%; Score 118: DB 1: Length 374; Sect Local Similarity 60.0%; Pred. No. 2.50e-03; Matches 18: Conservative 4: Mismatches 7: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.4%: Score 118: DB 1: Length 374; Hest Loral Similarity 60.0%: Pred. No. 2.50e-03: Matches 18: Conservative 4; Mismatches 7: Indels
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15-JNN 1993: US0139.
10-SUL-1992: WS-938990.
01-SFF-1992: US-938990.
(IMMC-) IMMULCGIC PHARM CORP.
(IMMC-) IMMULCGIC PHARM CORP.
WPI: 94-035C66/04.
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                                                                                                                    Evans S. Franzen HM, Kuo M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R45541 standard; Protein; 374 AA.
                                              06-APR-1995; U04249.
08-APR-1994; US-226248.
06-DEC-1994; US-350225.
(IMMC-) IMMCLOGIC FRARM CGRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptomeria japonica.
Crytpomeria japonica.
WO9527786-Al.
                                                                                                                                                                                                                                                                                                                                                                                                            :74 AA;
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                                 19-001-1995
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Gaps

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92 IFSCHMNIKLKMPMYIAGYKT-FDGRGAQV 120

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claim 1; Fig 13, 137pp: English.

The sequence is that of an isolated peptide of the Japanese reda:
pollen allergen CY (aring acids 71-90). The peptide, CJ1-8,
can be used for the treatment and diagnosis of allergies associated
with Japanese cedar pollen. I has enhanced therapeutic properties
but reduced side effects command to naturally occurring allergies.
                                                                                                                                                                                                                                                                                                                                                                     Antigens derived from Japane e cedar pullen allerden Gry ) I contain at least two I cell \{pltope(s)\} used to treat or diagnose
                                                                                                                                              Cry j I pollen allergen peptide CJ:-8.
Japanese cedar: detection: allergy: treatment; diagnosis:
T cell epitope: sensitiv'*y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.2%: Score 123: DB 1: Length 45: Best Local Similarity 75.0%: Pred. No. 7.48e-03: Matches 15: Conservative 3: Mismatches 2: Indeis
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15-JAN-1993: UOC139.
01-SEP-1992: WO-U05661.
01-SEP-1992: US-938990.
UMMC-) IMMULOGIC PHARM CORP.
BOND JJF. GATMAN RD. GILIFITH IJ, KUO M. POLIOCK J:
WPI: 94-035066/04.
1 IFSKNLNIKLNMPLYIAGNKRRFIKRVSNV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      completed: Mon Jun 19 16:01:15 2000
ne : 15 secs.
                                                                                          R45549 standard: Protein: 20 AA
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                                                                                                                                                                                                     Cryptomeria japonica
W09401550-A.
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US-09-142-524A-4.rai

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Release 3.1A John E. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Jun 20 13:34:00 2000: MasPar time 2.66 Seconds 168.026 Million cell updates/sec Run on:

Tabular output not generated.

1 IFSKNLNIKLNMPLYIAGNKRRFIKRVSNVI 31 >65-09-142-524A-4 (1-31) from USC9142524A.pep 225 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

145341 segs, 14437480 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing.

1:5A_COMB 2:5B_COMB 3:6_CCMB 4:PCT_CCMB 5:backfiles1 a-issued Dalabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 21.952; Variance 87.861: scale 0.250

Statistics:

Sequence 2. Application 6.12e-00 Sequence 76, Application 1.97e-01 Sequence 48 Application 2.38e-01 Sequence 48 Application 2.38e-01 Sequence 46, Application 4.22e-01 Sequence 76, Application 4.22e-01 Sequence 76, Application 4.22e-01 Sequence 76, Application 4.22e-01 Sequence 76, Application 5.09e-01 Sequence 76, Application 5.09e-01 Sequence 6, Application 5.09e-01 Sequence 7, Application 5.09e-01 Sequence 7, Application 6.15e-01 Sequence 7, Application 6.15e-01 Sequence 7, Application 6.15e-01 Sequence 3, Application 6.15e-01 Sequence 7, Application 6.15e-01 Description US-08-452 - 05-08-452 US-08-537 US-08-749 US-08-749 US-08-749 US-08-749 US-08-749 US-08-749 US-08-749 US-08-749 US-08-749 US-08-748 SUMMARIES Query Match Length DB Score

protein

MOLECULE TYPE:

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RESULT

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Sequence 76, Application PC/TUS9406528
GENERAL INCORMATION.
APPLICANT: New YORK University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND TOMPOSITIONS AND METHICS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARES PATENTIA PROSPERSION F1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: 05-7/943.236
FILING DATE: 05-SEP-1993
APPLICATION NUMBER: 05-7/943.236
FILING DATE: 10-SEP-1992
ATOMNEY/ASENT INPORMATION:
NAME: 10-SEP-1992
REGISTRATION NUMBER: 34.033
REGISTRATION NUMBER: 34.033
REFERENCE/POCKET NUMBER: 14.033
REFERENCE/POCKET NUMBER: 14.033
REFERENCE/POCKET NUMBER: 14.033
TELEPHONE: 202.628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.4%: Score 73: UB 4: Length 298.
Best Local Similarity 32.3%; Pred. No. 1.97e+01;
Matches 10: Conservative 10: Mismatches 10: Indels
                                                                                                                                                                                                                                           STREET: 419 Seventh Street, N.W., Suite 300 CITY, Washington STATE: 50.0.
 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 AA
 PKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Controlly integral McCECULE TYPE: peptide Willer 298 AA; 33548 MW; 4675/8 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 LESKAVIALLNMGTFL-GSFPDYVRKVSRIV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FSKNLNIKLNMPLYIAGNKRRFIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              Sequence 76, Application PC/1089308528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/U8537002A
Patent No. 577382
GENERAL INFORMATION:
APPLICANT: ISUSAM: Keiji
APPLICANT: KUBOTA, Michio
APPLICANT: SUGINOTO, ICShiyuki
                                                                                                                                                                                                                                          BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08537002A
 STANDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 248 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-5528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277715
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDELNESS
                                                                                                                                                                                                                                                                                                                 20004
 PCT-US93-08529-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-537-002A-3
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECCENCE
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                                 XXXXXX
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TILLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: POLYPEPTIDES OF G-COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWNY AND NEIMARK
STREET: 419 Sevent: Street, N.W., Suite 300
                                                               3
                                                               Caps
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                                                               .:
                                 Length 1018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waery Match
Hest Local Similarity 32.3%; Pred. No. 1.97e-01;
Matches 10: Penservative 10; Mismatches 10; Indels
                            Score 79; DB 1; Length 1018
Pred, No. 6.12e-00;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2rsion #1.25
                                                                                                                                                                                        298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJA 199E: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D/S
SOFTWARE: POLENTIN Release #1.6, 21
CURRENT AFFLICATION DATA:
APPLICATION NUMBER: US/28/118-270
FILING NATE: C9-SEP-1943
PRIOR APPLICATION CATA:
APPLILATION NUMHUR: US 07/94-246
TELE ARE 113102 MW: 5593274 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MURPHY-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 DESKAVIALLNMGIFL-GSEPDYVRRVSRIV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MODECULE TYPE: peptide
SEQUENCE 298 AA: 33548 MW: 467538 CN:
                                                                                                                                                                                          PRT
                                                                                             164 FPDDLSYBWLNEFPVFITMUKRRFVSGTN 192
                                                                                                                                                                                                                                                                                                                 Sequence 75, Application US/08118270 Patent No. 5508384 GENERAL INF.EMAILON:
                                                                                                                          Z PSKNINIK IN-MPLYIAGNKRRFIKRVS 28
                                                                                                                                                                                                                                                                                     Sequence 75 Application US/08118270
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FILLING (ALE)
FILLING (ALE)
FILLING (ALE)
AND TOWNSHIP (ALE)
NAME: CONTRIBUTION
NAME: 34, 0313
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REFERENTE/DOCKET NUMBER: MU
FELECOMMUNICATION INFORMATION:
TELEFHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248633
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                             usery Match
Rest Local Similarity 34.5%:
Matches 10: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY
STREET: 419 Sevent
CLTY: Washington
STATE: D.C.
COUNTRY: USA
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D.C.
USA
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 SEQUENCE
                                 Query Match
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Gaps ..

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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy o
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                                                                                                                                                                                                                                                                                                                                                              Query Match
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      Gaps
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE NUMBER OF SEQUENCES:

CRRESPONDENCE S. 17
CRRESPONDENCE S. 17
CRRESPONDENCE S. 17
CRRESPONDENCE S. 18
CRACE: 0.6
CONTRY: USA
2.19: 20.64
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: PATENTION SATA:
CRESPICATION NUMBER: US/08/537,002A
FILING DATE: 01-CR-1995
CRASSIFICATION NUMBER: JP 26C984/1994
FILING DATE: 01-CR-1995
ATTOMNEY NUMBER: JP NO. 5773282 yet received
FILING DATE: 01-CR-1994
PRIOR APPLICATION NUMBER: JP NO. 5773282 yet received
FILING DATE: 08-SEP-1995
ATTOMNEY NORDENTION:
NAMP: BPOWNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE CP. INVENTION: ETHYLENE
NUMBER OF SEQUENCES: 50
CCRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72: DB 1; Length 963; Pred. No. 2.38e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5: indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Richard F. Trecartin
STRUET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                         TSUSAK1-1
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JENCE 963 AA, 110142 MW: 4422259 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Application US/084841013 Patent No. 5824868 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08484101B
                                                                                                                                                                                                                                                                                              25,618
                                                                                                                                                                                                                                                                                                      REFERENCE/SOCKET NUMBER: TSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO: 3: SEQUENCE HARACTERISTICS: LENGTH: 963 amino acids TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 FRINLGIPPRIMPL-LGGDARRY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FSKNINIKIN-MELYIAGNKRRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                   NAME: BROWDY, RODER L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 43.5%;
Matches 10: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-484-1018-49
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Saps
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Patent NO. 5824668
GENERAL INFORMATION
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: FHYLENE
NUMBER OF SEQUENCES:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Match 31.1%; Score 70; DB 2; Length 613; Local Similarity 26.7%; Pred. No. 3.49e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3.49e+01;
11: Mismatches 11; Indeis
                                               SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/484,101B
FILING DATE: U7-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/0594/
FILING DATE: 01-301,1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/086.555
FILING DATE: U1-301-1993
CLASSIFICATION: 800
CLASSIFICATION: 800
CLASSIFICATION: 800
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COMPUTER: IBM PC comparible
OCREMING SYSTEM: PC-DOS/MS-DCS
SCFTWARE: PatentIn Release #1.0, Version #1.25
CURRENI APPLICATION DATA:
FILING DATE: US/08/484,101B
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613 AA
                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENI INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBE: 3,801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 48:
SECUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE 613 AA: 68332 MW: 1963596 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 LSINLILSADLPTYAIGDEKFLMCTILNIM 468
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FSKNLNIKLNMPLYIAGNKRRFIARVSNVI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application US/08484101B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 613 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8: Conservative
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MEDIUM TYPE: DISKELLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DIS
SOFTWARE: FASTESO VERSION 2.0
CURRENT APPLICATION DATA:
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                       TOPOJOGY: linear
IMMEDIATE SOURCE:
LIHRARY: GenBank
CL NE: 189508
ENCE 525 AA; 59139 MW; 1455254 CN.
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACIERISTICS:
LENGTH: 525 action acids
TYPE: arino acid
TYPE: arino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08749902
                                                                                                                                                                                                                                                                                                                                                                                                                                  302 IDKILKCKLNIPPYLTQEARDLLKKL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FSKNLNIKLNMPLYIAGNKRRFIKRV 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIANDARD
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.6%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3174 Por
CITY. Paje Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
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US-08-749-932-8
                                                                                                                                                                                                                                                                                          SEQUENCE
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Hest Local Similarity 26.7%: Pred. No. 3.49e+01:
Matches 8: Conservativo ii: Mismatches ii: Indels
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CLASSIFICATION: 800
PRIOR APPLICATION LATA:
APPLICATION UNBER: PCF/CS94/
FILING DATE: 01.00.1994
CLASS.FICATION: 800
PRIOR APPLICATION BOD PRIOR APPLICATION BOD PRIOR APPLICATION NUMBER: 01.00.1993
CLASS.FICATION NUMBER: 03.004/CRSS.FICATION NUMBER: 03.004/CRSS.FICATION NUMBER: 03.004/CRSS.FICATION NUMBER: A.57515-2/RFT
PECCOMMUNICATION NUMBER: A.57515-2/RFT
PELECOMMUNICATION NUMBER: A.57515-2/RFT
PELECOMMUNICATION NUMBER: A.57515-2/RFT
PELECOMMUNICATION NUMBER: A.57515-2/RFT
PELECOMMUNICATION NUMBER: A.57515-2/RFT
PELEFRAN: (415) 398-3249
INFOHMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
ILENGTH: 613 analto acids
INFOHMATION ACCOUNTS
INFOHMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 AA
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OPERATING SYSTEM: DOS
SOFTWARE: FRASEG VOESION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
FALOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATCRNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCLOSY Thear
MOLECULE TYPE: protein
MOLECULE SIGNA, 68332 MW: 1963596 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 USINLIDSADLPIYAIGDEKRIMQIILNIM 468
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Patest No. 5985635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08749902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDICM IYPE: Diskett
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Shore 69: UB 2: Length 525:
Pred. No. 4.22e-31:
10: Mismatches 7: Indels
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Patent No. 598565
GENERL INFORMATION:
APPLICANT Bandman, 13
APPLICANT Goli, Su;
APPLICANT HIllman, Occupter L.
ITILE OF INVENTION: NOVEL HUMAN SERINE/THRECNINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMAGEUTICALS.INC.
STREET: 3774 POILTER TOPE
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US-08-484-101B-50
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                                                                                                                                                                                                                                        xxxxxx
                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3400 Embarcadero Center, Suite 3400
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Pred. No. 4.22e+01;
10: Mismat.hes 11; Indels
                                                                                                                       Score 69: DB 2: Length 525: Pred. No. 4.22e+01: 10: Mismatches 7: Indels
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COMPUTER READABLE FORM:
MEDIJM TYPE: Floppy disk
MEDIJM TYPE: Floppy disk
COMPOTER: ISM PC compatible
COMPOTER: ISM PC compatible
CONFORTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version: #1.25
CURREII APPLICATION DATA:
APPLICATION NUMBER: US/C8/484,101B
FLING DATE: 07-7JN-1995
CLASSIFICATION: 800
PRIOR APPLICATION: BCO
PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 AA
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NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31.801
REFECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P3.
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JENCE 635 AA; 71134 MW; 2014758 CN;
LIBRARY: GerBank
CLONE: 1562
WCE 525 AA: 59109 MW; 1457206 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/08484101B Patent No. 5824368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 36, Application US/08484101B
                                                                                                                                                                                                                                                                 302 IDKILKCKLNLPPYLTQEARDLLKKL 327
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 30.0%;
Matches 9; Conservative
                                                                                                                           Suery Match
Sest Local Similarity 34.6%:
Matches 9: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
3Y: linear
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                                                                                                                                                                          Sequence 50. Application US/084841018
Patent No. 5824868
GENERL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANIS HAVING MODIFIED RESPONSE TY
TITLE OF INVENTION: PLANIS HAVING MODIFIED RESPONSE TY
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 15/08/484,101B
FILING DATE: 07-JUN-1 95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: /US94/
FILING DATE: 01-JUL
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 30.7%; Score 69; DB 2; Length 635; Best Local Similarity 30.0%; Pred. No. 4.22e+01; Matches 9; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Richard F. Irecartin
STREET: 3400 Embarcadero Center. Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Trecartin, Richard E.
REGISTRAILON NUMBER: 31.801
REFRENCE/DOCKET N. 1883: A-57515-2/BFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FINCE 635 AA: 71151 MW: 2014614 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                    Sequence 50, Application US/08484101B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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STATE: California
COUNTRY: USA
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Sequence 5, Application US/2864-74;
Patent No. 6017695
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Hemperly, John J.
ITLE CF INVENTION: Human Cell Adhesion Molecule and Nacleral CRRESPONDENCE & ACCRESPONDENCE & CORRESPONDENCE & ADDRESSE:
ADDRESSEE: ADDRESSE: and Company STREET: One Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sairs
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COMPUTER: IBM PC comp.tible
OPERATING SYSTEM: PC-20S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRNI APPLICATION DATA:
APPLICATION NUMBER: US/08/040,741
           ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 AA
                                                                                                                                                                                                                                                                                                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
JENCE 605 AA; 68102 MW: 1847099 GN:
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amino acid
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ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuery Match
Best Local Similarity 33.3%;
Matches 10: Conservative
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US-08-040-741-6
COUNTRY:
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APPLICANT: McCarthy. Sean A.
APPLICANT: Gearing. David P.
APPLICANT: Certinson. David P.
APPLICANT: Levinson. David P.
IIILE OF INVENTION: METHOE FOR IDENTIFYING GENES
IIILE OF INVENTION: ENCORING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 14
CURRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                 APPLICATION AND ACTOR SUSAN L.
TILLE OF ENVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR NUMBER OF SEQUENCES: 86
ACRRESONDENCE ADDRESS:
ACRRESONDENCE FOLEY, HOAG & ELICT LLP
SIRE: One Post Office Square
CITY: Roston
SIRE: MA
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                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109-2170
COMPUTER READSLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: Patentin Rolease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,980
FILING DATE: 10-JUL 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68, UB 2; Length 509:
Pred, No. 5.09e+01:
11; Mismatches 9: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/ASENT INFORMATION:
NAME: ARROIGH BELF E
REGISTRATION NUMBER: 35.430
REFERENCE/DOCKET NUMBER: MIA-005.61
TELECOMMULTOTION: DOCKMETION:
TELECOMMULTOTION: 617-832-1000
TELEFAM: 617-832-7000
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SEQUENCE 509 AA: 56973 MW: 1456590 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SKNINIKLNMEL-YIAGNKREFIKR-VSNVI 31
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Patent No. 5952171
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                                                                                   Sequence 2, Application US/08890980
Patent No. 5998141
                                          Sequence 2. Application US/08890980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
fest Local Similarity 29.0%;
Matches 9: Conservative
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                                                                                                                Patent No. 5998141
GENERAL INFORMATION:
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US-08-752-307B-8
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1018 AA; 113333 MW; 5493875 CN;
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                                                                                                                                                            NAME/KEY: Modified-site
LOCATION: 474
OTHER INFORMATION: /iabe:
OTHER INFORMATION: /note-
OTHER INFORMATION: a.ycos;
FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
     Modified-sit~
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STATE: NJ
                                          OTHER INFORMATION: OTHER INFORMATION:
    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .T :4
US-08-714-901-5
                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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     /label- FLR
/note- "conserved core of fibronectin type
III-like repeat"
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/note= "conserved core of fibromectin type
III-like repeat"
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/note= "conserved core of fibrosectin type
III-like repeat"
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/note- "conserved core of fibronectin type
III-like repeat"
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/note- "potential site of ASN-linked
glycosylation"
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OTHER INFORMATION: /note- "potential site of ASN-linked
OTHER INFORMATION: glycosylation"
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/note= "potential site of ASN-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosylation
                                            P-2630
ALIORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION UNBER: 22,135
REFERENCE/DOCKET NUMBER: P-263
INFORMATION FOR SEQ 15 NO. 6.
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 amino acids
IZPRE: AMINO ACID
IZPRE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
506..563
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332..371
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                                                                                                                                                                          NAME/KEY: Disulfide-bond LOCATION: 45..94
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LOCATION: 188
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                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Domain
LOCATION: 604..657
CTHER INFORMATION: //
OTHER INFORMATION: //
CTHER INFORMATION: II
FEATURE:
                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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NAME/KEY: Domain
LOCATION: 905..952
OTHER INFORMATION: /
OTHER INFORMATION: /
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LOCATION: #09. 857
OTHER INFORMATION: /
OTHER INFORMATION: I
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OTHER INFORMATION: ,
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: EMAITURE:
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LOCATION: 707..760
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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LOCATION:
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Patent No. 5739289
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: Acid Sequences
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson
ADDRESSEE: and Company
STREET: One Becton Drive
OTHER INFORMATION: /label. ASN-glycos
OTHER INFORMATION: /note= "potential site of ASN-linked
OTHER INFORMATION: gl=losylation"
                                                                       NAME/KEY: Modified-si e
LOCATION: 453
OTHER INFORMATION: /labei- ASN-glycos
OTHER INFORMATION: /mote- 'potential site of ASN-linked
OTHER INFORMATION: glycosylation'
                                                                                                                                                                                                                                                                                                                    LOCATION: 501
OTHER INFORMATION: /label- ASN-qlycos
OTHER INFORMATION: /note- "potential site of ASN-linked
OTHER INFORMATION: 9lycosylation"
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: Modified-site
LOCATION: 571
OTHER INFORMATION: /label- ASN-glycos
OTHER INFORMATION: /note- potential site of ASN-linked
OTHER INFORMATION: glycosylation*
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OTHER INFORMATION: /note- "potential site of ASN-linked
OTHER INFORMATION: glycosylation"
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/note- "potential site of ASN-linked
olycosylation"
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Best Local Similarity 33:3%; Pred. No. 5:09e+01;
Matches 10; Conservative 11; Mismatches 6; Indels
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CCMPUTER REACABLE FORM.
MEDIUM IYPE: Floppy disk
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Patest No. 5731154
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Hemperly, John J.
TIILE OF INVENTION: Human Cell Adhesion Molecule and Nucleic
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/note= "potential site of ASN-linked
glycosylation"
                                                                                 /label- ASN-glycos
/note- "potential site of ASN-linked
glycosylation"
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/noter "potential site of ASN-lloxed
glycosylation"
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/sote="potential site of ASN-linked
glycosylation"
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/note- "potential site of ASN-linked
qlycosylation"
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OTHER INFORMATION: /latel- ASN-glyccs
OTHER INFORMATION: / Lote- "potectial site of ASN-linked OTHER INFORMATION: glychylation"
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/note= "potential site of ASN-linked
qlycosy.atlon"
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THESE INFORMATION: Ziote (Petrital Site
CHEEF INFORMATION: 0/2008/at/lef
N°E (016 AA: 11)834 MM: Steep75 N;
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Pred. No. 5.09e-01;
11: Mismatches 6
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NAME/KEY: Modified-site
LOCATION: 453
OTHER INFORMATION: /labe:
CTHER INFORMATION: /note-
CTHER INFORMATION: qlycos;
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NAME/KEY: Mcd::1ed site
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NAME/KEY: Modified-site
                 NAME/KEY: Modified-site
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NAME/KEY: Modified-site
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LOCATION: 474
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NAME/KEY: Modified-site
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NAME/KEY: Modified-site
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Best Local Similarity 33.3%;
Matches 10; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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CTHER INFORMATION:
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OTHER INFORMATION:
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                                                    LOCATION:
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/solve- "nonserved core at iibiomostin type
!!!-like repeat"
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/note= "conserved core of fibromectin type
!!!-inke repeat"
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/note= "conserved core of fibronectin type
III-like repeat"
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/note= "conserved core of fibronectin type
!I:-like repeat"
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/note- "potential site of ASN-linked
glycosylation"
COMPUTER: IBM PC compatible
DPERATING SYSTEM: PC-DOS/MS-DOS
SOCHWARE: Petentin Release #1.0, Version #1.25
SUBSECT AND PATENT RELEASE #1.0, Version #1.25
SUBSECT AND PATENT RELEASE #1.0, Version #1.25
SUBSECT AND PATENT POST POST POST POST PAPELICATION NUMBER: US/08/74, PAPELICATION NUMBER: US/08/3045, 74, FILING DATE: 21-MAR-1995
APPLICATION NUMBER: US/08/3045, 74, FILING DATE: 26-MAR-1995
APPLICATION NUMBER: US/08/3045, 74, FILING DATE: 26-MAR-1995
APPLICATION NUMBER: US/08/3045, 74, FILING DATE: 26-MAR-1995
APPLICATION NUMBER: US/08/3045, 74, FILING DATE: DECOME REPRESENCE CORRESPONDER: USBERIED STATION FOR SEQ ID NO: 6: SEGGENCE CHARAITERISTICS:
LENGTH 1018 Amino acids
TYPE
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CCATION: 188
CTHER INFORMATION: //abe.'
CTHER INFORMATION: //cole*
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138..191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
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LOCATICN: 767.756
CTHER INFORMATION: /
CTHER INFORMATION: /
OTHER INFORMATION: /
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LOCATION: 664, 659
CTHEN INFORMATION: VOTHER INFORMATION: VOTHER INFORMATION: COTHER INFORMATION: 1
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LOCATION: 809.857
STHER INFORMATION: 7
OTHER INFORMATION: 7
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LOCATION: 905..952
OTHER INFORMATION: /
OTHER INFORMATION: /
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/note- "conserved core of fibronectin type
III-like repeat"
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/note- "conserved core of fibronectin type
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/note- "conserved core of fibronectin type
III-like repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= FLR
/note= "conserved core of fibronectin type
III-like repeat"
TITLE OF INVENTION: Acid Sequences
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: One Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: 05
                                                                                                                                                              COMPUTER READABLE FORM:
MEDCINT TYPE: Floppy disk
COMPUTER TO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARF: Patentin Release #1.0, Version #1.25
CURRY APPLICATION DATA:
APPLICATION NOMBER: US/08/408,120A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     III-like repeat
                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
AITORNEYAGENI INFORMATION:
NAME: Fudit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-26
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISICS:
LENGTH: 1018 amino acids
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416..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disultide-band
506..563
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPCLOGY: linear
MOLEGULE TYPE: protein
ORIGINAL SOYRE:
ORGANISM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
45..94
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138...91
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NAME/FEE:
NAME/FEE:
NAME/FEE:
SOCATION: 707,760
CTHER INFORMATION: 707 THER INF
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LOCATION: 905..952
OTHER INFORMATION: /
OTHER INFORMATION: I
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LOCATION: 634..657
OTHER INFORMATION:
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LOCATION: 809..857
OTHER INFORMATION:
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LOCATION:
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LOCATION:
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/note- "potential site of ASN-linked
dlycosy.ation"
NAME/KEY: Modified-site
LOCATION: 188
OTHER INFORMATION: /label- ASN-q:ycos
OTHER INFORMATION: /cote- "potential site of ASN-linked
OTHER INFORMATION: dlycosylation"
                                                                                                                                    NAME/KEY: Modified-site
LOCATION: 238
DTHER INFORMATION: /label= ASN-qlycos
OTHER INFORMATION: /note= 'potential site of ASN-linked
OTHER INFORMATION: qlycosylation'
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OTHER INFORMATION: /note- "potential site of ASN-linked
OTHER INFORMATION: glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- ASN-glycos
/note- "potential site of ASN-linked
:lycosylation"
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OTHER INFORMATION: /note= "potential site of ASN-linked
OTHER INFORMATION: glycosylation"
NCE 1018 AA: 113333 MW: 5493875 CN:
                                                                                                                                                                                                                                                                                                                          /label- ASN-glycos
/noie- "potential site of ASN linked
glycosylation"
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NAME/KEY: Modified-size
LOCATION: 453
CTHER INFORMATION: /label- ASN-qiycos
OTHER INFORMATION: /label- ASN-qiycos
OTHER INFORMATION: /note- polentia: site of ASN-iinked
OTHER INFORMATION: qiycosylation*
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/ncfr- "potential site of ASN-linked
glycosylation"
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30.2%; Score 68; DB 1; Length 1018;
Best Local Similarity 33.3%; Pred; No. 5.09e+01;
Matches 10; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 FPDDLSYRWLLNEFPVFIIMDKREFVSQIN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rch completed: Tue Jun 20 13:34:06 2000 time: 6 secs.
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LOCATION: 501
OTHER INFORMATION: /labe
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FEATURE: NAME/KEY: Modified:Site
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NAME/KEY: Modified-site
LOCATION: 913
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NAME/KEY: Modified-site
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OTHER INFORMATION: CHER INFORMATION: CHER INFORMATION: FEATURE:
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CTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:22:15 2000; MasPar time 15.47 Seconds 201:982 Million cell updates/sec Rufi On:

Tabular output not generated.

>US.09-142-524A-4 (1-31) from US09142524A.pep 225-31 I JESKNLNJKI.NMPLYJAGNKRRFIKRVSNVI 31

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

721208 segs, 100765575 residues Searched:

Post-processing: Minimum Match C% Listing first 45 summaries

a-pending liPCT 2.06 3.060 4.07 5.01% 6.081 7.082 8.083 9.084A lo.084B ll.085 12.086 13.047 14.088 15.089 16.090 17.091 18.092 19.093 20.094 21.095 22.NEWP 23.NEWU60 24.NEWU8 25.NEWU9 Latabase:

Mean 26.139; Variance 88.013; scale 0.297 Stitistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STWMARIES

Result No.	Score	Query Match	Query Match Length DB	23	ID	Description		Pred. No.
	225	100.0	31	17	US-09-142-	Sequence 4,	Applicatio	5.326-15
7	123	54.7	345	~	US-60-109-	Sequence 1,	Applicatio	416-03
ľ	123	54.7	367	10	US-08-467-	Sequence 95,	Applicati	1.416-03
7	123	54.7	367	10	-89 * -80-SD	Sequence 95,	Applicati	1.41P-03
'n	123	54.7	367	۲-	US-08-226-	Seduence 95,	Applicati	1.41P-03
w	123	54.7	367	80	JS-08-350-	Sequence 95,	Applicati	1.416-03
7	123	54.7	367	10	US-08-467-	Sequence 95	Applicati	1.416-03
ထ	:23	54.7	367	10	US-08-467-	Sequence 95	Applicati	416-03
σ	123	54.7	370	CT	US-08-467-	Sequence 97	Applicati	1.416-03
្ន	123	54.7	370		US-08-467-	Sequence 97	Applicati	1.416-03
11	123	54.7	370	7	US-08-226-	Sequence 97	Applicati	1.416-03
12	123	54.7	370	0,1	US-08-468-	Sequence 97	Applicati	1.416-03
13	123	54.7	370	10	US-08-467-	Sequence 97	Applicati	1 416-03
14	123	54.7	376	ω	US-08-350-	Sequence 97	Applicati	1.416-03
15	118	52.4	09	۲.	US-08-226-	Sequence 62	Applicati	4 74P-03
16	118	52.4	90	7.0	US-08-468-	Sequence 62.	Applicati	4.746-03
17	118	52.4	90	10	CS-08-467-	Sequence 62.	Applicati	4 746-03
13	118	52.4	9	ω	US-08-350-	Sequence 62	Applicati	4 746-03
1.3	118	52.4	90	7.0	CS-08-467-	Sequence 62,	Applicati	4 74P-03
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ADDRESSEE: ImmuLogic Pl
STREET: 610 Lincoln St
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Best Local Similarity 75.0%:
Matches 15; Conservative
                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                linear
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SIATE: MA
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.cs-08-468-940-95
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                                                                                                                                                                                                                                      SECUENCE
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                                                                                                                                APPLICANT: BECOKS, EDWARD G.
APPLICANT: BECOKS, EDWARD G.
APPLICANT: BECOKS, EDWARD G.
APPLICANT: BECOKS, EDWARD G.
APPLICANT: WIDDHO-HORTIT: TERUMI
APPLICANT: WIDDHO-HORTIT: TERUMI
III.E CF INVENTION: PROTEIN IN MOUNTAIN CEDAR POLLEN THAT BELCNGS TO A
TITLE CF INVENTION: PROTEIN IN MOUNTAIN PATHOGENESIS RELATED PROTEINS
FILE REFERENCE: 9753:230921
CURRENT APPLICATION NUMBER: US/65/109,165
CORRENT FILING DATE: 999-13-20
SOFTWARE: PALENTE: V98-13-20
SOFTWARE: PALENTE: V98-13-20
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APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Payers, Mark A.:
APPLICANT: Powers, Staven P.
IITLE OF INVENTION: Allergenic Proteins And Peptides From
IITLE OF INVENTION: Dapanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St. CIIY: Waltham
                                                                                                                                                                                                                                                                                                                                               Cuery Match 54.7%; Score 123; DB 3; Length 346; Pest Local Similarity 75.0%; Pred. No. 1.41e-03; Matches 15; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02154
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CMPUTER: IBM PC compatible
SPERATING SYSTEM: PC-D0S/MS-D0S
SOFTWARE: Patentin Release #1.6. Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 AA
           345 AA
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                                                                                                                                                                                                                                                                                                              CRGANISM: Juniperus ashei
NJENCE 346 AA: 37639 XW: 616983 CN:
           PRT:
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GENERAL INFORMATION:
                                                                                                           Sequence 1, Application US/60109165 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 95, Application US/08467723
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APPLICANT FOR CONTROL CONTROL CONTROL CAN FROM APPLICANT GARMAN RICHARD FOR APPLICANT KNO. Methodand
                                                                                   Sequence 1, Application US/60109165
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SOFTWARE: Pater
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RESULT 2
ID US-60-109-165-1
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CORRESPONDENCE ADDRESS: 261
APPLICATION NUMBER: US/U8/467,023
FILING DATE: June 6, 1945
CLASSIFICATION: 424
PRIOR APPLICATION 0474
APPLICATION NUMBER: 0.550,225
FILING DATE: December: 0.1994
ATTORNEY/AGENT INFORMATI N: NAME: Jane E: Remillar: RESISTRATION NUMBER: 38,82
REFERENCE/COCKET NUMBER: 025.6 USD2 (JMI-0290HIZ)
TELEPHONE: (617) 227-5941
INFORMATION PARACIENTICS: SEQUENCE CHARACTERISTICS: 455
SEQUENCE CHARACTERISTICS: LENGTH: 367 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ImmuLogic Pharmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                     Tore 123. DB 10: Length 467. Ved. No. 1,41e-63. 4: Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORPUTER: IBM PC COMPATIBLE
CORRENT PATENTION DATA:
PPELICATION NUMBER: US/08/468,946
FILING DATE:
CLASSITCATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/350,225
FILING DATE: DECEMBER 6, 1994
APPLICATION NUMBER: 08/250,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SET AA
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SENCE 367 AA: 39846 MW: 95078 CN:
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F.
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Page 3

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US-08-350-225-95
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                                                                                                                                                                            SEQUENCE
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     Gaps
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Bond, Julian F.:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard D.
APPLICANT: Kin, Mel-Chang:
APPLICANT: Kin, Mel-Chang:
APPLICANT: Strauer, Andrew:
APPLICANT: Allegraenic Proteins And Peptides From IITLE OF INVENTION: Japanese Cedar Poilen
COURSES OF SEQUENCES: 201
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610 Lincoln St
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ZIP: 02154

COMPUTER READABLE FCRM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/226,248A FTLING DATE: April 8, 1994

FTLING DATE: April 8, 1994
FILING DATE: April 8, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/938,990
FILING DATE: January 15, 1993
ATTONEN'AGENT INFORMATION:
NAME: DATE: 35,729
REGISTRATION NUMBER: 35,729
REPRENCE/POCKET NUMBER: 025.6 US (IMI-029CP2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEPHONE: (617) 466-6000
TELEFAK: (617) 466-6000
TELEFAK: (617) 466-6000
SECUENCE CHARACTERISTICS:
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FILING DATE: APRIL 0, -.
CLASSISTICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/00139
TIVE DATE: January 15, 1993
                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE 367 AA: 39846 XW; 695078 CN:
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**COLECTION OF TOPOLOGY: ::-...

**COLECTION OF TOPOLOGY: ::-...

**OLECTION OF TOPOLOGY: ::-...
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ADDRESSEE: Immulogic
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CITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                                              Length 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CU: RENT APPLICATION DATA:
APPLICATION NUMBER: U /08/350,225
FILING DATE: December 6, 1994
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,990
FILING DATE: April 8, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/0593/00139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Dariene A. Vanstone
REGISTRATION NUMBER: 35,729
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0%: Fred. No. 1.41e-03:
Matches 15: Conservative 4: Mismatches 1: Indels
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SIRED: 610 Lincoln St
CITY: Watcham
STATE: MA
ATTORNEY/AGENT INFORMATION:
NAME: Darlene A. Vanscone
REGISTRATION NUMBER: 35.729
REFERENCE/DOCKET NUMBER: C25.5 US (:MI-028CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6030
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 AA
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 367 AA; 39846 MW; 695578 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application ::S/38350225 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 95, Application US/38350225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 IFSONMNIKLKMPLYVAGHK 111
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TYPE: amino acid
TOPOLOGY: lines
MOLECULE TYPE: protein
SEQUENCE 367 AA: 39846 MW: 695078 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 amino acids
                                                                                                                                                                                                                                                                 STANDARES
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CIIY: Walthar
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                                                                                                                                                                                1 IFSKNENIKENMPLYIAGNK 20
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MEDIUM TYPE: FLOREY
COMPUTER: THE PO COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
21P: 02154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                            Query Match
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APPLICANT: Bond, Etchard D.
APPLICANT: Gardan, Richard D.
APPLICANT: Gardan, Richard D.
APPLICANT: Funder: Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Powers For D.
TITLE CF INVENTION: Allergenic Proteins And # ptides From TITLE CF INVENTION: Japanese Cedur Pollen
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSHE: //mmulcotic/pharmaceutical Corporation. Inc.
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                                                                                                                                                                                                             Length 367;
                                                                                                                                                                                                          / Match 54.7%; Score 123; DB 8; Length 367 Local Similarity 75.0%; Pred. No. 1.41e-03; conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (i) Immulaction Pharmaceutical Corporation.
610 Librain St
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-C28CP2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEPHONE: (617) 466-6000
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 957 amino acids
TYPE: amino acid
TOPOLOSY: Linear
                                                                                                                                                                                                                                                                                                                                                                                     367 AA
                                                                                                                                                                                                                                                                                                                                                                                  P.R.2.;
                                                                                                                                               TOPOLOGY: Tinear
MOLECULE TYPE: protests
SEQUENCE 367 AA: 39846 MM: 695079 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 95, Application US/38467006
GENNERL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Pollock, Joanne:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 95, Application US/08467005
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Pollock, Joanne:
Bond, Julian F.;
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                                                                                                                                                                                                                                                                                 92 IFSONMNIKLKMPLYVAGHK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
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Match S4.7%: Score 123; DB 10: Length 367. Local Similarity 75.0%: Pred. No. 1.416-04: nes 15; Conservative 4; Mismatches 1: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/OCKET NUMBER 055.6 USD4 (IMI-028CFD4)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 227-74.0
TELEFAX: (617) 227-5941
SEDENATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ImmuLogic Pharmuce.Lical Corporation.
                                                                                                                                                                                           367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERRIT AFPLICATION ON A DATA APPLICATION NUMBER - US/UH/167.697 FILLING DATE - 1945 CLASSIFICATION - 4.24 PRIOR APPLICATION DATA - REPLICATION DATA - REPLICATION DATA - REPLICATION DATA - REPLICATION DATA - PAPEL DECEMBER 6. 1994 ATTORNEY/AGENT - NFORWATION -
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367 AA: 39846 MW: 695078 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDICAL TYPE: Flopey disk
COMPOSED THE PS COMEDITION
PERALING SYSTEM: 1° 0.87881
SOFTWARE: Patens in Privise 1°
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APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Met. Chang;
APPLICANT: Kuo, Met. Chang;
APPLICANT: Frung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Ext.gv, Mark A.;
APPLICANT: Ext.gv, Mark A.;
APPLICANT: Powers, Steven P.
IIILE OF INVENTION: Japanese Cedar Polien
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ANDRESSEE: Immulogic Pharmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Gaps
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MEDIUM IYPE: Rloppy disk
COMPUTER: ISBM FC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
OPERATING DATE: DC CASSION #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PKIOR APPLICATION DATE:
APPLICATION NUMBER: 06/350,225
FILING DATE: December 6, 1994
AITORNEY/AGENT INFORMATION:
NAME: Jane E, Remillard
REGISTRATION NUMBER: C25.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SOIL 1000:
TELECOMMUNICATION FOR SOIL 1000: 97:
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Pred. No. 1.41e-03:
4: Mismatches 1: Indels
 Indels
:
                                                                                                370 AA
Mismatches
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 370 AA; 40191 MW; 725506 CN;
                                                                                                                                                                                                 Sequence 97, Application US/08467023
                                                                                                                                                                        Sequence 97, Application US/08467023
                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.,
APPLICANT: Policok, Joanne,
APPLICANT: Bond, Cilian F.,
APPLICANT: Garman, Richard D;
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LENGIH: 370 amino acids
TYPE: amino acid
                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 IFSONMNIKLKMPLYVAGHK 111
                        92 IFSONMNIKEKMPLYVAGHK 111
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                                       1 IFSKNENIKENMPLYIAGNK 20
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Best Local Similarity 75.0%;
Matches 15; Conservative
 Conservative
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                                                                                 RESULT 9
1D US-08-467-023-97
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  Matches
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APPLICANT
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Bond, Jul.: F.;
APPLICANT
Bond, Jul.: F.;
APPLICANT
Garman, Richard D;
APPLICANT
Garman, Richard D;
APPLICANT
Yeung, Stu-mei H.;
APPLICANT
Ex.ley, Mark A:
APPLICANT
Ex.ley, Mark A:
APPLICANT
TILLE OF INVENTION: Allegenic Proteins Acd Peptides From TILLE OF INVENTION: Allegenic Proteins Acd Peptides From TILLE OF INVENTION: Allegenic Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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COMPUTER: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: ImmuLogic Pharmaceutical Corporation, 1::C. STREET: 610 Lincoln St. CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 370;
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370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
PRT;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FORCE 370 AA: 4019: MW: 725506 CN;
                                                                                                                                                                                                                                                                                                                Sequence 97, Application US/08467697 GENERAL INFORMATION:
                                                                                                                                                                                                                                        Sequence 97, Application US/08457697
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    STANDARD:
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MEDIUM TYPE: Floppy
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ID US-08-226-248A-97
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US-08-467-697-97
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Query Match
Best Local Similarity 75.0%:
Matches 15: Conservative
Policck,
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US-08-467-006-97
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                                                                                                                                                                                                           COUNTRY:
            APPLICANT:
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SECUENCE 37
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                                   GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Gollock, Joanne.
APPLICANT: Boolock, Joanne.
APPLICANT: Garman, Richard D.
APPLICANT: Garman, Richard D.
APPLICANT: Yeung, Sim-mel H.;
APPLICANT: Yeung, Sim-mel H.;
APPLICANT: Exley, Mark A.;
APPLICANT: Stovens, Steven P.
III.E OF INVENTION: Japanese Cedar Polie:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amatch 54.7%; Score 123; DB 7; Longth 370; Local Similarity 75.0%; Pred. No. 1.41e-05; onservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPUTED: DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PALENTION NUMBER: US/08/25.248A FILING DATE: Bpril 8. 1994
CLASSIFICATION 1424
PRIOR PAPLICATION 1424
PRIOR PAPLICATION 0424
PRIOR DATE: September 1. 1992
APPLICATION NUMBER: PC-7/059/26/39
FILING DATE: September 1. 1993
ATTONEY/AGENT INFORMATION:
NAME: Darlene A. VANSTONE
REGISTRATION NUMBER: 35.729
REFERENCE/COCKET NUMBER: 35.729
REFERENCE/COCKET NUMBER: 025.5 US (IMI-028CP)
TELEPHONE: (617) 466-6000
TELEPHONE: (617) 466-6000
TELEPHONE: (617) 466-6000
INFORMATION FOR SEOUTH ON: 97: SEOUTH 370 MILES SOFTE
                                                                                                                                                                                                                   ADDRESSEE: ImmuLogic Pharmaceutical Corporation, STREET: 610 Lincoln St. CITY: Waltham STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 AA.
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MCLECULE TYPE: protein
SEQUENCE 370 AA; 40191 MW: 725506 CN:
                        Sequence 97, Application US/38226248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/08468940 GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
 Sequence 97, Application US/08226248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97. Application US/08468940
                                                                                                                                                                                                                                                                                                                Eloppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
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                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      ZIP: 02154
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                           USA
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US-08-468-940-97
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                                                                                                                                                                                                                                                                           CCUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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8170
                                     APPLICANT: Kuo, Mei-Chang:
APPLICANT: Yeung, Slu-m. H.:
APPLICANT: Yeung, Slu-m. H.:
APPLICANT: Brauer, Andrew.
APPLICANT: Erley, Mark A.:
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Pertides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 370;
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                                                                                                                                                                               ANDRESSEE: Immulogic Pharmaceutical Corporation. STREET: 610 Lincoln St. CITY: Waitham STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729
025-5 US (IMI-028CP2)
'N:
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTIBLE OPERATING SYSTEM: PC-002KMS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 GORENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 AA
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75.0%; Pred; No: 1.41e-03;
vative 4: Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 98/350,225
FILING DATE: December 6, 1994
FILING DATE: MOTH 9: 1994
APPLICATION NUMBER: 08/226,248
FILING DATE: SEPTEMBER: 07/98,999
FILING DATE: SEPTEMBER: 07/98,999
FILING DATE: JANUARY 1: 1993
APPLICATION NUMBER: 07/98,390
FILING DATE: JANUARY 1: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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370 AA: 40191 WW 725504 PR:
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SENERAL INFORMATION:
APPLICANI: Griffeth, Irwin J.;
APPLICANI: Pollock, Joanne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97, Application US/08457006
Bond, Julian F.;
Garman, Richard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 466 0
TELEFAX: (617) 466-6.40
INFORMATION FOR SEQ ID NO (

    376 amino acids
amino acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Darlene A. Vans:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 IFSONMNIKIKMPLYVAGHK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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APPLICANT: Brauer, Andrew:
APPLICANT: Exiey, Mark A.:
APPLICANT: POWERS, Steven
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 201
      TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen NUMBER OF SEQUENCES: 26.
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: ImmuLogic narmaceutical Corporation: Inc. STREET: 610 Lincoln S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 54.7%; Score 123; DB 8; Length 370; Best Local Similarity 75.0%; Fred, No. 1.41e-03; Matches 15; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-005/MS-DOS

SOSTWARE: Pacentin Release #1.0, Version #1.25

SOSTWARE: Pacentin Release #1.0, Version #1.25

CURRITION NUMBER: US/08/350.225

FILING DATE: December 6, 1934

PRICR APPLICATION DATA:

APPLICATION NUMBER: (7/256.248

FILING DATE: April 6, 1994

APPLICATION NUMBER: (7/38.990

FILING DATE: September 7, 1992

APPLICATION NUMBER: (7/38.990

FILING DATE: September 7, 1993

ATIORNEY/AGENT INFORMATI: ...

NAME: DATIENE A. PATIST ...
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SEQUENCE 370 AA: 40191 MW: 725596 CN:
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SENERAL INDOMMATION:
APPLICANT: Griffeth, Jrwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-chang:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 62, Application US/08225248A
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APPLICANT: Brauer, Andrew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARP
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LENGTH: 370 amino acids
IYPE: amino acid
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CITY: Waltham
                                                                                                                                                                                                                                                        USA
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US-06-226-248A-62
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APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard D.
APPLICANT: Kuo, Mel-Chang:
APPLICANT: Young, Sturmer H.:
APPLICANT: Brauer, Andrew:
APPLICANT: Exley, Mark A.:
APPLICANT: Correction and Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patent: PC COMPATIBL
COMPUTER: Patent: PC COMPATIBL
COMPUTER: Patent: PC COMPATIBL
SOFTWARE: Patent: PREPARE - 0.05
COMPUTER: Patent: PC COMPATIBL
CAPPLICATION DATA:
APPLICATION UNBER: 08/955,225
FILING DATE: December 6, 1994
FRIUNG DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Cane E. Remiliard
REGISTRATION NUMBER: 38.872
REFERENCE/DOCKT NUMBER: 38.872
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORM
                                                                                                                                                                                                                                                               CLUMESSEE: Immulogic Pharmaceutical Corporation, Inc. SIRET: 610 Lincoln St CITY: Waltham STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.2%: Prod. No. 1.41e-05:
Matches 15: Conservative 4: Mismatches 1: Indels
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MOLECULE TYPE: protein
JENCE 370 AA: 40191 MW: 725506 CN:
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
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Yeung, Siu-mei H.:
Brauer, Andrew;
Exley, Mark A.;
Powers, Steven P.
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MEDIUM TYPE: Floppy
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APPLICANT:
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APPLICANT:
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OF RESPONDENCE ADDRESS:

ADDRESSEE: Immittodic Pharmaceitical Corporation, Inc.
STREE: 610 Lincoln St.
STREE: 410 Lincoln St.
STATE: MA
STATE: MA
STATE: MA
STATE: MA
STATE: WA
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Sourch completed: Man Jan 19 16,22:45 20:00 Job time : 30 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:00:33 2000: MasPar time 6.43 Seconds 227.254 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-4 (1-31) from US09142524A.pep 225 I IFSKNLNIKLNMPLYIAGNKRFIKRVSNVI 31

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pirl 2:pir2 3:pir3 4:pir4

Database:

Mean 33.568; Variance 51.790: scale 0.545 Statistics:

Pred. No. is the number of results predicted by lance to have a score greater than or equal to the score of the lessit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Resu:t No.	91008	:	en : . h	::0 (1)	0	Description	SN Derry
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7	118	52.4	`	N	JC2123	major allergen cry j	
m	sy sp	ζ.	741	~	T16992	ethylene receptor hom	1.97e-01
-7	63	36.9	868	N	S52826	hypothetical protein	•
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ψ	81	Ġ	397	2	\sim	pectate lyase (EC 4.2	5.49e-01
7		36.0	460	-	E70132		5.49e-01
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o	81	vo.	3141	. 1	GNVSPD	qenome polyprotein -	5.49e-01
0.1		-3	143	~	545433	hypothetical protein	
7.7		4	480	7	B70367	hypothetical protein	
12			532	7	T16752	hypothetical protein	2.88e+00
13	7.6		569	N	E64427	hypothetical protein	2.88e+00
14	26		3140	~	S47508	н	2.88e+00
15	7.5	33.3	273	~	H64420	hypothetical protein	3.98e+00
16	75		347	7	S59837	probable membrane pro	3.98e+00
17	7.4		06	7	JQ1098	auxin-induced protein	5.49e-00
18	7.4		92	~	T10942	σ	5.49e+00
61	4.		189	~	E64371	hypothetical protein	5.49e+00
50			3	~	S76765		5.49e+00
27	74		393	7	F75130		5.49e+00
22			4	7	A35639	G protein-coupled rec	7.55e+00
23	7.3	32.4	3125	• •	SAVSPP	genome bolyprotein -	7.550+00

		AL GNMENTS					
2.630-01	ribosomal protein S6	A41687	7	525	30.7	, (A)	.t. πυ
275	pothetical prote	F7:274	7	1533	31.1	10	44
1	Enid - Si	PC0221	N	2	31.1	70	43
7.976.7	۵. ⊶		~	75	31.1	ر. د	42
10.075	Pg		~	346	31.1	70	4
<i>3</i> 1	conserved hypothetica	S	~	618	31.1	7.0	0
У.	ethylene response sen	007	~	613	31.1	70	36
	probable ethylene rec	1443	7	613	31.1	7.0	38
:. y2e-01	hypothetical protein	_	N	472	31.1	7.0	37
10-915	riborucleoside-diphos	WWBEV3		515	31.6	7.1	36
1.416.01	endopeptidase Cip ATP	C71533		854	31.6	7.1	35
• 7	endopeptidase Cir ATP	G72079	-	845	31.6	7.1	34
1,416.01	repressor modE homolo	B64175	C)	255	31.6	7.1	33
1.400-01	hypothetical protein	A75104	~	177	31.6	7.1	32
1.4.0-01	ribosomal protein S17	R5BY51	. •	136	31.6	7.1	3.
1.4.000	Ú	S20967	7	63	31.5	7.1	30
1.056+01	probable zinc finger	T09027	~	327	32.0	7.2	29
10.080.01	virB protein - Shael	S04379	~	303	32.0	7.2	28
9	IpaR - Shiqella dysen	A43859	7	306	35.0	72	27
1.096+01	ď	869201	~	308	32.C	7.2	56
10.460.1	ribosomal protein L17	850809	~	238	32.0	7.2	25
10.64-01	hypothetical protein	T01657	~	113	32.0	7 /	54

JC2124 *type complete major allergen Cry j I precursor (clone pCC1-15) · Japanese	_nam 1994	JC2124 JC2124 JC212 F. Komitama N. Shimizh K. Kusakake, T. Morikubo	Commun. (1994) 199:619-625	Cloning and sequencing of CDNA coding for Cry j 1, a major allergen of lapenese cedar polien.	Accession JC2124	1-374 ##label SON	across recreates delibebbbb Nilidae dono Diblo Jobob. Fillidae dono experimental_source polici ### ### Fillidae dono polici ### ################################	#Suppr	*domain signal sequence *status predicted *label SIGN *product major allergen Cry j I (clone pCCI-i5) *Status predicted *label MATN	*b length	Query Match Best Local Similarity 60.0%; Pred, No. 5.55e-07; Matches 18; Conservative 4: Mismatches 7; Indels 1: Gaps 1;	IFSGNMNIKLKMPMYIAGYKT-FDGRGAQV 120 .: ,: : : SKNLNIKLNMPLYIAGNKRRFIKRVSNV 30	JC2123 *type complete major allergen Cry j I precursor (clone pCCI-2-2) - Japanese ceda. *formal_name Cryptomeria Japonica *common_name Japanese cedar i4-Jul-1994 *sequence_revision 14-Jul-1994 *text_change
RESULT 1 ENTRY TITLE	ORGANISM DATE	ACCESSIONS REFERENCE	#journal	*title	*CICSS-rele *accession	**residues	SSOCION NO POLICE NO POLIC	CLASSIFICATION KEYWORDS FEATIOF	1-21	158,191,293,354 SUMMARY #	Query Match Best Local Matches	Db 92 IFS(Qy 1 IFS	RESULT 2 ENTRY TITLE ORGANISM DATE

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*domain signal sequence *status predicted *label SIGN *product major allergen Cry j : (clone pCCI-2-2) *status predicted *label MATN *pinding_site carbohydrate (Asn) (covalent) *status predicted
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Plant Physial. (1998) 117:125-1
Isolation and characterization of a broccoll cona (Accession
No. AF647477) encoding an ERS-Type HIBGlene receptor
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                                                                                                                                                                                                                                                                                                                                      22-53;58-61:219-232:236-258:299-307:346-372 **Label S02 the authors described carbohydrate binding site for residue 279
                                                      Sone, T.: Komiyama, N.: Shimizu. K.: K.sakabe, T.: Morikubo.
K.: King, K.
                                                                                                                                                                                       **residues :-374 **label SON
**renses-references GB-025544: NID:q493631: PID:d1006086; PID:q493632
**experimental_source pollen
reess.on P02565
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*formal_name Malus domestica *common_name apple tree
20:Sep-1999 *sequence_revision 20-Sep-1999 *text_change
                                                                                                 #journal Bicchem Blophys. Res. Commun. (1994) 199:619-625
#fitle Cloning and sequencing of cDNA coding for Cry j I. a altergen of Japanese cedar pollen.
#Cross.references MUID:94183234
#accession J02:23
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JC2123: PC2065
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**molecule_type mRNA
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S52826 #type complete hypothetical protein YMR066w - yeast (Saccharomyces

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S53852 #type_complete
ribosomal_protein_L5 - Acanthamoeba_castellanii_miteriion
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                                                                                                                                                                                                                                                                                                                                                                      ##residues :-898 ##Jabel PEA ##Cross-r ferences EMBL:248952; N.D.q763008; PID:q765013; N.DS:YMP.-Aw ##experimental_source strain AB972
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         hypothetical protein YM9916.05
#formal_name Saccharomyces cerevisiae
19-May-1995 #sequence_revision 01-Sep-1995 #text_chanae
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15-Jul-1995 *sequence_revision []:Sep-1995 *text_channe
26-Eeb-1999
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J. Mol. Biol. . -5) 245:522-537
                                                                                                                                                                                                                                                                                           *length 898 | molecular-weight 104747 | #checksum
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Pred. No. 2.786-01:
11: Mismatches 5: Indels
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submitted to the EMBL Gata Library, April:
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ss MUID:95147275
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Matches 16; Conservative
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#genetic_code 5GC6
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cerevisiae)
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             ALTERNATE_NAMES
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Clayton, R.: Lathigra, R.: White, D.: Ketchum, K.A.:
Dodson, R.: Hirkey, E.K.: Garnen, W.: Bougherty, B.: Tomb,
J.E.: Fletschwaren, R.D.: Richardson, D.: Peterson, J.:
Kerlayage, A.R.: Quackenbush, J.: Salzberg, S.: Hanson, M.:
Vuqt, R.V.: Palmer, N.: Adams, M.: Occapie, S.: Hanson, M.:
J.: Utterback, T.: Watthey, L.: McDonald, L.: Artiach, P.:
R.: Roberts, K.: Hatch, B.: Smith, H.O.: Venter, J.C.
Nature (1997) 390-586.
Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                  ##CICSS-references EMBL:X67158; NID:q19907; PIDN:CAA47630.1; PID:q19908
reession $26212
                                                                                                                                                                       ##cross-references GB:AE001137; GB:AE000783; NID:92588160; PID:92688209;
TIGR:BB0261
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Apportetion: protein BB0261 - Lyme disease spirochete
#formal name Horrella burgdorferi #common_name Lyme disease
Spirochete
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
E70112
translation of the nucleotide sequence is not complete
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translation not shown
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Post Local Similarity 50.0%; Pred. No. 5.49e-01;
Matches 10: Conservative 7: Mismatches 3: Indels
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GNVSRA *type complete
genome polyprotein - plum pox virus (strain Rankovic)
29K protein: Afk protein: coat protein: cylindrical inclusion
protein; help-r component protein; nuclear inclusion
protein a: nuclear inclusion protein b
#formal_name plum pox virus, PPV
host Nicotiana clevelandii (tobacco)
30-Jun-1993 #sequence_revision 30-Sep-1993 *text_change
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*product cylindrical inclusion protein *status predicted
*label CIPV
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**residues 2253-2874, \(\delta\) 2876-3146 **label LA1
**rresidues 2253-2874, \(\delta\) 1876-333361: PIDN:AAA85458.1: PID:\(\delta\) 333302
ression 842761
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*product 'uclear inclusion protein a *status predicted *label NIA\
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*domain tetratricopeptide repeat homology *labe; 713\
*domain tetratricopeptide repeat homology *labe; 714\
*domain tetratricopeptide repeat homology *status
atypical *labe! 75\
*domain tetratricopeptide repeat homology *labe; 775\
*domain tetratricopeptide repeat homology *labe; 775\
*th 460 *mc. 112ar-weight 54024 *checksum 9100
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#journal Virus Res. (1889) 13:157-172
#title The complete mucleotide sequence of plum pox potyvirus RNA
#cross:references MJID:89370814
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*binding_site phosphoryl-RNA (Tyr) (covalent) *status
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#product helper component protein *status predicted
#label HCPN
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*region nucleotide-binding motif B\
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Nucleotide seque of the 3' terminal region of pi-
potyvirus RNA.
A42761
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Fred. No. 5.49e-01:
10: Mismatches 10: Indels
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A60009; A42761; B42761; JA0138
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Best Local Similarity 33.3%;
Matches 10; Conservative
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**residues
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*product helper component protein *status predicted
*label HCP\
*product 29K protein *status predicted *label PRT\
*product 29K protein *status predicted
*label CIP\
*fabel CIP\
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*region nucleotide-binding motif A (P-loop)\
*region nucleotide-binding motif B\
*region nucleotide-binding motif B\
                                                                                                                                                                                                          GNVSPD *type complete
genome polypricein. plum pox virus (strain D)
genome polypricein. plum pox virus (strain D)
29K protein. 34K protein. coat protein: cylindrical inclusion
protein. helper component protein: nuclear inclusion
protein a. nuclear inclusion protein b
formal_name plum pox virus, PPV
30-Sep-1991 *sequence_revision 30-Sep-1991 *text_change
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#product nuclear inclusion protein a *status predicted
#label NIA/
#product nuclear inclusion protein b *status predicted
#product nuclear inclusion protein b *status predicted
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predicted
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*formal_name Saccharomyces cerevisiae
69-Jun-1994 *sequence_revision 09-Sep-1994 *text_change
                                          Gaps
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Dunez, J.
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hypothetical protein YBL077* - yeast (Saccharomyces
cerevisiae)
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pred. No. 5.49e-01;
Transches 5: Indels
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The complete nucleotide sequence of plum
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36.0%: Score 81: DB 1: Le
Hest Local Similarity 46.7%: Pred. No. 5.49e-01:
Matches 14: Conservative 8: Mismatches 5.
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S45433; S45813; S45819; S59230
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                                                                                2410 IFS-ALNWKAAVGALY-SGKKRDYFKNVSD 2437
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*cross-references MUID:90098790
*accession S06929
                 Rest Local Similarity 46.7%:
Matches 14; Conservative
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#title
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RETERENCE
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TITLE
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DATE
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NIO:4536121: PID:4536122: MIPS.YBU:774
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Obermaler, B.: Ga. Inhuber, J.: Piravandi, E.: Domdey. H. submitted to the 'L Data Library, May 1994
Sequence analysis: a 78,6 kb segment of the left endig.
Saccaromyces celevisiae chromosome II.
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Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, J.; Swanson, R.V.
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hypothetical protein aq-755 - Aquifex aeoli us
*formal_name Aquifex aeolicus
08-May-1998 *sequence_revision 08-May-1998 *text_change
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Nature (1998) 392-353-358
The complete geno: of the hyperthermophilic bacterium
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Audist 199
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**Coss references EMBL.X79489; NID:q496561; PID:q496706

**experimental_source strain S288C
SKS8C2
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SUMMARY *length 143 *mole ular-weight 16327 *checksum
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*title Sequence analysis of a 78.6 kb segment of the laaccharomyces cerevisiae chromosome 11.
*cross:references WUID:96076635
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d. No. 1.50e+00:
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**residues
**cross-references EMBL:235%
**experimental_source strair
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*cross-references MUID:98196566
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Best Local Similarity 33.3%;
Matches 7: Conservative
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Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
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##cross-references GB:AE000706; NID:q2983327; PID:q2983337; GB:AE000657
##experimental_scurce strain VF5
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                                                                                                                                                                                                                                                                                                                                                        hypothetical protein R144.5 - Caenorhabditis elegans *formal_came Caenorhabditis elegans 20.8ep.1999 *text_change 20.8ep.1999 *sequence_revision 20.8ep.1999 *text_change 20.8ep.1999
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                                                                                                                                                                              Gaps
                                                                        aq_765
#length 486 #molecular-weight 55991 #checksum 8726
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56/1: 1:0/1: 215/1: 264/1: 301/3: 419/3: 426/2:
#length 532 #molecular-weight 59809 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, March 1995. The sequence of C. elegans cosmid Ri44. 156752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues :-532 ##label FAV
##cross-references EMBL:023515; NID:9746492; PID:9746497;
PIDN:AAC46549 1; CESP:R144.5
##experimental_source strain Bristol N2
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                                                                                                                             Ouery Match 34.2%: Score 77; DB 2; Length 489; Best Local Similarity 32.1%: Pred. No. 2.06e+C0; Matches 9; Conservative 10; Mismatches 9; Indels
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*product protein it *status predicted *late! PIPA *product protein PF *status predicted *late! BFPA *product protein PF *status predicted *late! BFPA *product protein PF *status predicted *late! BFLA *product protein CI *status predicted *late! BFLA *quadomain DEMAPH box helicase homology *labe! BENDA *region nucleotide binding motif A (P-loop)A *region nucleotide binding predicted *labe! BENDA *product protein NIA *status predicted *labe! UPA *product protein NIA *status predicted *labe! UPA *Product Cod protein *status predicted *labe! UPA *Binding_ste phosphory! FNA (Tyr) (covalent) *status predicted
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genome polyprotein - plum pox virus (isolate PVV-SI)
coat protein protein 6K1; protein 6K2; protein vir pruteir
HCpro: protein Mia: protein MB; protein Pi; protein 19;
VPg protein
*Tornal_campe plum pox virus, PPV
isolate PVV-SC
20-Feb-1995 *sequence_revision 20-Feb-1995 *text_change
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**residues 1-569 **label BUL
**cross-references GB:U67545; GB:L77117; NID:q1591680; PID:q1499864;
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phosphoprotein: polyprotein
                                                                                                                       #map_position REV953676-951967
SJMMARY *Length 569 *molecular-weight 5558; #checksur
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Best Local Similarity 43.3%; Pred. No. 2.88e+00;
Matches 13; Conservative 9; Mismatches 5; Indels
                                                                                                                                                                                                           y Match 33.8%; Slore 76; DB 2; Length 569;
Local Similarity 40.7%; Pred. No. 2.886+60;
hes 11; Conservative 8; Mismatches 6; Indels
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Bolt, C.J.: White, O.: Olsen. G.J.: Zhou, L.: Fleischmann, #authors Bolt, C.J.: White, O.: Olsen. G.J.: Zhou, L.: Fleischmann, R.D.: Sutton. G.G.: Blake, J.A.: FlitzGerald, L.M.: Clayton. R.A.: Godgyne, J.D.: Kerkavage, A.R.: Dougherty, B.A.: Torb, J.F.: Adams, M.D.: Reich, C.L.: Overbeek, R.: Kirkness, E.F.: Weinstock, K.G.: Merrick, J.M.: Glodek, A.; Scott, J.J.: Geghagen, N.S.M.: Weilmen, J.E.: Fibrmann, J.C.: Cotton, M.D.: Roberts, K.M.: Hurst, M.A.: Kanna, M.C.: Cotton, M.D.: Roberts, K.M.: Hurst, M.A.: Kanne, B.P.: Borodovsky, M.: Klenk, H.D.: Roperts, C.M.: Gibberts, C.M.: Sonne (1996) 273:1058-1073
#title Complete genome sequence of the methanogenic archaeon, #cross-references MJD:96337999
#accession #64420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain ATPase nucleotide-binding domain homology #label
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##coss-references GB:U67540: GB:L77117: NID:q1591631: PIDN:AA558973.1:
##cross-references GB:U67540: GB:L77117: NID:q1591631: PIDN:AA558973.1:
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hypothetical protein MJ0968 - Methanococcus jannaschil
*formal_name Methanococcus ja: aschil
12-Sep-1996 *sequence_revisio: 13-Sep-1996 *text_change
29-Sep-1999
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CLASSIFICATION *superfamily hypothetical protein MJ0968; ATPase
cuclectide-binding domain homology
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Search completed: Mon Jun 19 16:00:43 2000 Job time : 10 secs.

4 KNUNIKLNMPLYIAGNKRR-FIKRVSNV 30

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 3.43 Seconds 274.849 Million cell updates/sec Mon Jun 19 15:59:18 2000; Run on:

Tabular output not generated.

(1-31) from 0599142524A.pep 225 1 JESKNINIKLNMPLYIAGNKRRFIKRVSNVI 31 >US-09-142-524A-4 Description: Perfect Score: :eduentes:

PAM 150 Gap 11 Scoring table:

83857 seqs, 36454973 residues Sourched.

Minimum Match 0% Listing first 45 summaries Fort-processing:

swiss-pro138 Database:

Mean 34.404; Variance 55.946; scale 0.615 Statistics:

::swissprot

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Prod. No.	2.9Ce-08	6.32e-02	1.34e-01	1.34e-01	1.34e-01	1.34e-01	4.06e-01	8.38e-01	8.38e-01	1.20e+0C	1.71e+00	1.7:e+00	1.71e+CC	2.42e+00	2.42e+00	3.43e+00	3.436+00	3.43e-00	4.83e-00	4.83e+00	4.83e+00	4.83e+00	6.78e+00	
Description	SUGI BASIC PROTEIN PRE	HYPOTHETICAL 154.7 KD	α,	PECTATE LYASE PRECURSO	GENOME POLYPROTEIN [CO	GENOME POLYPROTEIN (CO	VERY HYPOTHETICAL 16.3	HYPOTHETICAL 59.8 KD P	HYPOTHETICAL PROTEÍN M	DNA DAMAGE TOLERANCE P	AUXIN-INDUCED PROTEIN	INDOLE-3-ACETIC ACID :	HYPOTHETICAL PROTEIN M	PROBABLE G PROTEIN-COU	GENOME POLYPROTEIN (CO	MITOCHONDRIAL 60S RIBC	VIRULENCE REGULON TRAN	GENOME POLYPROTEIN (CO	40S RIBOSCMAL PROTEIN	HYPOTHETICAL PROTEIN K	MOLYBDENUM TRANSPORT P	RIBCNUCLEOSIDE-DIPHOSP	HYPOTHETICAL 38.7 KD P	
2	SBP_CRYJA	YMV6_YEAST	RM05_ACACA	PEL_TOBAC	POLG_PPVRA	POLG_PPVD	YBH7_YEAS:	YRRS_CAEEL	YA22_METJA	RH31_YEAST	AX6B_SOYBN	ARG7_PHAAU	Y573_METJA	RTA_RAT	POLG_PPVNA	RM08_YEAST	VIRB_SHIFL	POLG_PPVSK	R17A_YEAST	YC63_HUMAN	MODE_HAEIN	RIRI_HCMVA	YOL3_NPVAC	
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ALIGNMENTS

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"N-terminal amino acid sequence of a major altergen of Japanese cedar pollen (Cry j I)."; FEBS Lett. 239:329-332(1988).
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Sone T., Morikubo K.,
Kino K.;
Kino K.;
Cloning and Sequencing of CDNA coding for Cry ) I, a major alleran.
LT 1
SPECRYA
BP18632:
01-NCV-1990 (Rel. 16, Created)
01-NCV-1995 (Rel. 32, Last sequence update)
01-NCV-1998 (Rel. 37, Last aniotation update)
SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY 3 I) (CRY 3 I)
CTYPTOMETA 3 aponto (Japanese redet)
CTYPTOMETA 3 promise Conference (Steptoplyta: Embryophyta: Tracheophyta: Embryophyta: Cryptometals)
euphyllophytes: Spermatophyta: Conference Cryptometala.
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Taniai M., Ando S., Usui M., Kurimoto M., Sakaguchi M., Inouye S.,
Matuhasi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toridou K., Fukuda S., Kurimuto M.
to the EMBL/GenBank/PDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Japanese cedar pollen.",
Biochem. Biophys. Res. Commun. 199 619-625(1994).
                                                                                                                                                                                                                                                                                                                                                                                                AT. SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PAR
IISSUE-POLLEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTENCE FROM N.A.
TISSUE-POLLEN,
Namba M., Kurose M., To
Submitted (CUL-1994) to
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TISSUE=POLLEN;
      $\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac{\pi}{\pi}$$\frac
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                                                                 This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on this use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial.
                                                                                                                                                                               mudalled and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensellsb-sib.ch).
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Pearson D., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (APR-1995) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fundi: Ascomycota: Saccharomynetes: Saccharomycetales
Saccharomycethaeae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 1047 KD PROTEIN IN NCAL-HMS1 INTERGENIC REGION,
YMROGEW OR YM9916.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118: DB i: Length, J. Sc
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larity 37.0%: Pred. No. 5.32e-02:
Conservative II: Mismatches 5: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
74AB25950248F56F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUST BASIC PROTEIN.

L > F (IN CRY J 1-9).

H > Y (IN CRY J 1-9).

S > I (IN CRY J 1-9).

L > S (IN CRY J 1-9).

O > H (IN CRY J 1-9).

K > O (IN CRY J 1-9).

POTENTIAL.
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SIGNAL
22 374 SUGI BASIC PROTEIN.
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AMB A :/AMB A II/CRY J I SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: D26544: BAAG5542.1: ..
EMBL: D26545: BAAG5643.1: -.
EMBL: D34659: BAAG7020.1: -.
PIR: A44773. A44773.
PFAM: PFC0544: PEC_1yase: ..
PRINTS: PRO0807: AMBALLERGEN.
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50.08:
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Matches 18; Conservative
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898 AA: 1
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Sest Local Similarity
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361
158
191
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374 AA:
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Q04748;
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CARBOHYD
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VARIANI
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-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-MANN-4-ENURCNOSYL GROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
PECTATE LYASE PRECURSOR (EG 4.2.2.2).
Nicotiana tabacum (Common tobacco).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyjedons: core eudicots; Asteridae: euasterids I: Solanales; Solanaceae;
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*Isolation and characterization of a tobacco gene with homology pectate lyase which is specifically expressed during microsporogenesis.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burger G., Plante I., Lonergan K.M., Gray M.W.:
"The mitochondrial DNA of the ambebold protozoon. Acanthambetia castellanii: complete sequence, sene content and genore organization."
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Pred. No. 1.34e-01;
6: Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 AA; 21764 MW; BEA193CDBC375274 CRC64;
                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 39, Last annotation update)
MITCCHONDRIAL 60S RIBOSOMAL PROTEIN 15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   anthamoeba
7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Acanthamoebidae:
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Local Similarity 59.0%;
ies 13; Conservative
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STRAIN-ATCC 30010 / NEFF:
MEDLINE: 95147275.
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P40972:
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RM05_ACACA
P46764;
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'Nucleotide sequence of the
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2811
1919
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SEQUENCE
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 31, Last annotation update)
05-DEZ-1998 (Rel. 37, Last annotation update)
05-DEZ-1998 (Rel. 37, Last annotation update)
05-DEZ-1998 (Rel. 37, Last annotation parties (Pl): HELPER
05-DEZ-1998 (Rel. 37, Last annotation (Release)
1 (6KL), CYTPLASM.C INCLUSION PROTEIN (PR.);
05-DEZ-10 (PROTEIN (VPG), NUCLEAR INCLUSION PROTEIN (NICA) (NICA)
05-DEZ-10 (Rel. 37, Last annotation (Rel. 37, Last)
05-DEZ-10 (Rel. 37, Last annotation (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 1778-2342 FROM N.A.
MEDLINE: 89268456.
Garcia J.A., Riechmann J.L., Lain S.;
Froteolytic activity of the plum pox potyvirus NIa-like protein in Fraherichia coli ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE: 89370814.
Lain S., Riechmann J.L., García J.A.:
"The complete nucleotide sequence of plum pox potyvitus RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ö
                                   DEVELOPMENT. SELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
     A: THEIR NON-REDUCING ENDS.
-:- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED LATE IN POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 397
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POTENTIAL.
POTENTIAL.
POTENTIAL.
S-VC (IN MRNA).
S-VC (IN MRNA).
S-VC (IN MRNA).
H-VR (IN MRNA).
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H-VR (IN MRNA).
H-VR (IN MRNA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.0%; Score 81: DH 1; Le 50.0%; Pred. No. 1. te-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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   THEIR NON-REDUCING ENDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 IFGKNMKIKLSRELIVISNK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44351 MW;
                                                                                                                                                                                                                                                                                     PF00544; pec_lyase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IFSKNINIKINMPLYIAGNK 20
                                                                                                                                                                                                                  EMBL: X67159; CAA47630.1; -. EMBL: X67159; CAA47631.1; -. EMBL: X67100; CAA43414.1; -. PPR: X6221; S2621; PFAM: PFOGS44; PEC_lyase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Res. 13:157-172(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /irology 170:362-369(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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P17767:
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ACT_SITE
CARHOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                          SIGNAL
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P13529; Q84929; P89038;
P13529; Q84929; P89038;
P13529; Q84929; P89038;
P15-FEB-2000 (Rel. 13, Creared)
P15-FEB-2000 (Rel. 39, Last seruence update)
P5-FEB-2000 (Rel. 39, Last are seruence update)
P6-FEB-2000 (Rel. 30, Last are seruence 
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terminal region of plum pox potyvitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saps
                                                                                                                                                                  MAY BE INVOLVED IN REPLICATION.
-:- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTECLYTIC ACTIVITY
-:- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RRA.
-:- PTM: THE VIRAL RNA OF DIVIVIRGES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTECUTION PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                            ISION PROTEIN HAS HELICASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
F.
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-1- SIMILARITY: NI-A PROTEINA & BELONGS TO PEPTIDASE FAMILY G4.
-1- SIMILARITY: BELONGS TO THE POLYVIRGSES POLYPROTEIN FAXILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYTOPLASMIC INCLUSION PROJEIN. F. KD PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81; DB 1; Length 3140; Pred. No. 1.34e-01;
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JUCIEAR INCLUSION PROTEIN A.

JUCIEAR INCLUSION PROTEIN B.

UNAT PROTEIN.
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HELPER COMPONENT PROTEINASE
PROTEIN P3.
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3140 AA: 355577 MW: 5F3DBB079820F3F5 0RT64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR03966; NIAPOTYPIASE.
                                                                                 Virus Res. 10:325-342(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is coppetween the Swiss Institute the European Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: M21847; AAA85458.1; -. EMBL: M26965; AAA47085.1; -.
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Similarity 46.7%:
14: Conservative
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1856
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2810
3140
1919
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2411 IFS-ALNMKAAVGALY-SGKKROYFKNVSD 2438 !!: | | ! : : | | : : | | : 1 IFSKNLNIKLNM-PLYIAONKRRFIKRVSN 29

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                                                                                                                                                                                                                                                                            Submitted (DEG-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (DEG-1996) to the EMBL/GenBank/DDBJ databases.

ITRANSISSION AND ALSG HAS PROTEDLYITC ACTIVITY.

ITRANSISSION AND ALSG HAS PROTEDLYITC ACTIVITY.

HAY BE INVOLVED IN REPLICATION.

ITRANSIC COVALENT INCLUSION PROTEIN HAS HELLCASE ACTIVITY. IT HAY BE INVOLVED IN REPLICATION.

INDOLUTION: NUCLEAR INCLUSION PROTEIN HAS HELLCASE ACTIVITY.

INDOLUTION: NUCLEAR INCLUSION PROTEIN HAS PROTEDLYITC ACTIVITY.

INDOLUTION: NUCLEAR INCLUSION PROTEIN NA.

POLYPROTEIN WHICH UNDERGIES POSITARNSLATIONAL PROTEDLYITC PROTEINS A SINGLE POLYPROTEIN HATCH UNDERGIES POSITARNSLATIONAL PROTEDLYIC CONTROL NOT THE PRODUCTION OF AT LEAST EIGHT INDUNIDAL PROTEINS.

INDIVIDAL PROTEINS.

SIMILARITY: HC PROTEINASE BELONGS TO PEPTITOASE FAMILY CONTROL SIMILARITY: NIT A PROTEINASE BELONGS TO PEPTITOASE FAMILY CONTROL SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                             SEGUENCE FROM N.A.

MEDIINE: 90098796.
Teyencey P.Y., Tavert G., Delbos R., Ravelonandro M., Dunez J.:
"The complete nucleotide sequence of plum pox virus RNA (strain D).":
Nucleic Acids Res. 17:10:15-10:15(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiol protease: RNA-directed RNA polymerase: nr. Covalent protein-RNA linkage: Helicase:
Plum pox potyvirus (strain D) (PPV).
Viruses: ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                    SEQUENCE OF 2810-3141 FROM N.A., AND SEQUENCE OF 2812-2828. Ravelonandro M., Varveri C., Delbos R., Dunez J., "Nucleotide sequence of the capsid protein gene of plum pox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROJETA P3.

STOPLASMIC INCLUSION PROTEIN.

6 KD PROTEIN 2.
GENOME-LINKED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COVALENT LINKAGE OF VIRAL RNA SIMILARITY).
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HELPER COMPONENT PROTEINASE.
6 KD PROTEIN I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potyvirus.";
J. Gen. Virol. 69:1509-1516(1988).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1254 | 1261 | ATP
3141 AA: 355569 MW:
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Hydrolase: Transferase; Thi
Coat protein: Polyprotein:
ATP-binding.
                                                                                                                                                                                                                                                   REVISIONS TO C-TERMINUS.
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2811
3141
1920
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1805
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                                   Potyvirus.
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                                  01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 35, Last sequence update)
01-0CT-1996 (Rel. 33, Last annotation update)
VERY HYPOTHETICAL 16.3 KO PROTEIN IN NORIZO-THS: INTERJENT RECORN YBLO77W OR YBLC733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida:
Rhabditina; Rhabditoidea: Rhabditidae; Peloderinae: Caenorhabditis.
                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomyceres: Saccharomycetales:
Saccharomycetaceae: Saccharomyces.
                                                                                                                                                                                                                                            34.7%: Score 78, 18 1; Lenath 14v;
19.1%: Bred. No. 4.0% of;
cative 12, Rismatones 2, India
                                                                                                                                                                                                                                                                                                                                                               Contreras R., Fiers W., Louth M., Molemans F.;
Submitted (AUS-1994) to the Er (L/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1995) to the EMBI/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR: S45433; S45433.
Hypothetical protein.
SEQUENCE 143 AA; 16327 MW; 106F3FFCD9794CCD CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Re. 35, Created; 01-NOV-1997 (Re. 35, Last sequence update) 01-NOV-1997 (Rei 35, Last annotation update) HYPOTHETICAL 59,6 KD PROTEIN R144.5 IN CHROMOSOME III.
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   14 5 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservation
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   STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guery Match
Best (ocal Similarity
Matches
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                            MEDLINE: 96076635
                                                                                                                                                                                                                                                                                                                                                  SIRAIN-S286C;
                                                                                                                                                                                                         STRAIN-S288C
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YBB7_YEAST
P38183;
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3

Gaps

5: Indels

Mismatches

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Ouery Match Rest Local Similarity 46.7%; Matches 14; Conservative

Score 81: DB 1; Length 3141: Pred. No. 1.34e-01:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / AICC 43667;

MEDILE: 9637999.

MEDILE: 9637999.

Sutten G.G. Blake J.A. Fitzgerald L.M. Clayton R.A. Gonayne J.D. Kerlavage A.R. Doughbrty B.A. Tomb J.F. Adams M.D. Reich C.L. Souther G.G. Blake J.A. Fitzgerald L.M. Clayton R.A. Gonayne J.D. Kerlavage A.R. Doughbrty B.A. Tomb J.F. Fuhrmann J.L. Nguyen D. Scott J.L. Googhagen N.S.M. Weldmann J.E. Fuhrmann J.L. Nguyen D. Utterback T.R. Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D. Roberts K.M., Hurst M.A. Kaine B.F. Borodovsky M. Klenk H.-P., Fraser C.M., Smith H.O., Weese G.R. Venter J.C.:

"Complete, genome sequence of the methanogenic atchaeon. Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saps
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                 Score 75; DB 1; Length 532;
Pred. No. 8.38e-01;
11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 569 AA: 65581 MW; E29EC27908E366ED CRC64;
                                                                                                                                                                                  59809 MW; 103588FF445B4283 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN M:1022.
                                                                                                                                                                                                                                                                                                                                                                                                           569 AA
                                                                                                                                                                                                                                                                                                160 LESSAMK-KLVSPVLIC-NRRLFIRHVIDIV 208
                                                                                                                                                                                                                                                                                                                                   1 IFSKNLNIKLNMPLYIAGNKRRFIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 FCKHVDLIELEDADLYIIADGRRLIER 128
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                               EMBL: 023515; AAC46549.1; -. WORMPEP: R144.5; CE02035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jannaschii.7,
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.8%;
Local Similarity 40.7%;
hes ll: Conservative
                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.5%;
Matches 11: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
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                                                                                                                                                                    l protein.
532 AA: 5
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                                                                                                                                                                    Hypothetical
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058428:
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347 AA

PRI:

STANDARD;

RH31_YFAST Q06624:

RESULT

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Eukaryota; Viridiplantae; Stre tophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Manollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McClure B.A., Hagen G., Brown C.S., Gee M.A., Guilfoyle T.J.:
"Transcription, organization, and sequence of an auxin-regulated gene
cluster in soybean.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE, 97248684.
Shayeghi M., Does C.L., Tavassoli M., Watts F.L.;
"Characterisation of Schizcosaccharomyces ponce rad31, a SbA-related gene required for DNA damage tolerance.":
Nucleic Acids Res. 25.1162'1169(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saps
01-NOV-1997 (Rel. 35, Created)
15-DEC-1999 (Rel. 35, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).
SACSI OR RHC31 OR YPR180W OR P9705.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl: Ascomycota: Saccharomycetes: Saccharomycetalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- FUNCTION: COULD BE INVOLVED IN A UBIQUITIN-RELATED PROCESS INFORMATION TO THE AND 
                                                                                                                                                                                                                                                                                                                         STRAIN=S288C / AB972:
Johnston M., Andrews S., Brinkman N., Cooper J., Ding H., B.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jer M.,
Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Polu
Riffael L., Riles L., Taich A., Trevaskis E., Viquati D.,
Wilcox L., Wohldran P., Vaudin M., Wilson R., Waterston R.,
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA; 39273 MW; 1ADB7B817BA27F3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%: Score 75: DB 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C1-OCT-1993 (Rel. 27, Created)
O1-OCT-1993 (Rel. 27, Last sequence update)
O1-OCT-1993 (Rel. 27, Last annotation update)
AUXIN-IN UCED PROTEIN 6B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 AA
                                                                                                                                                                                                                                    Saccharomycetaceae: Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD: L0004031; AOS1.
PFAM: PF00899; Thir_family: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U25842; AAB68113.1; -.
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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EMBL; U67506: AAB98573.1: -.
                                                                                                                                                                                                                                                                                                                                                                 Science 2 3:1058-1073(1995).
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                                                                               Methanococcus jannaschii
                                                                                                                 Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
SEQUENCE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1 14
RTA_RAD
P23749:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT energy is suppringful it is included through a collaboration between the SMISS institute of Bloinformatics and the BMIS custation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license and removed. Usage by and for commercial entities requires a license and placement (See http://www.isb-sib.cf./announce/or sond an email to license*isb-sib.ch).
                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license/lish-sib.ch).
                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Visitatphattae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnollophyta: eudicotyiedons:
core eudicots: Rosidae: eurosids I: Fabales: Fabaceae: Papil:conoldeae:
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Pred. No. 1.71e+00;
11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                              udery Match
Best Local Similarity 33.3%: Pred. No. 1.71e+60:
Matches 9: Conservative 11: Mismatches 6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: D14414; BAAC3310.1; -; SEQUENCE 92 AA; 10212 WW; SEDE5A9CEBCF699E CRC64;
                                                                                                                                                                                                                                                  90 AA: 10068 MW: 6EE34736C46139D4 CKC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1993 (Fel. 27, Created)
01-0CT-1993 (Rel. 27, Last Sequence update)
10CT-1293 (Rel. 27, Last annotation update)
INDOLE-3-ACETIC ACID INDUCED PROTEIN ANGT.
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Plant Cell 1:229-239(1989).
-!- INDUCTION: BY AUXIN.
-!- SIMILARITY: BELONGS TO THE ARG7 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-HYPOCOTYL;
Yamamoto K.E., Mori H., Imaseki H.;
                                                                                                                                                                                                                                                                                                                                                   20 SKAVDVEKGYLAVYVGEKMRRFVIPVS 46
                                                                                                                                                                                                                                                                                                                                                                                   3 SKNINI-KINMPLYIAGNKRRFIKRVS 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI;
                                                                                                                                                                                               EMBL: 844175; AAB23281.1: -.
PIR: JQ1098: JQ1098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuery Match 32.9%;
Rest Local Similarity 34.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                    Multigene family
SEQUENCE 90 AA
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Y573_METJA
Q57993;
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P32295;
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RESULT

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RESULT 10 YS AC 053

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STRIN-SPRAGED-DAWLEY: TISSUE-ACRTA;

MEDLINE: 90222168.

A ROSS P.C., Figier N.A., Corjay M.H., Barber C.M., Adam N.,

Harcus D.R., Lynch K.R.;

T "RTA, a candidate of protein-coupled receptor: cloning, sequencend,

T and tissue distribution.", 87:3052-3056(1990).

Proc. Na-L. Acad. Sci. U.S.A. 87:3052-3056(1990).

Proc. Na-L. Acad. Sci. U.S.A. 87:3052-3056(1990).

T SUNCION: ORPHAN ECEPTOR.

TISSUE SPECIFICATION: INTEGRAL MEMBRANE PRCTEIN.

TISSUE SPECIFICATION: INTEGRAL MEMBRANE PRCTEIN.

TISSUE SPECIFICATION: INTEGRAL MEMBRANE GLAND AORTA BUT ONLY BARELY DETECTABLE IN LIVER. KIDNEY, LUNG, AND SALIVARY GLAND: IN THE BRAIN. RIA IS MARKEDLY ABUNDANT IN THE CREBBELLUM.

THE BRAIN: RIA IS MARKEDLY ABUNDANT IN THE CREBBELLUM.

STRILLARITY: BELCNGS TO FAMILY 1 OF G-PROTEIN COUDLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-JAL-1 / USM 2661 / ATCC 43067;

MEDLINE: 96337999.

Buil CO.J. WHite O. Olsen G.J., Zhou L., Fleischmann K.D., and the Duck of G., Blake J.A., Fitzgerald L.M., Guyton R.A., Bougherty B.A., Tomt G.F., Adams M.D., Reich G.J., Cerlavage A.R., Dougherty B.A., Tomt G.F., Adams M.D., Reich G.J., Googhagen N.S.M., Weidman J.F., Fuhrmann J.L., Nayawa A.C., Cotton M.D., Roberts K.M., Peterson J.D., Sadow P.W., Handa M.C., Cotton M.D., Roberts K.M., Bursh M.A., Kalne B.P., Bordursky M., Klomk H.-P., Fraser C.M., Smith R.J., Woese C.B., Venter J.C., Complete genome sequence of the methanogenic archaeon, Methanogous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-jpp
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Ruttus
                                                                                                                                                                                                                                                                   Archaea: Euryarchaeota: Methanococcales: Methanococcaceae.
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Best Local Similarity 33.3%; Pred: No. 1 71e-00;
Matches 11; Conservative
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189 AA: - 21198 MW: - 47174593ADBEDF69 GRC64.
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GLNAV 1991 (Rel. 20. Dast Sey Enne, Edate)
GLUGL-1993 (Rel. 26. Last annotation update)
PROBABLE G PROTEIN-COUPLED RECEPTOR RIA.
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
101-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN MJ0573.
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POLG_EPUNA

P1776E.

01-AG71950 (Rel. 15, Last sequence update)

15-DEC-1999 (Rel. 37, Last annotation update)

15-DEC-1999 (Rel. 37, Last annotation update)

15-DEC-1999 (Rel. 37, Last annotation update)

GENOME POLYPRUTEIN (COMTAINS: N-TERMINAL PROTEIN (PI): HELPER

COMPONENT PROTEINNEE (EC 3.4.22.) (HCPRC): WROTEIN P3: 6 KD PROTEIN

(GENOME-LINKED PROTEIN (VPG): NUCLEAR INCLUSION PROTEIN 2 (6K2):

GENOME-LINKED PROTEIN (VPG): NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)

(EC 3.4.22.) (49 KD PROTEINASE) (49 KD-PRO): NUCLEAR INCLUSION

PROTEIN (CP)]:

PULT POX POLYWING (isolate NAT) (PPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
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The complete nucleotide sequence of plum pox virus RNA.*:

J. Gen. Virol. 70:313-524(1989).

J. FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.

J. FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY.

MAY BE INVOLVED IN REPLICATION.

HEY DETAIN WOLLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

J. FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

J. FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

J. PIM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

J. PIM: THE VIRAL RNA OF POITVIRGES IS EXPRESSED AS A SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plum pox potyvirus (isolate NAT) (PPV).
Viruses; ssRNA positive-strand viruses, no DNA stage: Potyviridae;
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                                                                                                                                                                                                                                                                                                                                       PEAM: PFC001: 7tm_1: 1.

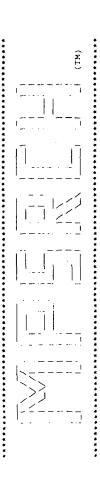
PFAM: PFC001: 7tm_1: 1.

G-protein coupled receptor: Transmembrane: Glycoprotein.
DOMAIN 45 66 1 (POTENTIAL).
DOMAIN 67 92 CYTOPLASMIC (POTENTIAL).
TRANSMEM 124 13 (POTENTIAL).
DOMAIN 105 123 EXTRACELLULAR (POTENTIAL).
TRANSMEM 124 134 EXTRACELLULAR (POTENTIAL).
TRANSMEM 124 134 (POTENTIAL).
TRANSMEM 125 140 CYTOPLASMIC (POTENTIAL).
TRANSMEM 126 180 CYTOPLASMIC (POTENTIAL).
TRANSMEM 127 198 EXTRACELLULAR (POTENTIAL).
TRANSMEM 129 220 5 (POTENTIAL).
TRANSMEM 129 220 5 (POTENTIAL).
TRANSMEM 129 220 5 (POTENTIAL).
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                      EMBL: M35297; AAA42087.1; -. EMBL: M35298; AAA42088.1; -.
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Local Similarity 32.3%;
les 10; conservative
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GCRDB: GCR_0155; -.
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Coat protein: Polyprotein: Covalent protein-RNA linkage: Hellouse:
ATP-binding:
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                                                                  SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6. SIMILARITY: NI-A PROTEINASE BELCNGS TO PEPTIDASE FAMILY C4 SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
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POLYPROTEIN WHICH UNDERGUES POSTTRANSLATIONAL PROJECTYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST FIGHT
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CYTOPLASMIC INCLUSION PROTEIN.
6 KD PROTEIN 2.
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Pred. No. 2.42e+00;
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NUCLEAR INCLUSION PROTEIN A.
N.YCLEAR INCLUSION PROTEIN B.
COAT PROTEIN.
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TE PER COMPONENT PROTEINASE.
TEIN P3.
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3125 AA: 354261 MW: EDCDD33C439CB712 CRC64:
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                                                                                                                                                                                                                                                                                                                                            EMBL, D13751; BAA02898.1; PIR: JOG003; GNVSPP.
PFAM; PF00275; EBAD; 1, PFAM; PF0068C; RNA_GOP, PFAM; PF00851; Poty_coat; 7, PFAM; PF00851; Peptidase_C6: 1, PFAM; PF00851; Peptidase_C6: 1, PFAM; PF00863; Peptidase_C6: 1, PFAM; PF01877; Poty_E1: 1, PR:NTS; PR00966; NIAPOTYPIASE.
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Best Local Similarity 43,3%;
Matches 13; Conservative
                                            INDIVIDUAL PROTEINS.
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Search completed: Mon Jun 19 15:59:38 2000 Job time: 20 secs.

US-09-142-524A-4.rspt



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MPsrch_pp = protein = protein database search. using Smith-Waterman algorithm

Mon Jun 19 15:59:55 2000; MasPar time 8.99 Seconds 239.116 Million cell updates/sec Run on:

Tabular output not generated.

>0S-09-142-524A-4 (1-31) from US09142524A.pep 225 : :FSKNLNIKLNMPLYIAGNKRRFIKRVSNVI 31

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 segs. 69334122 residues Searched:

Fost-processing: Minimum Match 0% Listing first 45 summaries

sptremb112 Calabase

isp_archea_2:sp_bacteria_3 sp_fungi_4:sp_human 5:sp_invertebrate_6:sp_mammil_7:sp_mhc_8:sp_organeile 9:sp_phaye_10:sp_plant_il:sp_rodent_12:sp_unclassified 13:sp_vertebrate_14:sp_virus

Mean 33,518: Variance 57,758: scale 0.580 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMAN DE

Resutt No.	Score	Query	Length	DB.	a	Description	Pred. No.
; ;		63.6	375	0.1	096385	CHAO1 PRECURSOR.	2.83e-12
7	123	54.7	367	10	CONZ 50	POLLEN MAJOR ALLERGEN	2.01e-08
m	68	39.6	707	S	017744	E03H4.4 PROTEIN.	2.17e-02
-7	8	37.3	747		081122	ETHYLENE RECEPTOR.	1.4Ce-01
ഗ	83	36.9	365		004580	SEQUENCE OF BAC F19K23	2.02e-01
9	81	36.0			051276	HYPOTHETICAL 54.0 KD P	4.17e-01
7	78	34.7	740	7,0	09XH5B	ETHYLENE RECEPTOR HOMO	1.21e+00
æ	11	34.2	73	S	C46181	HYPOTHETICAL 8.6 KD PR	1.72e-00
ď	Li	34.2	256		09XE03	ORF2 (FRAGMENT).	1.72e+00
10	77	34.2	180		066965	HYPOTHETICAL 56.0 KD P	1.72e+00
::	2.6	33.8	741	<u>.</u>	09XH57	ETHYLENE RECEPTOR HOMO	2.44e+00
12	97	33.8	3140		084925	COAT PROTEIN (FRAGMENT	2.44e+00
13	75			٦	Q58378	HYPOTHETICAL PROTEIN M	3.44e+00
14	75	33.3	1028	:	P97528	NB-3.	3.44e+00
15	46			N	P74570	HYPOTHETICAL 37.6 KD P	4.84e+00
3.6	7.4	32.9	637		094533	P70S5K PROTEIN KINASE	4.84e+00
17	7.4			m	P91656	70 KDA S6 KINASE.	4.84e+00
8	72		113		C81232	SEVEN IN ABSENTIA HOMO	9.49e+00
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20	7.7	32.0	176		085804	TINDECED - INNEGED CORONII	0 400400

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Sape Ö,

Query Match 63.6%; Score 143; DB 10; Lenath 375; Best Local Similarity 100.0%; Pred. No. 2.83e-12; Matches 20; Conservative 0; Mismatches 0; Indels

g ó RESULT 2 PRELIMINARY: PRT; 367 AA. 10 092NU7; PRUD UT NELL NINARY: SCHUT; 10 01-MAY-1999 (TEMBLED: 10, Last sequence update) DT 01-NAY-1999 (TEMBLED: 10, Last sequence update) DT 01-NOV-1999 (TEMBLED: 12, Last annotation update)

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PUTATIVE FLIPPASE. RCH2 PROTEIN. 100 KDA PROTEIN. IREGALCSE SYNIHASE. PFCG820W PROTEIN. SYNIAXIN. PUTATIVE DIHYDROPIEROA F1544 7 PROTEIN.	ETHYLENE RECEPTION. CLPC PROTEASE. CLPC PROTEASE ATPASE. TIG START CODEN. CONTACTIN A. TIGO24.6. VPIG. FC2H6.2 PROTEIN. FC2H5.2 PROTEIN. FC2H6.2 PROTEIN. FC2H6.2 PROTEIN. FC2H6.1 PROTEIN. FC2H6.1 PROTEIN. FC4H71ENE RESPONSE SENS ETHYLENE RESPONSE. FC4G01.3 FC4GMENT). FC4GMENT TAL TO FC PROTEIN FC4GMENT). REAPRAMANOSTORSE. HYPOTHETICAL 172.9 KD SENSORY TRANSOUTION H	is AA. nce ipdate) tilon update) Embryophyta: Tracheor ppsidu: Coniterales:	H., SONE T., KUNG K., T. Chornjar choping of Clar. (Japanese (Ypress) j. T.
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		1 6385, 6385, 6385, 6385, 1. NOV-1997 (7 1. NOV-1999 (1) 1. NO	SEQUENCE FROM N.A. IISSUE-POLLEN: WEDLINE: 96265194. SUZUKI M., KOMIYAMA N., ITC OHTA N.; PULIÉTCALION, CHARACHOLIZA PULIÉTCALION, CHARACHOLIZA MOI. ITALICO (NATABLE NO CHARACHOLIZA MOI. ITALICO (NATABLE NO CHARACHOLIZA EMBL. 165464 BAARB24611) EMBLI 17626 CHARACHOLIZA PRAM, PPCO0544; PPCLIVASC I I PRINTS; PRO0807; AMBALLERGE SIGNAL. SIGNAL. 1 22 SIGNAL. 22 375 SEQUENCE 375 AA: 40258 M
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051276
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          SORRER REPORTED THE CONTRACT OF THE CONTRACT O
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MEDLINE 94150718
MILSON R. ANDRESCN K., BAYNES C., REPKS M.
MILSON R., ALNSCHIGH R., CANNELL M., CAPSEY T., CHRES M., CHLES N. C., CRAXTON M., DEPK S., C. C., COREL M., CAPSEY T., CHRES M., CHLES M., CALL M. C., CORENER M., CARLAGER M., CARLAGER M., CARLAGER M., KERSHAW J., KIRSTEN J., LAISTEN N., LAFRETILE P., LIGHTHING J., LILLYD C., MCNORRAY A., WORTIMORS B., COALLAGRAN M., ENTRENCYS J., PERCY C., RIFKEN L., ROCPRA M., SAUNERS D., SHOWNKEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SOLSTON J., THERRY MICE J., THOMAS K., VADOLI M., VOUGHAN R., WEILSCON R., MATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                     MIDDAC HORIUIT T.M., GOLDBEIJM R.M., KURGSKY A., WOOD T.G., BROOKS E.G.;
BROOKS E.G.;
"Molecular cloning of monutain cedar (Juniperus ashel) pollen major alleraen, Jun a 1.".

BMELTAGE, Jun a 1.".

EMBL: AF106663: AADC3609.1: -

EMBL: AF106663: AADC3609.1: -

BMENDEL: 36545: Junas:1089:3654.

MENDEL: 36545: Junas:1089:3654.

SEQUENCE 367 AA: 39824 MM: 4C204630 CRC32.
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Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae: Cacnorhabditis.
                                          Juniperus ashel (Czark white cedar).
Bukarycta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta:
euphyllophytes: Spermatophyta: Coniferopsida, Coniferales:
Taxodiaceae, Juniperus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 123: DB 10: Length 367: Pred. No. 2.01e-08: 4; Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8: Indels
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Pred. No. 2.17e-62:
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Submitted (NOV-1996) to the EMBL/GeoBank/F BJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oreated)
Last sequence update)
Last annotation update)
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EMBL: 281492; CARD4026.1; -.
SEQUENCE 707 AA: 82664 MW: F805F519 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10: Mismatches
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017744 C1-5AN-1998 (TREMBLEEL, 05, Or
01-5AN-1998 (TREMBLEEL, 05, L8
01-5AN-1999 (TREMBLEEL, 09, L8
E0344.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 IFSONMULKLKMPLYVAGHK 111
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Similarity 37.5%:
12; Conservative
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
          MAJOR ALLERGEN 1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caencrhabditis elegans.
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Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Rest Local (
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ID CB1122
AC 081122
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Arabidopsis thallana (Mouselea: Cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Iracheu, byla:
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Iracheu, byla:
Conn eudiculs: Bosidae: Funcsias II Priessia.
                                                                                                                                                          Maius domestica (Apple) (Maius sylvestris).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta. Trachequipta.
euphyllophytes: Spermatophyta: Magnoliophyta: endicutyledius:
core eudicots: Rosidae: eurosius I: Rusales: Rosaceae: Maius.
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SCHOOL CVI COUCHEAN.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. GRANNY SMITH: IISSUE-FIPENING FRUIT:
LEE S.A. ROSS G.S. GABDNER R.C.:
The spoint ROSS G.S. GABDNER R.C.:
"An apple (Malus demestica L. Borkh: cv Granny Smith) home/cp ct. 13
ethylene receptor gene EIR! (Accession No. AF032448) (PGK be:125)
Exact Physiot. 117:126-1126(1998).
EMBL: AF033448: AAC31123.1:
MENDEL: 31773; Maldo:2116:31773.
MENDEL: 31773; Maldo:2116:31773.
PFAM: PF01560: GAF: 1
PFAM: PF01551: cspoint.
PFAM: PF01552: signal: 1.
SEQUENCE 741 AA: 82967 MW: D3508496 GRC72:
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01-JUL-1997 (TrEMBLrel. 64, Last Segmence update)
01-JUL-1998 (TrEMBLrel. 97, Last annotation update)
SEQUENCE OF BAC TIBXZ3 FROM ARABIDOPSIS THALLANA CHERE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 365;
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Best Local Similarity 57.1%: Pred. No. 2.02e-91;
Matches 12; Conservative 3: Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16: Mismatches 10: Indels
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01-JUN-1998 (TEMBLTEL 06, Created)
01-JUN-1998 (TEMBLTEL 06, Last sequence update)
01-NOV-1998 (TEMBLTEL 08, Last annotation update)
HYPOTHERICAL 54.0 KD PROTEIN.
                                Last sequence update)
Last annotation update)
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Pred. No. 1.40e-01;
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Overy Match
Best Local Similarity 33.3%;
Matches 10; Conservative
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PRELIMINARY

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Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Miscomotpha:
Ephydroidea: Drosophilidae: Drosophila.
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Best Local Similarity 29:0%: Pred. No. 1.72e+50;
Matches 9: Conservative : Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 256 AA: 30003 MW: FIFABGB3 CRC32:
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                                                                                                                                                                                                                                                                                                                                                                        256 AA
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                                                                                                                                                                                                                                                                        38 KKINGMVDMSLFFAGAISSFVSIIMSIF 65
                                                                                                                                                                                                                                                                                                     4 KNINIKLNMPLYIAGNKRRFIKRVSNVI 31
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ac
c
                                                                                                                                                                           73 AA; 8614 MM:
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                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY:
                                                                                                                                                Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                   SECUENCE FROM N.A.
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                                                                                                                                                                              SEQUENCE
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                                                                   SEQUENTE FROM N.A.

STRAIN-ATCC 35210 / B311,
MEDLINE: 98065943.

MEDLINE: 98065943.

FRASER C.M., CASSENS S., HURNG W.M., SUTTON G.G., CLAYTON R.A.,
DOUGHERT B., WHITE D., KETCHUM K.A., DODSON R.A., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., RERLANGER A.R., QUARKENBUSH J., SALZBERG S., HANSON M.,
VAN VGT R., PALMER N., ADAMS M.D., GOCAYNE J., WEIDMAN J.,
GARLAND S., FUJII C., COTTON M.D., HART R. BORMAN C.,
SMITH H.C., VENNER J.C., COTTON M.D., HORES Y., HATCH S.,
SMITH H.C., VENNER J.C., COTTON M.D., HORES Y., HATCH S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DERVINE C. CLARK D.G.:
DERVINE C. CLARK D.G.:
"Effect of Polination and Expanded Sthylene or Accimilation of ETR:
"Effect of Polination and Front Power Peral Abstract of Getanism, (Pelargonium x hortorum in H. Bailey).":
Submitted (APR-1949) to the EMBL/SenBank/NUBJ dutatises.
EMBL: AF141928: AAD37576.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (IrEMBLrel. 12, Created)
01-NOV-1999 (IrEMBLrel. 12, Last sequence update)
01-NOV-1999 (IrEMBLrel. 12, Last annotation update)
EIHYLEND RECEPTOR HOMOLOG.
PHETRI.
PELSTONIUM COTLORUM.
EUKARYOLA VITIGIPALATES, Streptophyta: Embryophyth: Tracheophyta; euphyllophytes: Spermatophyta; Magnoliophyta: edd: Otyledons: core exdicots: Rosidae; Geraniales: Geraniaceae: intargonium.
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046181.
046191.
01-JUN-1998 (TEMBLEEL 06, Cast Sequence update)
01-JUN-1998 (TEMBLEEL 16, Last sequence update)
01-MAY-1999 (TEMBLEEL 16, Last annotation update)
HPOTHETICAL 8.6 KD PROTEIN (FRAGMENT).
DEPOSOPHIAL subobscare (FRAMENT).
ELKARIYGTA: Metazoa: Arthropoda; Tracheata; Hexapoda: Insecta;
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                                                                                                                                                                                                                                              "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                     Score 81: DB 2: Length 460:
Pred. No. 4:17e-01:
10: Mismatches 10: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8: Indels
          BBC24].
Borrella burgdorfer: (Lyme disease spirochete).
Bacteria: Spirochaetales: Spirochaetaceae: Borrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78; DB 10;
Pred. No. 1.21e+60;
16; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  740 AA; 82956 MW; 96100075 CRC32;
                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 460 AA: 54024 MW; 54143655 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    320 ESKRLNENIALRIYLRSSKENFEKIANEII 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.8%:
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                          Substract 36.0%; Best Local Similarity 33.3%; Matches 10; Conservative
                                                                                                                                                                                                                                                                                         EMBL: AE001137: AAC66691.1;
TIGR: BB0261: -.
                                                                                                                                                                                                                                                                               Natire 390:580-586(1997).
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                                                                                                                                                                                                                                                                  burgdorferi
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SEQUENCE FROM N.A.
STRAIN-NOT08325;
MEDLINE: 99278010.
III TO I.I. KITATAMA Y., HIRAMATSU K.;
"Cloning and nucleotide sequence determination of the entire not UNA of pre-methicillin-resistant Staphylococcus aureus N315.";
Antimicrob. Agents Chemother, 43:1449-1458(1999).
NOM_TER 256. 256.
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RECKHAM D.E., OVERBEEK R., SERAD M.A., KELLER M., AUJAY M., HUBEF
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus"."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 256:
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                                                                                                                                                                                                                                                                                            Query Match 34.2%, Score 77, EB St Length, 73; Best Local Similarity 28.6%, Pred. No. 1.72e+00; Matches B: Conservative 12; Mismatches B: Indels
SIRAIN+H271:
BLESA D., MARTINEZ-SEBASIIAN M.J.:
BLESA (OCT-1996) to the EMBL/GenBank/CCGJ databases:
EMBL (17802): ABB92390.1:
FLYBASE; FBGNC023246: DsubNanon-1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AJG-1998 (TrEMBLrel. 07, Created) (1.40G-1998 (TrEMBLrel. 07, Last sequence update) (1.40G-1998 (TrEMBLrel. 08, Last annotation update) HYPOTHETICAL 56.0 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel, 12, Cheated)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-NOV-1999 (TrEMBLrel, 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORF2 (FRAGMENT).
Staphylococus aureus.
Bacteria: Firmicutes: Bact..us/Clostrid.um group:
Bacillus/staphylococcus group: Staphylococcus.
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PFAM; PF0C680; RNA_dep_RNA_pcl: 1
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1857
2292
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1168
1169
1803
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309
765
767
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SEQUENCE 27
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CHAIN
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NON_TER
SEQUENCE
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NON_CONS
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058378
058378;
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DERVINIS C., CLARK D.G.:
    "Effect of Pollinarion and Exegenous Ethylene on Accumination of ETRI
    "Effect of Pollinarion and Exegenous Ethylene on Accumination of ETRI
    "Endering Transcript During Flower Peral Abscission of Geranium
    (Pelargonium x hortorum L.H. Bailey).":
    Submitted (APR-1949) to the EXBL/GenBank/DSBJ databases.
    Receptor:
    Receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DERIVED FROM N.A.
STRAIN-DERIVED FROM SOUR CHERRY MAINTAINED ON NICCTIANA CLEVELANDII;
MAISS E., DERORRE G., JELKMANN W., CASPER R.;
SUDMILLED (AUG-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: X81093: CAA56974.1: -.
PFAM: PFOCRST; DEAD: 1.
PFAM: PFOCRST; Peptidase_C4: 1.
PFAM: PFOCRST; Poty_coat: 1.
PFAM: PFOCRST; Poty_coat: 1.
               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
DECKERT G. WARREN P.V., GAASTERLAND T., YOUNG W.G., LENCX A.L.,
GRAHAM D.E., OVERBEEK R., SMEAD M.A., KELLER M., AUJAY M., HUBER R.,
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, ABCONOSE, AACONOSE, ACCOSSED.
EMBL, ABCONOSE, ACCOSSED.
EMBL, ACCONOSE, ACCOSSED.
EMBL, ACCONOSE, ACCOSSED.
EMBL, GENERAL P. SESSON C. S. SESSON C. S. SEQUENCE 48, AA. SESSON C. S. SECOLENCE 48, AA. SESSON C. S.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sukaryota, Viridplantae: Streptophyta; Embryophyta: Tracheophyta;
euphyllophytes: Spermatophyta: Nagnollophyta: eudicotyledons:
core eudicots: Rosidae; Geraniales: Geraniaceae: Pelargonium.
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                                                                                                                                                                                                                                                                                                                                      Score 77; DB 2; Length 480:
Pred. No. 1.72e+00:
10; Mismatches 9; Indels
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01-NOV-1996 (I-EMBLEE). U. Last sequence update)
01-NOV-1999 (I-EMBLEE). C1. Last sequence update)
01-NOV-1999 (I-EMBLEE). C2. Last annotation update)
COAT PROTEIN (FRAGMENS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plum pox potryirus (strain SK 69) (PPV).
Viruses: ssRNA positive-strand viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 TESTAYQISAELAFYVPGNPRIYVFBVN 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TESKNINIKINMPLYIAGNKRRFIKRVS 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 NENIKENMPLYIAGNKRHFIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                            Query Match
Hest Local Similarity 32.1%;
Matches 9; Conservative
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Pred, No. 2,44e+00:
9: Mismatches 5: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.3%; Score 75; DB 1; Length 273; Best Local Similarity 35.7%; Pred. No. 3.44e+00; Matches 10; Conservative 10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                            11.NCV-1998 (TrEMBLrel. 06, Created)
01.NCV-1998 (TrEMBLrel. 08, Last sequence update)
01.NCV-1998 (TrEMBLrel. 08 and administron update)
HYPOTHETICAL PROTEIN MJC96.
MJC968.
Methanocognus jannaschii.
                                                                                                                                                                                                   355547 MW: 203FB949 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein.
273 AA: 30739 MW: 98CEF898 CRC32:
                                                                                                                                                                            COAL PROTEIN.
                                                                                                                                                                                                                                                                            2410 IFS-ALNMKAAVGALY-SGKKKDYFKNVSD 2437
                                                                                                                                                                                                                                                                                             148 KOLK-DUGVKVFIASGDRKGFIKRLAEI 174
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Local Similarity 43.3%;
nes 13; Conservative
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1857
1857
>2049
>2293
>2810
>3140
767
>1116
1117
>1169
>1803
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STRAINT-ECCEDING
STRAINT-ECCEDING
MEDIINE: 97561201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA I.,
MIYAJIMA N., HIROSAWA M., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMMOD S., TAKEUCHI C., WADA T., WATANABE A., YANADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-WISTAR: TISSUE=BRAIN;
MEDLINE: 97101230
MEDLINE: 97101230
MEDLINE: 97101230
MASSUA T., NAGATA S., HOSOYA H., WATANABE K.:
"Novel neural adhesion molecules in the Contactin/F3 subgroup of the immunoslobulin superfamily: isolation and characterization of cDNAs from rat brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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EMBL: D90916: BAA18677.1: -.
HYPOTHELICAL PROTEIN.
SEQUENCE 331 AA: 37593 MW: B50A856C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :
ن
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ن
                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NAY-1999 (TrEMBLrel. 12, Last annotation update)
NB-3.
NB-3.
Ratius norventous (Rat)
Eukaryota: Metazca: Chordata; Cran.ata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Mutinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75: DB 11: Length 1028;
Pred, No. 3.44e+00:
3: Mismatches 2: Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.9%; Score 74; DB 2; Length 331; Best Local Similarity 32.0%; Pred. No. 4.84e+00; Matches 8; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
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PRELIMINARY: PRT: 331 AA.
P7457C
P7457C
P7457C
P7457C
P7457C
P7457C
P7457C
P7457C
P7457C
P7477C
P7477
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EMBL; D87248; BAA:3320:1; ...
FISSP; P20241; 1CFB.
FFAM; PF00041; 1CFB.
PFAM; PF00042; iq: 6.
SEQUENCE 1628 AA; 114065 MW; 4798F057 CRG32;
                                  PRI: 1028 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
Local Similarity 58.3%;
es 7: Conservative
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 PLYVQEDKRRFV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PLYIAGNKRRFI 24
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SEQUENCE FROM N.A.
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IABAIA S.:
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P97528:
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Search completed: Mon Jun 19 16:00:15 2000 Job time : 20 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:03:25 2000: MasPar Lime 4.36 Seconds 168.264 Million cell updates/sec Run on:

Tabular output set generated.

>CS-09-142-524A-5 (1-31) from US09142524A.pep (2-31) scgnueGTNIYNNNEAFKVERRFIKRVSNVI 31 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 Post-processing:

summar:es

a-geneseg35 l:genesegp Catabase

Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 22.687; Variance 86.099; scale 0.264

SHWMARIES

7 7 7 7 7 7							
No.	Score	Water.	Length	an an	a :	Description.	Fred. No.
	207	ວ∵ຄວ ∶	3.1	_	W27373	Multi-epitope peptide	1.53e-12
(7	125	\$0.0	20	_	W42154	I-cell eritope peptide	3.4
e	1.25	60.4	354	-	W04344	usa	3.4.e
√*	125	60.4	354	-	W42121	Japanese Cypress polle	3.4.e-04
'n	125	0	375	-	W04345	Chamaecyparis obtusa p	3.4%e-04
Ş	108		367	_	R45577		1.49e-02
7	63	4	20	,-ı	R82522	٠,	.80e-
æ	65	4	20	٠, ٦	R45573	Cry j I pollen allerge	
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10	93	44.9	2:	-	W80355		ω.
11	66	44.9	26	•-4	R45599	Cry j I pollen allerge	3.80e
12	93	6.47	28	1	R92180	, ,	ς.
13	93	44.9	30	. 1	R45598	Cry j I pollen allerge	~
14	93	6.44	353	. 1	875388	nese	۳.
15	66	44.9	353	٠.	R81587	Cedar polien allergen	3.80e-01
15	93		374	-	R31937	Cry) I.	
17	93		374	-	R60165	ese	3.80e-0:
18	93		374	-	345541	Cry j I pollen allerde	
19	93		374	-	R82490	Н	
20	06		81	-	W80358	craen protein	
2;	68	43.0	19	_	Y01802	used f	8.85e-01
22	87		61	~	Y01801	nsed for	1.35e-00
23	85	41.1	18	~	Y01804	sed for	2.046-03

RESULT 2
M42154 standard; peptide: 20 AA.
AC M42154:
DT 16-JUN-1998 (first entry)
DE 1'c-li epitope peptide 34 from Japanese cypress pollen antigen Chaol.
KW Japanese cypress pollen; antigen: T-ceil epitope; Chaol; Chaol.
KW Japanese cypress pollen; antigen: T-ceil epitope; Chaol; Chaol.
KW diagnosis; aliergy; spring tree pollen disease; pollinosis.

24 83 40.1 18 1 Y01803 Peptide used for the 25 82 39.6 24 1 R4560 Cry 1 pollen altera 27 80 38.6 24 1 R4560 Cry 1 pollen altera 28 76 36.7 105 1 W27375 Wilti-epitope peptide 29 76 36.7 105 1 W27379 Wilti-epitope peptide 29 76 36.7 134 1 W27379 Milti-epitope peptide 29 76 36.7 134 1 W27371 Milti-epitope peptide 29 76 36.7 134 1 W27371 Milti-epitope peptide 29 76 36.7 134 1 W27371 Milti-epitope peptide 29 70 33.8 360 1 W42870 Thermotoga OCI/4V end 33 70 33.8 360 1 W42870 Thermotoga OCI/4V end 33 70 33.8 360 1 W42870 Thermotoga OCI/4V end 35 8 32.9 264 1 Y00911 S. aureus ffh protein 36 8 32.9 264 1 Y00911 S. aureus ffh protein 36 68 32.9 264 1 Y00911 S. aureus ffh protein 36 68 32.9 264 1 Y00911 S. aureus ffh protein 36 68 31.9 428 1 Y00911 S. aureus ffh protein 36 68 31.9 428 1 Y00911 S. aureus ffh protein 36 68 31.9 428 1 W1643 S. Aureus ffh protein 36 67 31.4 4 4 8 130 1 W3735 Calulase from Me 4 65 31.4 4 97 1 W3735 Cytochrome P450RAJ IS 65 31.4 4 97 1 W3735 Cytochrome P450RAJ IS 65 31.4 4 97 1 W3735 Cytochrome P450RAJ IS 65 31.4 4 97 1 W43735 Cytochrome P450RAJ IS 65 31.4 1266 1 W48721 Human Cytoplasmic is 79 CHI epitope Peptide used as immunotherapeutic agent is 1 Ergen i Tymphocyte; immoglobiulin: Synthetic: Tell epitope Fegion: alergen: lymphocyte; immoglobiulin: Synthetic: Tell epitope Fegion: alergen: lymphocyte; immoglobiulin: W2787 W2787 K. K.me A. Sone T: W2787 K. Iwama A. Kino K. K.me A. Sone T: W2787 W2787 K. Iwama A. Kino K. K.me A. Sone T: W2787	contains multi-epitobe peptide contain from different allegens. Claim 9, Page 31: 58pp. Japanese. The present sequence represents a multiple process. The present sequence represents a multiple process. The present sequence represents a multiple process. Greater than 100 as measured to applicate that a vide value of the alternative season be used to prevent and treat a wide value season to prevent and treat a wide value consistination. Side effects, e.g. that Match Sequence 1 AA: 100.0%: Score 207 st Local Similarity 100.0%: Pred. No. tohes 11: Claim Illing Ill	SGKNEGINIYNNNEAFKVERRF K
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ID R4
AC R4
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O
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                                     18-DEC-1997.
12-JUN-1997.
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18-DEC-1997
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NA-PSON: T46319.

NA-PSON: T46319.

NA-PSON: T46319.

NA-PSON: T46319.

NA-PSON: Characoparis obtusa polico allergen - ficeli
epiloge(S) of Wilch are userni in development of preventative and
treating ugent for C. chimsu pollen pollinosis

The present sequence of the state of the present of the present sequence of which can be used in the bresupment of the present epiloges of which can be used in the bresupment of preventive and freuting agent for C. coticsa police, pullinosis.

C. obtusa pollen (2.4 kg) was degreased with diethyl other, and
died at soom temp. Oversight. Oha oli was sept. From it and
purified at soom temp. Oversight. Oha oli was sept. From it and
purified. RNA was extracted from C. obtusa pollen, and mRNA and
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28-NOV-1996 (lirst entry)
Chamaecyparis obtusa pollon allergen Cha O I (A).
Pollen allergen: Cha O I: T-ceil epitope: prevention: treatmest.
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W42121
16-JUN19419-6 (first entry)
Japanese Operess pollen antigen Chabl.
Japanese Operess pollen antigen Treal epitopen Chabl.
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C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mainh 60.4%: Score 125: DB 3: Length 20; Local Similarity 100.0%: Pred. No. 3.41e-04: cs. 26; Conservative 6; Mismatches C: Indels
                                                                                                                                                                                                                                      polien disease
Graim 1: Fage 32: 71pp: Japanese.
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21.2EC-1994: 335089.
21.DEC-1994: DF-335089.
(MEP) MEDI MIK PROD CO LID.
WPI: 96-368225/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pollinosis.
Chamaecyparis obtusa.
308176192-A.
Chamaeyparis obtusa
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Example 1: Page 14-15: 71pp; Japanese.
The present sequence represents Japanese cypress pollen antigen Chadi. The present invention describes peptides which correspond to the Toell epitope sites on Japanese cypress pollen antigens Chad, and Chaoi. The peptides can be used as a reacent for the diagnosts of allergy to Japanese cypress pollen, and as an antigen in the treatment and prevention of spring tree pollen disease in which the pollingsis involves reactivity to Japanese cypress pollen.
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12-JUN-1995. JUN-1997.
12-JUN-1995. JUN-1995.
13-JUN-1995. JUN-1995.
14-JUN-1996.
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The frescnt seguence as the C. obtuse policy acceptant of a the frescnt seguence of the C. obtuse policy and the coll epitopes of which can be used in the development of a preventate and treating agent for C. obtusa policy politicasis.

C. obcusa policy (2.4 kg) was degreased with distributions; and dried at room temp, overnight. Cha o I was sepd, from it and publised. NNA was extracted from C. obtusa polien, and mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1996 (first entry)
Chamaecyparis obtusa pollen allergen Cha o I CDNA (B).
Pollen allergen: Cha o I: T-cell epitope: prevention: meatmen
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diagnosis; allergy; spring tree polled disease; pollinosis
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Best Local Similarity 100.0%; Pred. No. 3.41e-04;
Matches 10; Conservative : Mismatches 0; Indels
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R45577 standard, Protein: 367 AA.
R45577.
13-501-1994 (first entry)
Jun s I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ... 5
WO4345 standard; Prote:n: 375 AA
WO4345;
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21-DEC-1994: 335089.
21-DEC-1994: JP-335089.
(MIEP) MEILI MILK PROD CG LTI
WPI: 96-368225/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 SSGKNEGTNIYNNEAFKVE 330
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J08176192 A.
                                                        Chamaeyparis obtusa.
WC9747648-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified Cryptomeria japonica (Cry j) I peptide(s) - useful for treating allergy to japanese cedar pollen allerae, or treating allergy to japanese cedar pollen allerae, or laminologically cross reactive allergens.

Disclosure, Figure 2: 60pp, English.

Disclosure, Figure 2: 60pp, English.

Novei peptides of cry j I have been modified as a part of a preformulation scheme to develop an optimised drug product for therapeutic treatment of humans suffering from allergy to Japanese cedar pollen allergen or an allergen which is immunologically cross reactive with Japanese cedar pollen allergen. Such modified peptides possess certain characteristics which reader them particularly suitable for drug product formulation. Peptide fragments of Cry j I modified and unmodified, are given in R82491-R82555. This peptide fragment corresponds to amino acids 31:330 of the allergen mature
                                                                                                                                                                                                                                                                                              Discrésure: Fig 16: 137pp: English.
The sequence is that of Jun s I, a homologue of the Japanese cedar pollem allorgen Cry j I. Antigenic peptides derived from it can be used for the treatment and diagnosts of allergies associated sequence. 16: AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #82522;
15-APR-1996 (first entry)
Cry j I Japanese Cedar pollen allergen: modified: drug production;
Cry j I. japanese cedar pollen allergen: modified: drug production;
allergy: Crytpomeria japonica.
Crytpomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                            Antiques derived from Japanese cedar pollen allergen Cry j I -
contain at least two T cell epitope(s), used to treat or diagnose
Japanese ondar: polies allerges: allergy: treatment; diagnosis;
T cell epitope; sensitivity: detection.
Juniperus sabinoides.
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8est Local Similarity 85:08: Pred. No. 1.49e-02;
Matches 17: Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93; DB 1; Length 20; Pred, No. 3,80e-01; 3; Mishatches 3; Indels
                                                                                                                                        20-JAN-1994; UG0139;
15-JAN-1992; WO-105661;
01-SEP-1992; WO-105661;
01-SEP-1992; US-938990;
(IMMU-) IMMULOGIC PHARM CORP.
HAPI: 34-035066704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1995: U04249.

08-APR-1994: US-226248

06-DDC-1994: US-320225.

CHMM-1 ZMMLLOGIO FRARM O'NEP.

CHEL X, Evans S. Franco HM, NOO M, Powers SE;
                                                                                                            "mature peptide"
                                                                            /note= "signal peptide"
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R82522 standard; Protein: 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 SSGKTEETNIYNSNEAFKVE 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Hest Local Similarity 70.0%;
Matches 14: Conservative
                                                                                         22. 367
                                                                                                         /aote-
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                                                                                                                                                                                                                                                N-PSDB: Q55272.
                                                                                                                         W09401550-A
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                                                                pept;ded
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08-0CT-1998: 059701.
PR 1996: 059701.
PR 10-1996: 059701.
PR 10-1997: JP-276054.
PR 01-APR-1997: JP-16908.
PR 25-JUN-1997: JP-169088.
PR 25-JUN-1997: JP-16908.
PR 25-JUN-1997: JP-1690
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Control peptide P16.

Fast optiope: HEE7A; monocion; antibody; hymanised untibody.

Fast optiope: HEE7A; monocion; antibody; hymanised untibody.

Maran: apoptosis: HEE7A; autoimouse disease; Hashimoto's disease;

System systemic lupus erytheratosus; gial refers host disease;

System systemic lupus erytheratosus; gial referse host disease;

System system; Goodpasture systeme; Addison's disease;

R. Hemmatoid arrhitis; autoimenne haemosytic anaemia;

M. Masthenia gravis; multiple sclerosis; Basedow's disease;

R. Arromopopala purpura; insulin-dependent diabetes; allergy;

atopy: atteriosolerosis; myocaiditis; cardomyopathy;

M. Gomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

Franksplant rejection; therapy.
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The sequence is that of an isolated peptide of the Japanese cedar pollen allergen Cry 1 (amino acids 311-330). The peptide, C11-32, can be used the treatment and diagnosis of allergies associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects come; d to naturally occurring allerges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigens derived from Japanese cedar pollen allergen Gry : . . contain at least two T cell apprope(s), used to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-3CL-1994 (first entry)
Cry ) I pollen allerger peptide CJI-32.
Japanese cedar: detection: allergy: treatment: diagnosis: i cell epitope: sensitivity.
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44.9%; Scure 93; FB 1; Length 20:
Best Local Similarity 70.0%; Pred. No. 3.80e-01;
Matches 14; Conservative 7. Vinc. 3.80e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bond JF, Garman RD, Griffith IJ, Kuo M, Poliock J; WPI: 94-035066/04.
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W83058 standard; Peptide; 20 AA.
                                                                                                                                                                                                                                                                                                T 8
R45573 standard: Protein: 20 AA.
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                                                                   1 SSGKNEGTNIYNNEAFKVE 20
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SSGKYEGGNIYTKKEAFNVE
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10-JUL-1992; WO-UC5661.
01-SEP-1992; US-938990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptomerla japonica
W09401560-A.
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AU9859701-A.
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US-09-142-524A-5.rag

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A linked T cell epitope peptide - used for the treatment of significals: Pages 19-20; 21pp; Japanese. Claim 8: Pages 19-20; 21pp; Japanese. Gerived from the sugi allergen proteins Cryji (W80339-44, K80350-53 and W80355 58) and Cryj2 (W80345-49 and W80354-59). The peptides are useful for the treatment of sugirpullances, an allergic reaction of the body to poller.
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ن
                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases that involve Fas/Fas ligand interactions, and also to treat
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Synthetic peolides PI-PIS (see W83643-57) are partial sequences of amino acids 1-157 of the extracellular domain of himan Fas. With between 9 and 11 amino acid residues overlapping one another. Pis See W81059) is a negative control having no homology with human Fas. Pi-PIE were used in an ELISA, Which demonstrated that novel mustine anti-luman Fas conoclonal antibody HPEPA specifically binds and amino acid sequence contain antibody HPEPA specifically binds was subsequently identified. The invention provides humanised HPEPA antibodies (see W82131-3) produced by CDR craftling. These antibudies are capable of inducing apoptosis in abnormal cells expressing Fas. and in contain general models, treatments of cells. They are used to evaluate, in animal models, treatments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cryj2: treatment:
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Japanese cedar: detection: altergy: treatment: diamnosis:
T cell epitope: sensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WB035 standard: peptide: 21 AA. WB035 standard: peptide: 21 AA. WB0355: 11-385. Ill-3855: 11-385 statement protein Cry32 derived epitope for I cells. Sugi alleraen protein Cry32 derived epitope for I cells. I cell epitope: sugi alleraen proteins Cry3: Cry32: tree sugi:pollinosis; alleraic reaction: pollen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     query Match.

44.9%; Score 93; DB 1: Length; 20: best Local Similarity 70.0%; Pred. No. 3:80e-01; Matches 14: Conservative 3; Mismatches 3: Indels
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10-UCL-1992; WC-UC5661.
01-SEP-1992; US-G9861.
(IRMC-) ZMUCLOGIC PHARM CORP.
Bond JP, Garran RD, Griffith IJ, K.O M. Pollock JP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HAYB ) HAYASHIBARA SEIBUISU KASAKU
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13-JUL-1994 (first entry)
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29-SEP-1998.
22-DEG-1997: 353448.
24-DEG-1996: UP-343441.
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WPI: 98-577037/49.
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Wo9401560-A.
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WPIN 95-366391/47.

Woiltied Cryptomeria japonica (* y j) 1 peptide(s) - iseful for treating allergy to japanese char pollen allergen or immunologically cross reactive progress.

Claim 1: Figure 3: 60pp. Engl.

Solid 1: Figure 3: 60pp. Engl.

Novel peptides of cry j 1 have an modified as a part of a preformulation scheme to devel an optimised drug product for the rapecutic treatment of humans inferring from allergy to Japanese cedar pollen allergen or an allergen which is immunologically cross reactive with Japanese cedar pollen allergen modified in the postess certain characteristics which render them fortunels (*) possess certain characteristics (*) possess certai
                                                                                                                                                                                                                                                                                                                                                                                              Sire
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Cry : Lapanose Cedar pollen illergen modified peptide (FUI-44.8)

Cry : Lipapanese cedar pollen allergen; modified; drug piodumilion,
allergy: Crytpomeria japonica.
                                                                       allergy clark 18: 137pp; English.
Clark 76: Fig 18: 137pp; English.
Clark 76: Fig 18: 137pp; English.
Clark 76: That of an isolated peptide of the Japanese counties allerge Cry 7: The profite, CJ7-44.1, can be used for the treatment and diagnosis of clerates associated with Japanese cedar pollen. It has enhanced inerapetic properties but redured side effects compared to naturally occurring allergens.
Sequence 26 AA:
                 Antiques derived from Japanese cedar pollen allergen fry licopiain at least two I cell epitope(s), used to treat or diam
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Japanese cedar: detection: allergy; treatment; diagnosis.
T coll petupe: sensitivity.
Cryptomeria japonica.
W09401560-A.
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                                                                                                                                                                                                                                                                                                                             Query March
44.9%: Score 93; DR 1: Length 26;
Best Local Similarity 70.0%: Pred. No. 3.80e-61;
Matches 14; Conservative 3: Mismatches 3: Indels
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R92186 standard; Protein: 28 133
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R45598:
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19-CCT-1995.
C6-APR-1995: U04249.
C8-APR-1994: US-22648.
C6-DEC-1994: US-350225.
(IMMU-) IMMULOGIC PHARM CORP.
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Local Similarity 70.0%;
les 14; Conservative
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15-JAN-1993: U00139.
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94-035066/04
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R81587 standard: Protein: 353 AA
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Claim 75: Plu 18: 137pp: English.

Claim 75: Plu 18: 137pp: English of the Japanese redar policy allorder for policy allorder.

The proalment and diagnosis of allergies associated with Japanese redar policy. It has enhanced therapeutic properties but reduced solder treatment and diagnosis of allergies associated with Japanese Side vilens. It has enhanced therapeutic properties but reduced side vilens.
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Japanese codar: pollen allergen: Gry; I: T-cell epitope: peptides:
prevention: treatment: cryptomeria pollinosis.
                                                                                                                                                                     Antiwors derived from Japanese cedar pollen allerado Cry j I ^{\circ} contain at least two I cell epitope(s), used to treat or diagnose
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RESULT

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DI Cacar pollen allergen: Immunociobuin E; idE: Tree! epituper

KW Gedar pollen allergen: Immunociobuin E; idE: Tree! epituper

KW artibody: pollinosis; therapy: immunotherapy.

Cryptomeria japonica.

PP 7002954A.

PP 10-SEP-1996: JP-202137

PR 10-SEP-1996: JP-202237

PR 10-SEP-199
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MPsrch_pp protein protein database search, using Smith-Waterman algorithm Jul Jun 20 13:34:24 2000; MasPar time 2.63 Seconds 170.246 Million cell updates/sec Tabular output not generated. Run cn:

>US-09-142-524A-5 (1-31) from US09142524A.pep 2-207 : SSGKNEGTNIYNNNFAFKVERRFIKRVSNVI 3: Title: Description: Perfect Score: Sequence:

РАМ 150 Сар 11 Scoring table:

145341 seqs, 14437480 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 21.454; Variance 83.581; scale 0.257 Statistics:

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or egual to the score of the risuit being printed, and is derived by analysis of the total score dis ribution.

SUMMARIES

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60 29.0 128 3 US-08-804- Sequence 2, Applicatio 1.73 (2. 29.0 128 3 US-08-720- Sequence 34, Applicatio 1.73 (2. 29.0 249 1 US-08-152- Sequence 34, Applicati 1.73 (2. 29.0 249 2 US-08-152- Sequence 35, Applicati 1.73 (2. 29.0 249 2 US-08-740- Sequence 6, Applicatio 1.73 (2. 29.0 249 2 US-08-144- Sequence 6, Applicatio 1.73 (2. 29.0 249 2 US-08-145- Sequence 6, Applicatio 1.73 (2. 29.0 249 2 US-08-145- Sequence 6, Applicatio 1.73 (2. 29.0 24) 2 US-08-145- Sequence 6, Applicatio 1.73 (2. 29.0 24) 2 US-08-544- Sequence 6, Applicatio 1.73 (2. 29.0 25) 2 US-08-544- Sequence 30, Applicatio 1.73 (2. 29.0 25) 2 US-08-544- Sequence 30, Applicatio 1.73 (2. 29.0 25) 2 US-08-544- Sequence 30, Applicatio 1.73 (2. 29.0 25) 3 US-08-	74	£ 1	29.5	541		9	. 4	
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60 29.0 248 1 US-08-152 Sequence 34, Applicati 1 US-08-152 Sequence 35, Applicati 1 US-08-154 Sequence 35, Applicati 1 US-08-160 Sequence 6, Applicati 1 US-08-135 Sequence 6, Applicatio 1 US-08-144 Sequence 1 US-08-144 Sequence 6, Applicatio 1 US-08-144 Sequence 1 US-08-144 US-08-1	16	90	29.0	128		8	7	1.71
50 29.0 249 1 US-08-152- Sequence 35, Application 1 60 29.0 249 2 US-08-460- Sequence 6, Application 1 60 29.0 249 2 US-08-135- Sequence 6, Application 1 60 29.0 249 2 US-08-144- Sequence 6, Application 2 60 29.0 249 2 US-08-124- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29.0 249 1 US-08-544- Sequence 6, Application 1 60 29 20 20 20 20 20 20 20 20 20 20 20 20 20	17	99	29.C	248		8	34,	, 1
50 29.0 249 2 US-08-460- Sequence 6, Applicatio 1 50 29.0 249 2 US-08-735- Sequence 6, Applicatio 1 50 29.0 249 1 US-08-144- Sequence 6, Applicatio 1 50 29.0 249 1 US-08-125- Sequence 6, Applicatio 1 50 29.0 251 1 US-08-544- Sequence 6, Applicatio 1 50 29.0 251 1 US-08-544- Sequence 7 30, Applicatio 1	18	9	29.0	249		8°-	35,	_
50 29.0 249 2 US-08-735- Sequence 6, Applicatio 1,718-60 29.0 249 2 US-08-144- Sequence 6, Applicatio 1,718-60 29.0 249 2 US-08-155- Sequence 6, Applicatio 1,718-60 29.0 251 US-08-544- Sequence 30, Applicatio 1,718-60 29.0 251 US-08-544- Sequence 70, Applicatio 1,718-60 29.0 251 US-08-544- Sequence 70, Application 1,718-7	5.1	90	29.0	249		-08	9	_
50 29.0 249 1 US-08-144- Sequence 6. Applicatio 1.71e+ 50 39.0 249 2 US-08-125- Sequence 6. Applicatio 1.71e+ 50 29.0 251 1 US-08-544- Sequence 30. Applicatio 1.71e+	20	90	29.0	249		80 -	ý,	1.716+
60 39.0 249 2 US-08-125- Sequence 6, Applicatio 171e+ 60 29.0 261 1 US-08-544- Sequence 30, Application 71e+	2:	90	29.0	249		38-144	9	1 7 0+
60 - 29.0 - 261 1 US-08-544 - Seduence 30 Applicated 1 715+	22	90	39.0	249		9	9	'
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RESULT
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                                                                                                                       upery Match 34.8%: Score 72: DB 2: Lendin 317: Hest Local Similarity 40.0%: Pred. No. 1.69e+01: Matches 10: Conservative 7: Mismatches 7: Indels
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Patent No. 6/8012
GENEVAL INFORMATION:
GENEVAL INFORMATION:
TITLE OF INVENTION: Carboxymethyl Cellulase from TITLE OF INVENTION: Thermotoda Maritima NIMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARFILA, BYRNE, BAIN: GILFILLAN, ADDRESSEE: CARFILA, BYRNE, BAIN: GILFILLAN, STREET: 6 BECCRI, STEMAT 6 01.STEIN
STREET: 6 BECCRE FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 AA
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SOFTWARE: MOND PERFECT 5.1
CLERENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/951,889
PILING CATE:
CLASSIFICATION: 0415
PHIOR APPLICATION: 0A1A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: LINEAR MALECULE TYPE: PROTEIN 525334 CN;
FOPOLOGY: LINEAR MALECULE TYPE: PROTEIN SEQUENCE 317 AA: 37355 MM: 525334 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER USA
ZIP: J7068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08951889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISEEFAX: 201-994-1744
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                57 STHAYAFP-PYKIMDRFFKKVDEVI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 STHAYAFP-PYKIMDRFFKRVDEVI 80
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                                                                                                                                                                                                                                                                                                                               7 GINIYNNNEAFKVERRFIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Sequence 2, Application US/09066075
Patent No. 5925749
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TILLE FINVENTION:
Carboxymethyl Cellulase from Element of Mattifina NUMBER of SEQUENCES:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: CECHILLA, BYRNE, BAIN SILFILLIAN,
STREET: GENERAL SECONDER SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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   317 AA
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PROR APPLICATION DATA:
PROR APPLICATION DATA:
APPLICATION NUMBER: US/08/518.61.C
FILING DATE: August 23. 199E
ATTORNEY/AEBMT INCRMATION:
NAME: FERRARO, GREGT 10.
REGISTRATION NUMBER: 134
REFERENCE/ORCET NUMB: 231400-20
TELECOMMUNICATION INFORMALION:
TELECOMMUNICATION INFORMALION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DGS
SOFTWARE: WCRD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NORBER: US/09/064,075
FILING DAIE;
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317 AA: 37455 WW: 52544 ON.
   F. X.
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Patent No. 5792642
GENERAL INFORMATION:
                                                                                                                                                                                                                              Sequence 2. Application US/0905075
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7 GINIYNNEAFKVERFIKRVSNVI 31
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AMINO ACID
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   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NEW JERSEY
COUNTRY: USA
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TOPOLHGY: LIN
MOLECULE TYPE:
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US-09-066-075-2
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBW FOC DOMPATIDE
OPERATING SYSTEM: PC DOS/KS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.35
CUSPTANENT APPLICATION DATA:
APPLICATION NUMBER: US/28/459,264
FILING DATE: US-JUN.1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAMME: ROBINSON, JOSEPD, R
REGISTRATION NUMBER: 0646/18026-US3
REFERENCE/DOCKET NUMBER: 0646/18026-US3
TELEPHONE: 212-527-7706
TELEFAN: 212-753-6237
TELEELEX: 236687
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sc re 71; 28 1; Length 255;
Pr.: No. 2.05e+01;
5: Mismatches 1; Indels
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APPLICANT: CAPON, DANIEL J.:LASKY, LAURENCE A.
TILLE CE INVENTION: RECOMBINANT DNA ENCODING HYBRID
IMMUNOSLOBULLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/38/185,670
FILING DATE: 21-5AN-1954
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-5E-1772
APPLICATION NUMBER: 6-5,122
FILING DATE: 16-5EC-1991
APPLICATION NUMBER: 6-5,122
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 45,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AA; 27847 MW: 349604 CN;
       ADDRESSEE: Darby 6 Darby PC
STREEI: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOLECULE TYPE: peptide OKIGINAL SOURCE: ORGANISM: Bacillus cereus IMMEDIATE SOURCE: CLONE: B-LACTAWASE
                                                                                                   CCUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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APPLICANT: TALLY, Francis P
APPLICANT: CLUSTON STATEMENT OF TALLY, Francis P
APPLICANT: GLUSTON STATEMENT OF TILLE OF TINENTION: OF CLASS BETA-LACTAMASE ENZYMES FROM BACTEROIDES
TITLE OF INVENTION: OF CLASS BETA-LACTAMASE ENZYMES FROM BACTEROIDES
NUMBER OF SEQUENCES: BETA-LACTAMASE ENZYMES FROM BACTEROIDES
NUMBER OF SEQUENCES:
ADDRESSES: Darby PC
SIREET: 805 TALLA AVENUE
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RASMUSSEN, Beth A
APPLICANT: TALLY, Francis P
APPLICANT: GLUZMAN, Yakov
TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCES
TITLE OF INVENTION: OF CLASS B BETA-LACTAMASE ENZYMES FROM BACTEROIDES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :
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CUMPUTER READABLE FORM:

MEDITUM TYPE: E.CPPY disk

COMPUTER: IBM PC compatible

CLASSITIATION NUMBER: US/06/459,263

FLICE COMMUNICATION INFORMATION:

TELEFICATION NUMBER: U646/18026-US2

TELEFICATION NUMBER: U646/18026-US2

TELEFICATION INFORMATION:

TELEFICATION INFORMATION:

TELEFICATION INFORMATION:

TELEFICATION NUMBER: U646/18026-US2

TELEFICATION NUMBER: U646/18026-US2

TELEFICATION NUMBER: U646/18026-US2

TELEFICATION COMPATION INFORMATION:

TELEFICATION COMPATION INFORMATION:

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TELEFICATION COMPATION 
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Pred. No. 2.06e+01;
5: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacilius cereus
NMMEDIATE SOURCE:
CLONE: B-LACTAMASE
JENCE 255 AA: 27847 MW: 349604 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08459264 Patent No. 5705340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4. Application US/08459264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPCLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 34.3%;
Local Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 MVEKKFQKRVIDVI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 KVERRFIKRVSNVI 31
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                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE
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Patent No. 575933
GENERAL INFORMATION:
APPLICANT: Shidan Knyotaka
APPLICANT: Shidan Knyotaka
APPLICANT: Shidan Knyotaka
APPLICANT: Schinge E.
APPLICANT: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPAR: US
COMPATED S
ZIP: USING
COMPUTER READABLE FORM:
MEDIUM TYPE: Élopyy dis
COMPUTER: IBM PC COMPA!
COMPATING SYSTEM: PC-DN: WS-DNS
SUSTANCE: Patentin Relu ew el n. Vets:: el.Nn
SUSHENI APPLICATION NUMBER: US/ e/4**/**
FILING DATE: 06-JUN-3-5
GLASSIFICATION: 435
PRIOR APPLICATION: ATA:
APPLICATION: NUMBER: US/ e/4**/**
ATIORNEY/AGENT INFORMATION:
NAME: BIOOK DATE:
REFERENCE/OOKET NUMBER: CP194-13A
TELECOMMUNICATION: NUMBER: CP194-13A
TELECOMMUNICATION: NUMBER: CP194-13A
TELECOMMUNICATION: NUMBER: CP194-13A
TELECOMMUNICATION: 10-0000-10-0000-10-0000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10-000-10
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Local Similarity 45:5%: Fivd: No. 6:52e-51:
Nes 16: Conservative 5 Mismatches 5: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1255 AA
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1266 AA; 144957 MW; .588372 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT:
                                                                                                                                               TOPOLOGY: Linear MOLECULE TYPE: protein FENCE 130 AA: 15301 MW: E+1'% CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08468557 Patent No. 5759833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08468557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Militia Drive
CIIY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1256 amino ac: 1s
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                                                                                                 130 amino acids
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                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acid
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                                                                                                                                 TYPE: amino acid
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TELEX: 899149
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MOLECULE TYPE:
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AC XXXXX

AXX XXXXX

DI XXX XXXXX

EX SEQUENCE 4, APPLI XXX

SEQUENCE 4, APPLI XXX

SEQUENCE 4, APPLI XXX

CO SEQUENCE 1, NO. 57596

CO SECRET 1, NO. 57596

CO CORRESPONDENC APPLICANT: S APP
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                     Query Match
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                                                           Score 66: DB 5: Lenuth 86: Pred. No. 5.45e-01: 6: Mismatches 7: Indels
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C.MPDTER READSHE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/467.046
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    130 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRICK APPLICATION:
PRICK APPLICATION DATA:
APPLICATION UNPER: US 37/944,055
FILING CATE: 26 - UN 1992
APPLICATION NUMBER: AU POLGE!
FILING CATE: 26 - SUP-198
PRICK APPLICATION NUMBER: AU POLGE?
FILING DATE: 26 - SUP-198
FRICK APPLICATION NUMBER: AU POLGE?
FRICK APPLICATION NUMBER: AU POLGE?
FRICK APPLICATION NUMBER: AU POLGE?
FRICK DATE: 26 - SUP-198
PRICK APPLICATION NUMBER: AU POLGE?
FILING DATE: 26 - SUP-198
PRICK DATE: 26 - SUP-1989
PRICK DATE: 26 - SUP-1999
FRICK DATE: 26 - SUP-1999
ATTORNEY AGENT INFORMATION:
NAME: YAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BENT, STEPHEN A
REGISTRATION NUMBER: 29,768
REFRENCE/FOCKET NUMBER: 16786/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9309
TELEPHONE: (703)836-9109
                                                                                                                                                                                                                                                                                                                                                                                                    P. F. F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/U8467046
Patent No. 5348644
GENERAL INFORMATION:
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85 AA; 9549 MW: 41530 CN;
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                                                                  Match
Cocal Similarity 38.1%;
es 8: Conservative
                                                                                                                                                                                                   57 YXDIIVFKCUKGFVLKGSSVI
                                                                                                                                                                                                                                                                                                                                                                                                    US-08-467-046-12
      SECUENCE
                                                                         Query Match
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Gaps

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Sequence 2, Application US/07584135A
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                                                                                                  CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.8%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                linear
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 YNNNEAFKVERRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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US-07-684-135A-2
                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                   APPLICANT: Law, Marcus
APPLICANT: Hebara, Ledare
APPLICANT: Reddick, Bradford B.
TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and
TITLE OF INVENTION: Jose Therefor
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
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                                                                                                                                                                                                                                                                                                                                  CUCDANTIAN 25466
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18th PC COMPALIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/08/416,603
                                                                                                                                                                                                                                                                               ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street. Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FNCE 3457 AA: 388866 MW, 61731914 CN:
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTORNEY AGENT INFORMATION:
NAME: Lloyd, Jeffrey
REGISTRATION NUMBER: 35,589
FELEPHONE: 904-375-8130
INFORMATION FOR SECUTION: 4,589
ENOUGH FOR SECUTION: 4,580
                                                                                                                                                                  Sequence 4, Application US/08416603
Patent No. 5866780
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08452083
Patent No. 5756327
                                                                                                                                             Sequence 4, Application US/08416503
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                                                                            STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 NNEAFKVERREIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYPE: amino acid
TOPOLOGY: linear
                      11 YNNNEAFKVERRF 23
        75 YAHQSGFHVDRRF 87
                                                                                                                                                                                                                                                                                                                              USA
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ID US-08-452-083-2
                                                                           05-08-416-603-4
                                                                                                                                                                                                                                                                                                                            COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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APPLICANT: Sassanfar, Mandana
APPLICANT: Schimmel, Paul R.

IIILE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISTLEUCHITENA
IIILE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS
NUMBER OF SEQUENCES:
ADDRESSEE: Hamilton: R.OCK. SEITH & REYROLDS. P.C.
STREET: Two Militia Dr.Ve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52: DB 1: Length 1045:
Pred. No. 1.17e-02;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07684135A
Patent No. 5243039
GENERAL INFORMATION:
APPLICANT: Schendel, Frederick J. and
APPLICANT: Flickinger, M. C.
TITLE OF INVENTION: Bacillus MGA 3 Aspartokinase
TITLE OF INVENTION: II Gene
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant 6 Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUNESSEE: Merchant & Gould STREET: 3100 No. 5243039west Center CITY: Minneapolis STATE: Minnesota CCUNTR: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LE TYPE: protein
1045 AA; 117659 MW: 5476572 CN;
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Sequence 18, Application US/08%67941
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                                                                                                                                                                                                                                                                                            : 500 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANCARD:
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.5%;
Best Local Similarity 27.3%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                              LENGTH:
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Parent No. #1972
GENERAL No. #1972
GENERAL No. #1972
APPLICANT WINCHE FINALS WASPLICANT WINCHELD FOR STATE FOR THE STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 29.5%: Snore 61: DB 1: Length 411;
Local Similarity 30.4%; Pred. No. 1.42e+02;
les 7; Conservative 5; Mismatches 10: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/307,499 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Aspartokinase II '- dimer subunit
LOCATION: 1 to 411
GE 411 AA: 44310 MM: 899934 CN:
                                                                                                                                                        NAME: WOOSSNET. MATHEN D.
HEGISTHATION NUMBER: 30,440
AETERRENCE/SOCKET NUMBER: 600,215-US-C1
TELEPHONE: (612) 33-5300
TELEPHONE: (612) 33-5300
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: AMINO ACID
TOTAL AND ACID
TOTAL AND ACID
TOTAL AND ACID
         MEDIUM TYPE: Diskette, 3.5 inch, 77 KE COMPUTER: No. 5243039thqate 386 OPERALING SYSTEM: DGS 4.0 SOFTWARE: MordPerfect 5.0 CURRENT APPLICATION DATA: DS/O7/684,135A FILING DATE: 19910412 CLASSIFICATION: 435 AIRONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PHIOS APPLICATION DATA:
APPLICATION NUMBER: US 27/908,241
FILLING DATE: 1-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08307499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 KAEKCDIYIDVIGVETTDPRYVK 187
                                                                                                                                                                                                                                                                                                                                            GY: Linear
TYPE: Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KNEGINIYNN-NEAFKVERRFIK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy of
OUMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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SEQUENCE 411 A
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Sequence 18, Application US/1886/341
Patent No. S947301
GENERAL INFORMATION
APPLICANT LOSSOCIE, Sheena M
APPLICANT LOSSOCIE, Sheena M
APPLICANT WANG, UGL)UG
APPLICANT WANG, UGL)UG
APPLICANT WANG, VALPING
APPLICANT WANG, UGL)UG
APPLICANT WANG, MANGERE CONTRES ON GENERAL ADDRESSEE SAME AMBURED
ADDRESSEE SIME AMBURED
STREET GENERAL FLOOR, 330 INIVERSITY AVENUE
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STREET: 6th Floor, 330 University Avenue
STREET: 18th Floor, 18t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24 4973
REFERENCE/DOCKET NUMBER: 1038-681 MIS: 3b
TELECOMMUNICATION INFORMATION:
TELEPRONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF35.1.FWCC3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-U0N-1992
CLASSIE/CATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/142,212
FILING DATE: 21-APR-1992
CLASSIE/CATION: 435
ATOMES ABINACHIS, DAVID R.
NAME: SAINACHIS, DAVID R.
REGISTRATION NUMBER: UF 95.1.FWCCCNOKET NUMBER: UF 95.1.FWCCCCNOKET NUMBER: UF 95.1.FWCCCCNOKET NUMBER: UF 95.1.FWCCCNOKET NUMBER: UF 95.1.FWCCCNOKET NUMBER: UF 95.1.FWCCCCNOKET NUMBER: UF 95.1.FWCCCCONOKET NUMBER: UF 95.1.FWCCCCO
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MOLECULE IYPE: protein
JENCE 500 AA; 57475 MW; 1384311 CN:
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                                                                                                                                                                                                                                                                        APPLICANT: Lossmore, Sheera M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Van Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: LATOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                   STATE: OLDSTICE
STATE: OLDSTICE
STATE: OLDSTICE
COUNTRY: Canada
ZERE: MSJ 187
COMPUTER: Eloppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: APPLICATION NOWABER: US/08/467,941
FILING DATE: 03-UOK-1997
CLASSIFICATION NOWABER: 1038-681 MIS:)b
FELECOMMUTCATION NUMBER: 24,973
REFERENCE/DOCKT NUMBER: 24,973
REFERENCE/COCKT NUMBER: 1038-681 MIS:)b
FELEPHONE: (416) 595-1163
INFORMATION FOR SEQUENCE CHARACTERISTICS:
FENCTH: 541 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 2; Length 541;
Pred. No. 1.42e+62;
5; Mismatches 3; Indels
                                                                                   Length 538;
                                                                                 Score 61; DB 2; Length 538;
Pred. No. 1.42e+02;
5; Mismatches 3; Indeis
                                                                                                                                                                                541 AA
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sim & McBurgey
STREET: 6th Floor, 330 University Avenue
CITY: Toron, 530 State: 5tate: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OGY: linear
541 AA: 50740 MW; 1494681 CN;
                                                        TOPOLOGY: linear
CE 538 AA: 60417 MW: 1483780 CN:
                                                                                                                                                                                                                                                       Sequence 14. Application US/08867941
Pathot No. 5977337
                                                                                                                                                                                                                                      Sequence 14, Application US/08867941
TELEFAX: (416) S95-1163
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                            : 538 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 541 amino acids IYPE: amino acid
                                                                                                                                                                               STANDARD;
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ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                               single
                                                                                 Query Match
Best Local Similarity 56.0%:
Matches 8; Conservative
                                                                                                                       6 KTNPALKVKHRFLKQV 21
                                                                                                                                   : 1 | 1:.. : 11:1:1
12 NNNEAFKVERRFIKRV 27
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GENERAL INFORMATION:
APPLICANT: LOSSICE
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Best Local Similarity
Matches 8: Conserv
                                              STRANDEDNESS:
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US-C8-867-941-14
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                                                                 SEQUENCE
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6 KINPALKVKHRFLKQV 21

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                                                                                                                                                                         Sequence 2, Application US/08804439A
Patent No. 601555
GENERAL INFORMATION:
APPLICANT: ROSE, Marchy M.
APPLICANT: Bose, Marchy M.
APPLICANT: Strand, Wurt
TITLE OF INVENTION: GLYCOPROJEIN B OF THE REHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION FU-DCS/MS-DGS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.439A
FILING DATE: Februa 11, 1997
VITORNY APPLICATION: 424
                   128 AA
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson P.C. SIREET: 4225 Executive Square, Ste 1400 CITY: La Jolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 39176/204001
ELECOMMUNICATION INFORMATION:
TELEPHONE: (519) 678-5070
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
I.P. 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LE TYPE: protein
128 AA; 14821 MW: 97091 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: Tue Jun 20 13:34:29 2000 Job time : $ secs.
                                                                                                                                        Sequence 2, Application US/08804439A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMA. N:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 128 amino acids TYPE: amino acid STRANDEDNESS: single
                     STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEC 10 NU-SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSS: Single
linear
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US-08-804-439A-2
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyriant (c) 1993-1998 University of Edinburgh. U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp - protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:23:02 2000: MasPar time 16:08 Seconds 194:302 Million cell updates/sec Run on:

Tabular output not generated.

>US-16-142-524A-5 (1-31) from US09142524A.pep 207 | SSCKNEGINIYNNNEAFKVERREIKRVSHVI 31 Title: Description: Perfect Score: Sequence:

FAM 150 Gap 11 Scoring table:

721208 seqs. 100765575 residues Searched.

Post processing:

Minimum Match 0% Listing first 45 summaries

Satabase:

a-pending liPCT 2.05 3.050 4.07 5.080 6.081 7.082 8.083 9.084A liCEB4R 11:085 12:086 13:087 14:088 15:089 16:090 17:091 18:092 19:093 20:094 21:09 22:NEWP 23:NEWU60 24:NEWU8 25:NEWU9

Mean 25.118; Variance 80.992; scale 0.310 Statistics:

Pred. No. 18 the number of results predicted by charce to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	5.98e-14	1.73e-C2	1.73e-02	1.73e-02	1.73e-02	1.73e-02	1.73e-02	1.73e-02	2.60e-01	2.60e-01	2.60e-01	2.60e-01	2.50e-01	6.84e-01	6.84e-01	5.84e-01	6.84e-01	5.84e-01	6.84e-01	5.84e-C1	
	ption	se 5, Applicatio	-4	9.5	n)	55	in in	S, S,	95	261,	261,	261,	251,	261,	57, 2	57,	5.7	91,	. 5	91,	132,	
	Description	Sequence	Sequence	Sednence	Sednerce	Sednesce	Sequence	Sequence	Sequence						Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	
CO TAMANDA	01	US-09-142-	US-60-109-	US-08-226-	US-08-467-	US-08-467-	US-08-467-	US-08-350-	US-08-468-	US-08-467-	CS-08-320-	CS-08-467-	US-08-467-	US-08-468-	US-09-468-	US-07-938-	US-08-320-	US-08-226-	US-08-350-	CS-08-457-	us-08-468-	
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	Length	3.5	346	367	367	367	367	367	367	36	3C	30	30	30			20	26	26	25	28	
.*	Opery Manch	100.0	52.2	52.2	52.3	52.2	52.3	52.2	52.2	6.00	46.9	6.34	46.9	46.9	44.9	6.44	44.9	44.9	44.9	4.9	4.0	
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ID US-08-467-023-95
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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GENERAL INF-MANION:
APPLICANT GULDSMARD G.
APPLICANT: MIDARO-HURCITI, TERUMI
TITLE OF INVENTION: PROTEIN IN MOUNTAIN CEDAR PULLEN THAT BELCONGS TO A
TITLE OF INVENTION: PROTEIN IN MOUNTAIN CEDAR PULLEN THAT BELCONGS
TITLE OF INVENTION: PRAMILY OF PLANT PATHOGENESIS ACLATED PROTEINS
CURRENT APPLICATION NUMBER: 1998-11-20
CURRENT FILING DATE: 1998-11-20
SOFTWARE: PATHOLIC VAE: 2.0
SOFTWARE: PATHOLIC VAE: 2.0
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APPLICANT: Praint, Andrew;
APPLICANT: Braint, Andrew;
APPLICANT: Edwars, Steven P.
ITLE OF INVENTION: Allergence Proteins And Peptides From IIILE OF INVENTION: Allergence Cedar Poilen
NUMBER OF SECUENCES: 201
AUMBER OF SECUENCES: 201
AUMBERSEE INVENTION: Allergence Cedar Poilen
STREET: 610 Lincoln St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 108: DB 3: Length 346:
Pred. No. 1.73e-02;
1: Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRCANISM: Juniperus ashei
SEQUENCE 346 AA: 37639 MW; 616983 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95, Application OS/08/22/248A OSEBEAL INPRMATICAN
APPLICANIES STATEMENT OF THE APPLICANIES POILORS, CONDUCT
APPLICANIES POILORS, CONDUCT
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                   PR1:
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                                                                                                                                         Sequence 1. Application US/60109165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carman, Richard D: APPLICANT: Kuo, Melichang:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 SSGKTERRINIYNSNEAFKVE 330
                     STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Hest Local Similarity 85.0%:
Matches 17: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIREET: 610 Li
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AC XXXXXX
DI SEQUENCE 95, APPLION
XX DE SEQUENCE 95, APPLION
CO GENERAL INP-MANING
CO APPLICANI BYA
CO CONTRACTOR

RESULT 2
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CC RASPICATION WROPER. 1979/226.248A

CC RASPICATION WROPER. 12, 1959

CC RASPICATION WROPER. 1, 1959

CC RASPICATION WROPER. 1, 1950

CC RASPICATION WROPER. 1, 1950

CC RASPICATION WROPER. 1, 1950

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COUNTRY:
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                                                                                                                                                                                                                                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Policek, Joanne:
APPLICANT: Bond, Julian F.!
APPLICANT: Bond, Julian F.!
APPLICANT: Garman F.!
APPLICANT: Brauer, And Mei-Chang:
APPLICANT: Brauer, Andrew:
APPLICANT: Braner: Steven P.
IITLE OF INVENTION: Japanese Cedar Pollen
NYMBER (FF SEQUENCES: 26:
APPLICANT: ALREWSES:
APPLICANT:
                                                                                                                                                                                                                                                                                 ::
                             Query Match 52.2%, Score 108; Us 10: Length 367; Best Local Similarity 85.0%; Prod. No. 1.73e-02; Astobes 17: Conservative 1: Mismatches 2: Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TITTEL FLORDY disk
COMPUTER: 15M PC COMPATIBLE
DEFRAINS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIS Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,006
FILING DATE: Jone 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATIONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jace E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/JOCKET NUMBER: 025.6 USD6 (IMI-U28CPD6)
IELECONALIDATION INFORMATION:
TELEPHNINE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                         367 AA.
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F. 3.
                                                                                                                                                                                                     E TYPE: protein
367 AA; 39846 MW: 695078 CN:
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FILING DATE: December 6, 1994
ALTORNEY/AGENT INFORMATION:
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Waltham
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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SEQUENCE 36
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APPLICANT: Yeung, Siurnei h.;
APPLICANT: Yeung, Siurnei h.;
APPLICANT: Brauer, Andrew:
APPLICANT: Exley, Mark A:
APPLICANT: Exley, Mark A:
APPLICANT: POWERS, Steve: P.
TILE OF INVENTION: Alle Genic Protess: And Peptides From NUMBER OF SECUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLoqic Planmaceutical Corporation, Inc
STREET: 610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.2%; Score 108: FB 10: Length, 367:
Best Local Similarity 85.0%; Pred. No. 1.73e-02;
Matches 17: Conservative 1: Mismatches 2: Indels
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MOLECULE TYPE: protein
SEQUENCE 367 AA: 39846 MW: 695078 CN:
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APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.;
TELEFAX: (617) 227-5941
INFORMATION FOR SEC 1D NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD
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STATE: MA
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ID US-08-467-697-95
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SEQUENCE
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APPLICANT GILIGECH, JANN J.;
APPLICANT Pollock, Joanne;
APPLICANT Garman, Richard J.
APPLICANT Garman, Richard J.
APPLICANT Garman, Richard J.
APPLICANT Young Sidence;
APPLICANT FILEY, MARY A.;
APPLICANT POWERS, Steven P.
ITTLE OF INVENTION: Alerquic Proteins And Peptides From JITLE OF INVENTION: Japanese Gedar Follen
NURBER OF SEQUENCES: 261
                                                                  Ö
                               cuery Maich
Best Local Similarity 85.0%; Pred. No. 1.736-02:
Matches 17: Conservative 1: Mismatches 2: Indols :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ImmuLoqic Pharmaceutical Corporation, STREET: 610 Lincoln St. CITY: Waltham
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SOFTWARE PALENTIN BAIN
CURRENT APPLICATION DAIN
FILLS
FILLS
CLASSIFICATION 44
PRICE APPLICATION 144
PRICE APPLICATION 144
FILLS
FIL
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REGISTRATION NUMBER: 35,729
REFECONATION NUMBER: 025.6 US (IMI-028CP2)
TELECONATINICATION INFORMATION:
TELEPHICNE: (617) 466-600
TELEFAX: (617) 466-604
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: September 1, 1992
APPLICATION NUMBER: PGI/US93/60139
                                                                                                                                                                                                          PRT:
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357 AA: 39846 MW: 695078 CN:
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
367 AA: 39846 MW: 695078 CN;
                                                                                                                                                                                                                                                                                                                                               Application US/08350225
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             Sequence 95, Application 05/08350225
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anino acid
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                                                                                                     332 SSCHTEETNIYNSNEAFKVE 351
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CUMPUTER FRACABLE FORM:
MEDIUM TYPE: FLORBY 4'
COMPUTER: IRW
OPERATOR
                                                                                                                           1 SSGKNEGINIYNNNEAFKVE 20
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APPLICANTS STIFFE
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IYPE: amin
TOPCLOGY:
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 SECUENCE
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DB 8: Length 367;

52.2%: Score 108:

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APPLICANT Griffell, Irwin J.
APPLICANT Bold-Cak, Joannel
APPLICANT Bond, Julian F.
APPLICANT Kuo, Mai Chan
APPLICANT Yeung, Surve, H.
APPLICANT Yeung, Surve, H.
APPLICANT Power, Surve, H.
APPLICANT Powers, Steven P.
IIILE OF INVENTION: Allergenic Proteins And Peptides From
IIILE OF INVENTION: Japanese Gedar Poilen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immuloqic Pharmaceutical Corporation. Inc
STREET: 610 Lincoln St
CITY: Waltham
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CC APPLICATION NUMBER: C/294
CC APPLICATION NUMBER: C/294
CC ALLING DATE: September 1, 1994
CC FILING DATE: January 15, 1994
CC FILING DATE: January 15, 1993
CC FILING DATE: January 16, 1993
CC FILING 
                                                Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comina* ble
COMPUTER: SEM PC comina* ble
COMPUTER: Batch PC-FC-8/MS-DC-S
SOFTWARE: Patchtin Peleise #1.0. Version #1.25
CURRENT APPLICATION DATA:
Best Local Similarity 85.0%; Pred. No. 1.73e-02;
Matches 17; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                           367 AA
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Best Local Similarity 85.0%; Pred. No. 1.73e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/468,940 FILING DATE: US/08/468,940 TIANSISTONIEN 424 PRICE AFFICATION DATE: 9/15 22 PILING DATE: DECEMBER 4/15 22 PILING DATE: DECEMBER 4/15 22
                                                                                                                                                                                                                                                                                                                                                                                                           58.7
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JENCE 367 AA: 39846 MW; 695078 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08468940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 95, Application US/08468940
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD.
                                                                                                                                  332 SSGKIEETNIYNSNEAFKVE 351
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TOPCLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Griffe
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COUNTRY: USA
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Gaps
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GENERAL INFORMATION:
APPLICANT Griffeth, Irwin J.:
APPLICANT Pollock, Joanne:
APPLICANT Pollock, Joanne:
APPLICANT FORMATION:
APPLICANT Garman, Richard D:
APPLICANT Kuo, Mei-chang :
APPLICANT Kuo, Mei-chang :
APPLICANT Kuo, Mei-chang :
APPLICANT Braver, Andrew:
APPLICANT Braver, Andrew:
APPLICANT Braver, Steven P.
TILLE OF INVENTION: Allerqunic Proteins And Peptides From ITILE CF INVENTION: Allerqunic Cedar Polien
NUMBER OF SEQUENCES: 261
CORRESPENDENCE ADDRESS:
APPLICANT STANDARD ST
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MEDIULY IYEE: Floppy disk COMPUTER FEADABLE FORM:
MEDIULY IYEE: Floppy disk COMPUTER ISM PC COMPATIBLE COMPUTER ISM PC COMPATIBLE COMPUTER ISM PC COMPATIBLE CONTRIBUTION DATA:
SOFTWARE: PALENTIN RELEASE 1.C. Version 1.25
CURRENT APPLICATION DATA:
FILING NATE: June 6, 1995
CLASSIFICATION LAST AND APPLICATION NUMBER: C. 1995
FILING THE UP-COMPATION COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATION NUMBER: SEGISTATION NUMBER: 38.872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-0285PD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-74 00
TELEPAX: (617) 227-5541
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Indels
                                                                                                                                  30 AA
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Local Similarity 55.7%; Pred, No. 2.60e-01;
es 14; Conservative 4; Mismatches 3;
Mismatches
                                                                                                                                  PRT;
                                                                                                                                                                                                                                Sequence 251. Application US/08467023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 30 AA: 3375 MM: 4852 CN:
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                                                                                                                                 STANDARD:
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                                 332 SSGKTEETNIYNSNEAFKVE 351
                                                     1 SSGKNEGINIYNNNEAFKVE 20
17: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
SY: linear
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                                                                                                                  RESULT 9
ID US-08-467-023-261
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STATE:
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.9%; Score 97; DB 8; Length 30; Best Local Similarity 56.7%; Pred. No. 2.60e-01; Matches 14; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PE-Tase *.C. Version *1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/350,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Carlene A. Varistone
REGISTRATION NUMBER: 55.725
REFERENCE/DOCKET NUMBER: 25.6 US (IMT-028CP2)
TELECOMMUNICATION INFORMATION:
   30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROD APPLICATION DATA:
APPLICATION NUMBER: 08/226.248
FILING DATE: APRIL 9. 1 con 4
APPLICATION NUMBER: 07/98.990
FILING DATE: September: 1, 1992
APPLICATION NUMBER: PT (0593/00139
FILING DATE: 3acusty 15, 1993
ATICKNEY/AGENT INFORMATION:
   PRT;
                                                                                                     Sequence 251, Application US/08350225
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CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 30 AA; 3375 MW: 4852 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 261:
   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 SSGKYEGGNIYTKKEAFNVEK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-350-225-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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RESULT

1 SSGKNEGTNIYNNEAFKVER 21

SSGKYEGGNIYIKKEAFNVEK 29

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APPLICANT: Bond, Julian: Bapplicant: Garman, Richaru E. APPLICANT: Garman, Richaru E. APPLICANT: Woung, Siu-mei H. APPLICANT: Weung, Siu-mei H. APPLICANT: Brauer. Andrew. APPLICANT: Exley. Mark A. Bapplicant: Exley. Mark A. Bapplicant: Provers. Sieven P. TITLE OF INVENTION: Allerquence Cedar Follen WABBE OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%: Pred. No. 2.60e-51,
Matches 14; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lenath 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         025.6 USD4 (IMI-028CHD4)
No
                                                                                                                                                                                                                                               ADDRESSEE: Immuloqic Pharmaceutical Corporation, STREET: 610 Lincoln St CIIY: Waltham
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMMUTER: IBM PC compatible
COMMUTER: IBM PC compatible
CORRATING SYSTEM: PC-FCS/NS-DOS
SOFTWARE: Patentin Release #1.6. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/U8/467,697
FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 261 Application US/08468940
GENERAL INFORMATION:
APPLICANT: GIffeth, Irwin J.;
APPLICANT: POLicek, Joanne:
                           261, Application US/08467697 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 261, Application US/08468940
 Sequence 261, Application US/08467697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/350.225
                                                       Griffeth, Irwin J.
Pollock, Joannel
Bond, Julian F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 38/3
FILING DATE: December '
TATORNEY/AGBNI INFORMATION
NAME: Jane E. Remilian-
REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER TELECOMMUNICATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 227-59: INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 amino acius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 SSGKYEGGNIYTKKEAFNVEK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODERALE TYPE: preptude
FRAGMEN: TYPE: interna-
ENCE (0 AA: A*TS MW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGKNEGTNIYNNEAFKVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-468-940-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                       02154
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                              Sequence 261
                                            GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECTINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                     APPLICANI ... us/U8467006

APPLICANI GILLELH, Irwin J.;
APPLICANI Belid, Johns F.;
C APPLICANI Baman, Ribard D.;
APPLICANI Samman, Ribard D.;
APPLICANI Samman, Ribard D.;
APPLICANI Samman, Ribard D.;
APPLICANI Belid, Julian F.;
APPLICANI Belid, Mark M.;
APPLICANI EXLEY, Mark M.;
APPLICANI EXLEY, Mark M.;
APPLICANI EXLEY, Mark M.;
APPLICANI BALLON Japanese Cedar Pollen
NUMBER OF SEQUENCES: 26;
CORRESPENDINGE ADDRESS:
ADDRESSES: Inmutox. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                 Match 46.9%; Score 97; DB 10; length 30; Local Similarity 66.7%; Pred. No. 2.60e-31; es 14; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jack E. Remillard
REGISTATION NUMBER: 36.82
REFEREN'S/COCKET NUMBER: 025.6 USD6 (IMI-128CPD6)
PELECOMMUNICATION INFORMATION:
TELEPHINE: (617) 227-7400
INFORMATION FOR SEQ. U.No. 261;
SEQUENCE PRARACTER/SPICS:
LENGTH 30 amino acids
IVPE: GAILLO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible chemating system: PC DOS/XXS-DOS COSTEMATING SYSTEM: PC DOS/XXS-DOS COSTEMATES: PATENTIAL RElease #1.0. Version #1.25 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/467.036 FILING DATE: June 6. 1995 CLASSIFICATION: June 6. 1995 PRIOR APPLICATION: DATA:
 30 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 AA
PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: C8/350,225
FILING DATE: December 5, 1994
ATTORNEY/AJENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
MCLEGULE IVPE: peptide
FRAGMENT IVPE: internal
JENCE 36 As: 3375 MW: 4852 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                      CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 SSGKYEGGNIYTKKEAFNVEK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-457-697-251
 38-08-467-006-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY
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15 US
XX
XX
XX
XX
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XX
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APPLICANT: Garman.
APPLICANT: Garman.
APPLICANT: Kuo, Mei-chanu:
APPLICANT: Fung. Siu mei H.:
APPLICANT: Brauer. Andrew;
APPLICANT: Brauer. Andrew;
APPLICANT: Brauer. Andrew;
APPLICANT: Powers. Stew n.P.
TITLE OF INVENTION: All tuanic Proteins And Peptides From TITLE OF INVENTION: All tuanic Proteins And Peptides From TITLE OF INVENTION: All tuanic Proteins and Peptides From NUMBER OF SEQUENCES: 26;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immiliagic Pharmaceutica; Corporation. Inc STREET: Tham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
44.9%: Score 95, 3B 10; Lenath 23;
Best Local Similarity 76,0%: Pred. No. 6.84e-01;
Matches 14: Conservative :: Mismatches 3; Indels
                                                                                                                                                                                                      CONTROL CAN
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC S/MS-DCS
SOFTWARE: PARENTIN Re ease *1.0, Version *1.25
CURRAY APPLICATION DATA
APPLICATION NUMBER: 18/09/466.940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Datlene A. Vanstone
REGISTRATION NUMBER: 35.729
RECISTRATION NUMBER: 35.729
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 18F08MATION:
TELECHONE: (617) 466.6040
INFORMATION FOR SEC ID NO: 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AA
                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 0 350,225
FILING DATE: December: 1994
APPLICATION NUMBER: 0 1994
APPLICATION NUMBER: 0 1994
APPLICATION NUMBER: 0 1994
APPLICATION NUMBER: 0 1993
APPLICATION NUMBER: 0 1993
APPLICATION NUMBER: 0 1993
APPLICATION NUMBER: 0 1993
ATTORNEY/AGENT INFORMATION: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/07938990A
GENERAL INFORMATION:
APPLICANT: GILFLICH, ITWIL J.
APPLICANT: POLIOCK, JOANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/07938990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODECTAR TYPE: POPULA
FRASMENT TYPE: Internal
SECORNOR 20 NA: 2221 MM. 2174 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 20 amino acida
TYPE: amino acid
TOPCLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SSGKYEGGNIYTKKEAFNVE 20
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US-07-938-99CA-57
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                    APPLICANT: Garman, McChang D:
APPLICANT: Veung, Stu-met H.;
APPLICANT: Veung, Stu-met H.;
APPLICANT: Extery, Mark A.;
APPLICANT: Extery, Mark A.;
APPLICANT: Extery, Mark A.;
TILLE OF INVENTION: Altergenic Proteins And Peptides From TILLE OF INVENTION: Japanese Cedar Pollen
VUMBER OF SEQUENCES: 26;
CARRESPONNENCE ADDRESS:
ADDRESSEE: Irrulouic Pharmaceutical Corporation. Inc.
STREE: MA
COUNTRY: USA
STREE: MA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
FLING DATE:
FLING DATE:
CLASSIFICATION 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
RESCREMENSCHOOLOGE (IM:-028GP2)
TELECRAMINICATION INFORMATION:
TELEPHONE: (617) 466-600
INDOMATION FOR SEC ID NO: 261:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350.225
FILING DATE: December 6, 1994
APPLICATION NUMBER: 08/226.249
FILING DATE: APTI 8, 1994
APPLICATION NUMBER: 07/938.990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/0593/06139
FILING DATE: January 15, 1993
ATTORNEY/ADENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/08468940
GENERAL INFORMATION:
APPLICANI: Griffeth, Irwin J.;
APPLICANI: GLIFETH, JOANNE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/38468943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.DECLE TYPD: poptide
FRAGMENT TYPE: 2010/0003/
SEQUENCE 30 AA: 837f MW: 4852 CN:
               Garman, Richard D:
 Bond, Julian F.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 amino acids
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US-38-468-940-57
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APPLICANT: Bond Julian
TILE OF INVENTION: Aliergenic Proteins And Peptides From
ITILE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: OCKETED
CORRESPONDENCES: Calive & Cockield
STREET: Sixty State Street
CITY: Boston
STATE: Was
CCUNTRY: Usa
CCUNTRY: Usa
CCUNTRY: Usa
CCUNTRY: Usa
CCUNTRY: Usa
CCUNTRY: Usa
CCHAILING SYSTEM: PC-DOS/WS-DOS
SUSTRMET: Parentle Foam:
MEDIOW ITYPE: Ploppy disk
CCMPUTER: TBW PC Compatible
CPERATING SYSTEM: PC-DOS/WS-DOS
SUSTRMET: Parentle Release 41.0, Version #1.25
CMPUTER: TBW PC Compatible
CPERATING SYSTEM: PC-DOS/WS-DOS
CHAME: Parentle Release 41.0, Version #1.25
CMPUTER: Day 10.5
CMPUTER: Day 10.5
CMPUTER: Day 10.739, 134
FILING SATE: July 10.199
APPLICATION NUMBER: US/729,134
FILING DATE: July 10.199
ATTORNEY/AGEN: UNDER 190, 199
ATTORNEY/AGEN: UNDER 190, 199
ATTORNEY/AGEN: NUMBER: 190, 199
ATTORNEY/AGEN: NUMBER: 190, 199
ATTORNEY/AGEN: UNDER 190, 190
IELERAN: (617) 227-14.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cuery Match 44.9%; Score 93: DB 4: Leath 20:
Hest Local Shilarity 70:0%; Pred. No. 6.846-01:
Matches 14; Conservative 3; Misratches 3; Chels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FRACMENT TYPE: internal
SEQUENCE 20 AA; 2221 MW; 2174 CN:
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S. C. S.

Search completed: Mon Jun 19 16:23:33 2000 Job time : 31 secs

1 SSGKYRGGINIYIKKEAFNVE 20 | 1111 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131 | 131

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Release A.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:02:46 2000; MasPar time 5.20 Seconds 281.442 Million cell updates/sec Rup on:

Tabular output not generated.

>US-09-142-524A-5 (1-31) from USO9142524A.pep (207 : SSGKNEGINIYNNNEAFKVERRFIKRVSNVI 31

Description: Perfect Score: Sequence:

PAM 150 Cap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir62 lipirl 2:pir2 3:pir3 4:pir4 Satabase:

Mean 32.523; Variance 57.974; scale 0.561

Statistics

Pred. No. is the number of results predicted by mance to have a score greater than or equal to the score of the mosult being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score	r.	Quorry Materi		Jenett	Ę.	QI .	Description	Pred. No.
, , , ,	93	•	. o		i na	JC2124	major alleraes Gry A	2.65e-03
~	63	4	œ	374	~	JC2123	allergen	2.65e-03
~	82	39	9	344	~	A47025	abortive phage resist	
•	82	w S	٥	344		527587	ein - Lacto	.54e-
	80		s.	1161		S66730	pr	3.14e-01
	30	33	r-	1308		E71622	probable membrane ass	6.32e-01
	75	36.	~	2380		E71604	hypothetical protein	1.77e+GC
	7.2	34.		256		A32017	beta-lactamase (EC 3.	4.84e+00
	7.5	34	ø	260		S11984	fapR protein - Escher	
	22	34	œ,	317		B72216	endoglucanase - Therm	4.84e+00
	72	34.	œ	1355	~	S51995	probable ATPase (EC 3	4.84e+00
	5	3.4	٣.	257		PNBS28	beta-lactamase (EC 3.	6.72e+00
	۲,	, M	m	257		PNBSU2	beta-lactamase (EC 3.	5.72e+00
	70	ж ЭЭ	œ.	259	ď	150727	sensory organ homeobo	9.31e+C0
	7.0	tr)	œ.	641		F71810	type III DNA modifica	9.31e+00
	69	(*)	٣.	323		H64130	glycosyl transferase	1.29e+01
	59		٣.	266		S17477	hypothetical protein	
	69		٣.	1356		S	ROM2 protein - yeast	1.29e+01
o.	80	32.	6	453		_	probable permease - C	۲.
ی	80	3.5	σ.	61C		161	asparagine tRNA liga	۲
r 1	99	32.	σ.	623		A45050	transketolase (EC 2.2	1.77e+01
	89	32.	6	626		A42891	beta-galactosidase (E	1.77e+01
	68	32.	σ.	929		151027	type XII collagen alp	1.77e+01

	2.4 158 2 F65103 PTS system, n-acetylg 2.41e-0 2.4 168 2 PN0660 nitrogenase (EC 1.18, 2.43e-0 2.4 440 2 114436 conserved hypothetica 2.43e-0 2.4 440 2 114436 probable sexime/threo 2.43e-0 2.4 1234 2 B56186 I factor 2 (transposo 2.44e-0 1.9 169 2 S77820 probable excludingses 3.32e-0 9 298 2 57820 knoothetical probable assituates 3.32e-0	4444444444	# CC212 # form major cedd # form #	### ##################################	JCJ123 *type complete major aliergen Cry j I precursor (clone pCCI-2-2) - Japanese cedar *formal_name Cryptomeria japonica *common_name Japanese 14-Jul-1994 *sequence_revision 14-Jul-1994 *text_change
NO SM	4W&\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	(ИК 4 00 0 C 00 0 C 11 0 M 4 0	ISM ISM ISM INDE INDO INDI INDI INDI INDI INDI INDI INDI	374 191,2 7 Matc 7 Matc 191,2 1 1 SS	ENIKI TITLE ORGANISM DATE

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Alb
                                                                                                                                                    Durmaz, E.; Higains, D.L.; Klaenhammer, T.K.
submitted to the EMBL Data Library, June 1992
Molecular characterization of a second austrive plane
resistance gene present within Lactocommus lantus ME.
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probable membrane associated protein PFB0125c - malaria
paraziace (Plasmodium falciparum)
*formal_name Plasmodium falciparum
13.Nov-1998 *text_change
                                                                   #Sequence_revision 06-Jan-1995 #text_change
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C.: Voss, H., Lemann, S.
Submitted to the Protein Sequence Database, July 1996
866730
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hypothetical protein Yol045w · yeast (Saccharomyces
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*region protein Kinase ATP-binding motif
*length 1161 *molecular-weight 124371 *checksum
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                    abic protein "Lacrococcus lactis (tragment) #formal_mane Lactoroccus lactis
06-Jan-1995 #sequence_revision 06-Jan-1995 #
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Pred. No. 1.54e-01:
12: Mismatches 6: Indels
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*formal_name Saccharomyces ceruvisiae
12-Jul-1996 *sequence_rowision 12-Jul-1999
$66730
  #type fragment
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Best Local Similarity 28.0%;
Matches 7; Conservative
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Best Local Similarity 26.9%;
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**molecu.e_type DNA
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839-1099
847-855
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##Molecule_tipe protein
##residues 22-53;56-81:219-242;236-258;299-367;346-372 ##!abel S02
##residues 22-53;56-81:219-242;236-258;299-367;346-372 ##!abel S02
##residues 279
CLASSFEIGATION #Superfamily pectate lyase LAT59
KENWORDS @!ycoprotein; poilen
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abortive phage restrance protein abid - Lactococcis lactis
sibsp. lactis (strain ME2) plasmid phys0
*formal_dare Lactococcus lactis subsp. lactis
-(9-May 1994 *sequence_revision 03-May-1994 *text_change
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NID:g493631: PID:d1006086: PID:g493632
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2. Bocteriol, 1992) Thirtigial-1469
Malecular characterization of a second abortive phage
resistance gene present in Lactococcus lactis subsp.
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Fleagth 344 *molecular-weight 40128 *checksum 3503
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tor Cry 5 I.
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NID:q149359; PID:q149360
                                                                                            #journal Blocken, Blophys. Res. Commun. (1994)
#Litle Cloning and sequencing of cDNA coding
active of Japanese cedar pollen.
#accession | 0:2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *molecular-weight 40645
                    JC2123: PC2065
JC2123
Sone, T.: Komiyama, N.:
K.: Kibo, K.
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##cross-references GB:M95956;
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##molecule_type DNA
26-Aug-1999
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#authors #journal #title ACTESSIONS REFERENCE

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Best Local Similarity 57.18;
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*Author Alayind L.; Koonin, E.V.; Shallon, S.; Mason, T.; Yu, K.;
*Eujin, C.; Pedoritz, D.C.; Shen, K.; Jing, J.; Aston, C.;
*Lai, Z.; Schwartz, D.C.; Pertea, M.; Salzberg, S.; Zhou,
**Li, Sutton, G.G.; Clayton, R.; White, C.; Smith, H.O.;
**Finser, C.M.; Adams, M.D.; Venter, J.C.; Hoffman, S.L.
**Schore (1998) 28:11126-1132
**Tille Plasmodium faltering human malaria parasite
**Toss:reference MJD:99021743
**Faccession #71604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
##cross-references GB:AE001374; GB:AE001362; NID:q3845100: PID:q3845132;
TISR:PFB0125c
              Authors Gardner, M.J.: Tettelin, H.; Carucci, D.J.; Cummings, L.M.;
Aravind, L.; Koonin, E.V.; Shallom, S.; Mason, C.;
Tujii, C.; Pederson, J.; Shen, K.; Jing, JJ; Aston, C.;
Tai, Z.; Schwartz, D.C.; Pertea, M.; Salzberg, S.; Zhou,
L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Fraser, C.M., Adams, M.D.; Venter, J.C.; Hoffman, S.L.
Fille Chromosome 2 sequence of the human malaria parasite
Across:references MILD:99021743
accession E71522
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hypothetical protein PFB3876w - malaria parasite (Plasmodium
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13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change
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Pred. No. 1.77e+00;
13; Mismatches 3; Indels
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Pred, No. 6.32e-01;
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Similarity 29.2%;
7; Conservative
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Best Local Similarity 46.2%:
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ANISM FORMER DESCRIPTION OF SEP-1999 REQUIRED OF SEP-1999 REGUIRED OF SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       *authors Lim, H.M.; Pene, J.J.; Shaw, R.W.
*journal J. Bacteriol. (1989) 170:2873-2878
*title Cloning, nuclectide sequence, and expression of the barillus cereus S/B/6 beta-lactamase II structural qune.
*cross-references MUID:88227879
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                                                    precursor - Bacillus celeus
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                                                                                                                                                              *formal_name Bacillus cereus
07-Jun-1990 *sequence_revision 07-Jun-1990 *text_Channe
22-Jun-1999
A32017
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endoglucamase - Thermotoga maritima (strain MSB8)
*formal_name Thermotoga maritima
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DNA binding: transcription regulation
#length 260 #molecular-weight 30349 #checksum
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Pred, No. 4.84e+00;
5; Mismatches 1; Indels
A32017 *type complete beta-lactamase (EC 3.5.2.6) II (strain 5/8/6)
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##residues 1-250 ## Del KLA
##cross-zeferences EMBL:X53494
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ORGANISM
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#authors Nison K.E.: Clayton, R.A.: Gill, S.R.: Gwinn, M.L.: Dodson, R.J.: Harkey, E.K.: Pereson, J.D.: Nelson, N.C.: Kernin, M.A.: McDonaid, L.: Utterback, T.K.: Malek, J.A.: Linher, K.D.: Garrett, M.M.: Stewart, A.M.: Cotton, M.D.: Pratt, N.S.: Phillips, C.A.: Richardson, D.: Heidelbero, J.: Sutton G.S.: Fleisthmann, R.D.: White, C.: Salzberg, S.L.: Smith, H.O.: Venter, J.C.: Fraser, C.M.: Riche (1999), 399:323-329

#Litle Backerie Irom genome Sequence of Thermotoga and Backeria Irom genome Sequence of Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                #authors Ripmaster T.L.: Vaughn, G.P.: Woolford Jr., J.L.
#journal Nol. Cell. Biol. (1993) 13:7901-7912
#fitle DRSI to DRS7, novel genes required for ribosome assembly and turction in Saccharomyces cerevisiae.
#cross-references MUD:94067151
#accession B54591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS1995 *type complete
probable ATPase (EC 3.6.1.1) DRS2 + yeast (Saccharomyces
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05-May-1995 #sequence_revision 01-Sep-1995 #text_change
11-Jun-1999 #sequence_revision ii-Jun-1999 #text_change
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#.esqth 317 #molecular-weight 37383 #checksum
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Pred. No. 4.84e+00;
7: Mismatches 7: Indels
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##residues 1-890,'NT',893-1355 ##label RIP
##Cross-references EMBL:L01795
ENCE S20768 T
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###Esidues
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Just Local Similarity 40.0%:
Matches 10: Fosservative
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#domain Signal Segmence #Status predicted #label SIGN #product beta-lactamase II #status predicted #label BL2N #active_site Glu #status predicted\
10 #binding_site Zinc, high affinity (His, His, Cys. His) #status predicted
#length 257 #molecular-weight 28153 #chtcksum 2375
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beta-lactamase (E. 3.5.2.6) II precursor · Bacillus cereus
cephalosporinase II; penicilinase II
#formal_name Bacillus cereus
04.Dec-1986 *text_change
                                                                                                                                                                                                                                                                                                         #formal_name Bacillus sp.
31-Dec-1988 #sequencc_revision 31-Dec-1988 #text_chanae
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#domain transmentiane #status predicted #label
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*journal J. Gen. Microbiol. (1985) 131:3317-3324
*title Nucleotide sequence of the beta-lactamase gene 
*alalophilic Bacillus sp. strain 175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1355
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3, No. 4.84e-00:
Mismatches 5: Indels
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Pred. No. 6.72e+60;
5; Mismatches 1;
                                                                                                                                     probable hydrolase
hydrolase, transmembrane protein
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Best Local Similarity 33.3%;
Matches 10; Conservative 12
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cession B24393
                             ##cross_references SGD:SGCU
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Best Local Similarity 57.1%;
Matches 8; Conservative
SGD: DRS2; FUN38
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                                                               #map_position 1L
FUNCTION
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                                                                                                                                                               FEATURE 251-267 258-464 498 514 1099-1115
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1162-1178
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                                                                                                                                                                                                                                                                                                                                                                                                                               **authors Arbler, R.P.; Daniel, M.; Fleming, J.; Hermoso, J.M.; Pang, C.; Waley, S.G.
**journal FEBS Lett. (1985) 189:207-211
**itle The amino acid sequence of the zinc-requiring beta-lactamase li from the bacterium Bacilius cereus 569.
**across-references MUID:86095446
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CLASSIFICATION *superfamily unassigned homeobox proteins; homeobox homology
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#product beta-lactamase II #status experimental #label
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*formal_name Gailus gallus *common_name chicken
13-Sep-1996 *sequence_revision 13-Sep-1996 *text_change
24-Sep-1999
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                                                        Hussain, M.: Carlino, A.: Madonna, M.J.: Lampen, J.C. J. Bacterio, (1995) 164:223-229 Cloning and sequencing of the metallothioprotein betallacturactenase II gene of Bacillus cereus 569/H in
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**ccss-references EMBL:035815; NID:91016799; FIDN:AAA79164.1;
P*CCSS-references PID:91016800
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5: Mismatches 1: Indels
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J. Neurosci. (1994) 14:486-498
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A91806
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#cross-references MUID:85068056
#accession A91806
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**authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Sauthors Doig P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; defonge, B.L.; Carrel, G.; Tummino, P.J.; Carres, G.; defonge, Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, K.; Merberg, D.; Mills, D.M.; Ives, C.; Gibson, K.; Merberg, D.; Mills, S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.J.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.J.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.J.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.S.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.S.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.S.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.S.; S.D.; Jiang, Q.; Tayior, D.E.; Vovis, G.F.; Trust, T.S.; S.D.; Jiang, Q.; Tayior, D.E.; S.D.; Jiang, D.E.; S.D.; Jiang, G.; The human, gastric pathogen Helicobacter pylor;
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strain 39
12-Feb-1999 *sequence_revision 12-Feb-1999 *text_culduam
12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F71810 #type complete type III DNA modification enzyme (methyltrausterase) Helicobacter pylori (strain 399)
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DNA binding: homeobox: nucleus: transcription
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Best Local Similarity 52.4% Fred. No. 0.4337 J.
Matches III Conservative it Mishafiches S. Inders
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                                                                     #domain homeubox homology #label HOX
th 259 #molecular-weight 27926 #ch
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 3.92 Seconds 241.115 Million cell updates/sec MPsrch_pp

Sabular output not generated.

Mod Jun 19 16:01:31 2000;

Run on:

1 SSGKNEGINIYNNNEAFKVERRFIKRVSNVI 31 >US-09-142-524A-5 (1-31) from USC9142524A.pep 207 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 seqs, 30454973 residues Searched

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 l:swissprct Satabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Variance 51.934; scale 0.640

Mean 33.239:

Statistics:

SUMMARIES

Score Match Length DB 15 93 44.9 374 1 SEP_CRVJA SUGI BASIC PROTEIN PRE 93 44.9 374 1 SEP_CRVJA SUGI BASIC PROTEIN PRE 94 94.9 374 1 SEP_CRVJA SUGI BASIC PROTEIN PRE 95 34.6 135 14 14 14 14 14 14 14 1			æ			0.1.00		
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71 34.3 257 1 BLAZ_BACSP BETA-LACTAMASE. TYE 69 33.3 523 1 YEP8_HAEIN UNTATIVE GLYCOSYL 69 33.3 503 1 CPV1_RABIT CYTOCHROME BLYCOSYL 69 33.3 566 1 YCCO_YEAST HYDOTHETICAL 64.9 K 69 32.9 623 1 TYT_HUMAN TRANSKETOLASE (EC. 268 32.9 626 1 BGAL_LEULA BETA-GALACIOSEDASE 68 32.9 626 1 BGAL_LEULA BETA-GALACIOSEDASE 68 32.9 1 CAIC_MOTVI COLLAGEN ALPHA 1(XI 67 32.4 158 1 PTPB_ECOLI PTS SYSTEM, N-ACETYI 67 32.4 158 1 DL92_HSV7J PROTEIN U63. N-ACETYI 66 31.9 597 1 C4BP_HUMAN C4B-BINDING PROTEIN 66 31.9 956 1 SYV_TREPA VALYL-TRNA SYNTHETR 65 31.4 135 1 ES30_TRICO 30 KD ANTICENIC GLS 65 31.4 149 1 GL32_MCRMR GLOBIN III.	9	7.1	٠	257	۲-,	BLA2_BACCE	ETA-LACTAMASE,	1.95e-00
69 33.3 1 YF78_HAETN PUTATIVE GLYCOSYL TO PUTATIVE	7	7.1	34.3	257	. 4	BLA2_BACSP		1.95e+00
69 33.3 503 1 CPV1_RABIT CYTOCHROME P450 19 69 33.3 566 1 VCDC_EAST RHOI GDP-TGL 64.9 K 69 32.9 623 1 TKT_HUMAN TRANSKETCLASE (EC 2 68 32.9 626 1 BGAL_LEULA BERA-GAALACTOSIDASE 68 32.9 626 1 BGAL_LEULA BERA-GAALACTOSIDASE 68 32.9 929 1 CAIC_NOTVI COLLAGEN ALPHA 1(X) 67 32.4 158 1 YIAC_BPT4 HYPOTHETICAL 9.5 KI 67 32.4 211 1 UL92_HSV7 PROTEIN U63. 66 31.9 35.3 1 TP6A_MATTH PYPE II DM TOPOISE 66 31.9 35.3 1 TP6A_MATTH PYPE II DM TOPOISE 66 31.9 550 1 C4BP_HUMAN G4P-BINDIN SPECURE 65 31.9 956 1 SYV_TREPA NALYL-TRNA SYNTHETE 65 31.4 149 1 GLB3_MCRMR GLOBIN III.	αυ	69	33.3	323	٠,	YF78_HAEIN		4.01e-00
69 33.3 566 1 YCD6_YEAST HYPOTHETICAL 64.9 K 69 35.3 1356 1 ROM2_YEAST FROI GDF-GTP EXCHANGE 68 32.9 628 1 TAT_HUMAN TRANSKTOLASE (EC 26 8 32.9 626 1 BGAL_LEULA BETA-GALACTOSIDASE 68 32.9 929 1 CAIC_NOTVI COLLAGEN ALPHA 1(X) 67 32.4 158 1 YI4C_BPT4 HYPOTHETICAL 9.5 KC 67 32.4 158 1 PIPR_ECOLI PIS SYSTEM, NACETICAL 9.5 KC 63 31.9 133 1 TPA_METTH TYPE II DNA TOPOISC 66 31.9 956 1 SYV_TREPA VALYL-TRNA SYNTHETIC 65 31.9 956 1 SYV_TREPA VALYL-TRNA SYNTHETIC 65 31.9 135 1 ES30_TRICO 30 KD ANTICENIC CLIS	2	69	33.3	503	-	CPV1_RABIT		4.01e+00
69 33.3 1356 1 ROMZ-YBAST RHOI GDP-GIP EXCHANG 68 32.9 623 1 YIX_HUMAN TRANSKETOLASE (EC. 2. 68 32.9 626 1 BGAL_LEULA BETA-GALACTOSIDASE (EC. 2. 68 32.9 929 1 CAIC_NOTVI COLLAGEN ALPHA 1(XII) 67 32.4 158 1 PIPE_ECOLI PTS SYSTEM, N-ACETVIL 67 32.4 211 1 UL92_HSV7] PROTHEITCAL 9.5 KD 65 31.9 353 1 TP6A_METH TYPE II DNA TOPOISON 66 31.9 550 1 CABP_HUMAN CAB_BINDING PROTEIN 65 31.4 135 1 ES30_IRICO 30 KD ANTIGENIC GLYGES 11.0 1 CABP_HUMAN CAB_BINDING PROTEIN 65 31.4 135 1 ES30_IRICO 30 KD ANTIGENIC GLYGES 11.0 1 CABP_HUMAN GLOBIN III.	10	69	33,3	566	r-1	YCD6_YEAST	×	4.01e-00
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68 32.9 626 1 BGAL_LEULA BETA-GALACTOSIDASE I CAIC_MOTVI COLLAGEN ALPHA 1 (XII 6 3 2.4 80 1 Y14C_BPT4 HYPDTHETICAL ALPHA 1 (XII 6 2 3 2.4 158 1 PTPB_ECOLI PTS SYSTEM, N ACETYL 6 3 1.9 113 1 UL92_HSV7 PROTEIN U63. 66 31.9 135 1 TP6A_METH TYPE II DNA TOPOISON 6 11.9 956 1 SYV_TREPA VALYL-TRNA SYMTHETAN 6 3 3.4 149 1 GLB3_MORMS GLOBIN III.	12	58	32.9		e 1	TKT_HUMAN	TRANSKETOLASE (EC 2.2.	5.72e+00
68 32.9 929 1 CAIC_NOTVI COLLAGEN ALPHA 1(XII) 67 32.4 158 1 PTPB ECOLI PTS SYTEM, N-ACETVII 67 32.4 211 1 UL92_HSV7J PROTHEIN U63. 66 31.9 113 1 UL92_HSV7J PROTEIN U63. 66 31.9 35.3 1 PP6A_METH TYPE II DNA IOPOISON 66 31.9 956 1 SYV_TREPA VALYL-TRAR SYMTHETAR 65 31.4 135 1 ES30_TRICO 30 KD ANTIGENIC GLYG 65 31.4 149 1 GLB3_MORMS GLOBEN III.	13	68	32.5		٦	BGAL_LEULA	BETA-GALACTOSIDASE LAR	5.72e+00
67 32.4 80 1 Y14C_BPT4 HYPOTHETICAL 9.5 KD PTPB_ECOL PTS SYSTEM, NACETYL 67 32.4 211 1 UL92_HGYD1 PROTEIN U63. 66 31.9 113 1 GUAU_PIG UROCIANI'IN PRECURCG 66 31.9 553 1 PF6A_METH FYPE II DNA TOPOISON 66 31.9 956 1 SYV_TREPA VALYL-TRAN SYMTHETAK 65 31.4 135 1 ES30_TRICO 30 KD ANTIGENIC GLYG 65 31.4 149 1 GLB3_MORMS GLOBIN III.	4	69	32.9		4-1	CAIC_NOTVI	COLLAGEN ALPHA 1(XII)	5.72e+00
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67 32.4 211 1 GL92_HGV7 PROTEIN U63. 66 31.9 133 1 DAM_DFT GROCJANYLIN 66 31.9 597 1 C4DP_HUMAN C4B-BINDING 66 31.9 566 1 SYV_TREPA VALYL-TRA S 65 31.4 135 1 ES30_HRICO 30 KD ANTIGE 65 31.4 149 1 GLB3_MORNIS GLOBIN III.	15	29	32.4		٠,	PIPB_ECOLI	PIS SYSTEM, N-ACETYLGA	8.12e+00
56 31.9 113 1 GUAU_PIG URGCJANYLIN 66 31.9 353 1 PF6A_MBTH TYPE II DNA 56 31.9 597 1 CABP_HUHAN CAB-BINDING 66 31.9 956 1 SYV_IREPA VALYL-TRNA S 65 31.4 135 1 ES3O_IRICO 30 KD ANTIGE 65 31.4 149 1 GLB3_MORMS GLOBIN III.	17	67	32.4		۲-1	UL92_HSV7J	PROTEIN U63.	8.12e+00
66 31.9 353 1 TP6A_METTH TYPE II DNA 56 31.9 597 1 C4BP_HUMAN C4B-BINDING 68 31.9 956 1 SYV_TREPA VALYL-TRNA S 65 31.4 135 1 ES30_TRICO 30 KD ANTIGE 65 31.4 149 1 GLB3_MORMR GLOBIN III.	18	55			-	GUAU_PIG		1.15e+01
56 31.9 597 1 C4BP_HUMAN C4B-BINDING 56 31.9 956 1 SYV_IREPA VALYL-TRNA S 65 31.4 135 1 ES30_IRICO 30 KD ANTIGE 65 31.4 149 1 GLB3_MORNE GLOBIN III.	19	99	31.9		-	TP6A_METTH	TYPE II DNA TOPOISOMER	1.15e+01
66 31.9 956 1 SYV_IREPA VALYL-TRNA SYNTH 65 31.4 135 1 ES30_IRICO 30 KD ANTIGENIC 65 31.4 149 1 GLB3_MCRMA GLOBIN III.	20	99	31.9			C4BP_HUMAN	C4B-BINDING PROTEIN AL	1.15e+01
65 31.4 135 1 ES30_IRICO 30 KD ANTIGENIC 65 31.4 149 1 GLB3_MCRMR GLOBIN III.	21	99	31.9		-	SYV_IREPA	VALYL-TRNA SYNTHETASE	1.1Se+01
1 GLB3_MCRMR	22	65	31.4	135	-	ES30_IRICO	30 KD ANTIGENIC GLYCOP	1.62e+01
	23	65	31.4	577	r 1	GLB3_MCRMR	GLOBIN III.	1.62e+01

	2.27e+01 2.27e+01 3.17e+01
METHIONYL-TRNA SYNTHET GLUTAMINE SYNTHETASE (CCTOCHEMER ES 26 (EC) PROBABLE DNA POLYMERAS DNA POLYMERAS ENOLEUCYL-TRNOSINE PROSE DNA POLYMERASE I (EC 2 ESOLEUCYL-TRNOSINE PROSE DNA POLYMERASE I (EC 2 ESOLEUCYL-TRNOSINE ENOLEUCYL-TRNOSINE ENOLEUCYL-TRNOSINCHET GENOME POLYPROTEIN [CO CINNAWYL-ALCOHOL DEHYD HYPOTHETICAL 45.1 KG P HYPOTHETICAL 45.1 KG P HYBOTHETICAL 45.1 KG P HYBOTHETICAL 45.1 KG P HYBOTHETICAL 45.1 KG P HYBOTHETICAL 5.1 KG P HYBOTHETICAL 5.1 KG P TRANSKETOLASE (EC 2.2 THANSKETOLASE (EC	VALYL-TRNA SYNTHETASE, TESTIS SPECIFIC PROTEI NINAC LONG PROTEIN (EC
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ALIGNMENTS

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01-NOV-1990 (Rel. 16, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY J :) (CRY J :).
Cryptomeria japonica (Japanese cedar)
Eukaryota; Viridiplantae; Szreptophyta; Embryophyta: Tracheophyta;
euphyllophytes; Spermatophota; Coniferales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-POLLEN:
MEDLINE: 89031257.
Tantai M., Ando S., Usui M., Kurimoto M., Sakaquchi M., Inouye S.,
Matuhasi T.;
"N-terminal amino acid sequence of a major allergen of Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and sequencing of CDNA coding for Cry ) I, a major allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sone I., Komiyama N., Shimizu K., Kusakabe I., Morikubo K.,
Kino K.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Torigoe K., Fakuda S., Kuilmoto M., to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Japanese cedar polien.".
Biochem: Biophys. Res. Commun. 199.519-525(1994).
                                  374 AA
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARITAL SEQUENCE. TISSUE-POLLEN;
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pollen (Cry j I).";
FEBS Lett. 239:329-332(1988).
                                                                                                                                                                                                                                                                                                                                   Taxodiaceae: Cryptomeria
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-POLLEN;
Namba M., Kurose M.,
Submitted (JUL-1994)
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LT 1
SBP_CRYJA
P18632;
PACEUS SECOND SE
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BLAB_BACCE
P14488;
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Plasmid.
SEQUENCE
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SEQUENCE
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Ricinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its centent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/ancounce/or send an emain to licenseitsb.ch).
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Bacteria: Firmicutes, Bacillus/Glostridium droup: Streptococcaceur:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE: 93054365.

Durmaz E., Hissins D.L., Klaenhammer T.R.:

"Molecular characterization of a second abortive phage resistance gene present in Lactococcus lactis subsp. lactis ME2.";
J. Bacteriol. 174.7463-7469(1992).
-!- FUNCTION: PROVIDES RESISTANCE TO BACTERIOPHAGE BY ABORIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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QQ1457-1993 (RCL. 27, Created)
Q1-067-1993 (Rel. 27, Last sequence update)
Q1-067-1993 (Rel. 27, Last annotation update)
ABCRIT-1993 (Rel. 27, Last annotation update)
ABCRIT-1993 (Rel. 27, Last annotation update)
ABCRIT-1893 (Rel. 27, Last annotation update)
ABCRIT-1893 (Rel. 27, Last annotation update)
ABCRIT-1894 (Rel. 27, Last annotation update)
Lactoroccus Lactis (subsp. lactis) (Streptococcus Lactis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; DB 1; Length 374;
No. 3.04e-04;
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                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: 026544; BAA05542.1: -.
EMBL: 026545; BAA05543.1: -.
EMBL: 0.31639; BAA057020.1: -.
PIR: A44773; A44773.
PFAM: PF00544; poc.2.ivasc: 1.
PRIMS: PR00544; poc.2.ivasc: 1.
Allergon; 01yroprotein; Multiqene tamily: Signal.
                                                                                                                                                                                                                                                                                                                                                                                                      SUG: BASIC PROTEIN
H -> F (IN CRY U.)
S -> T (IN CRY U.)
S -> T (IN CRY U.)
C -> S (IN CRY U.)
C -> S (IN CRY U.)
K -> U (IN CRY U.)
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  AMB A I/AMB A II/CRY J I SUBFAMILY
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Local Similarity 70.0%;
ses 14; conservative
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PIR; A47025; A47025
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374 AA;
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EMBL: 274786; CAA99047.1: -.
HSSP: G63450; 1A0.4
HSSP: G63450; 1A0.7
HSSP: G63450; 1A0.7
HSSP: G63450; PROTEIN_KINASE_ATP: FALSE_NEG.
PROSITE: PS00108; PROTEIN_KINASE_ST: 1.
PROSITE: PS0011; PROTEIN_KINASE_ST: 1.
PROSITE: PS0011; PROTEIN_KINASE_DOM: 1.
Hypothetical protein: Transferdase. Settine/Threentheticales.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Bukk is yeast).
Eukaryota: Fungi: Ascomycota: Jaclaromycetes: Saccharomycetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ansorge W., Benes V., Rechmann S., Schwager C., Teodoru C., Voss H., Wiemenn S., Schwager C., Teodoru C., Submitted (JUL-1996) to the PA C/Gerbank/CDBJ databases -:- SIMILARITY: WITH THE CONE, VEO CATALYTIC DOMAINS OF SEE/THE-
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01-JAN-1990 (Rel. 13. Last sequence update)
15-JUL-1999 (Rel. 38. Last annotation update)
BETALACTAMASE, TYPE II PRECURSOR (EC 3.5.2.6) (PENICILLINASE)
Bacilius cereus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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01-NoV-1997 (Rel. 35, Last Sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROBABLE SERING/THREONINE-PROTEIN KINASE YOLG45W (EC 2.7.1...)
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Pred. No. 6.38e-02;
11; Mismatches 8: Indels
                                                                                       39.6%; Score 82; DB 1; Length 344; larity 28.0%; Pred, No. 2.89e-02; Conservative 12; Mismatches 6; Indeis
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344 AA: 40128 MW; AA6E41E71B4A003C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria: Firmicutes: Bacillus/Clostridium group:
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AIP (BY SIMILARITY)
AIP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                            271 GINLFGDEKDFKIDQHFVIPKPETI 295
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                                                                                                                                                                                                                                                                                                                                                                               7 GINIYNNNEAFKVERRFIKRVSNVI 3:
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Local Similarity 26.9%;
les 7; Conservative
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                                                                                                  Query Match
Best Local Similarity
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EMBL, L01795, AAA16691.1;
EMBL, U12980, AAC05006.1;
PIR; S30768; S30768
SCD: L0000826; DRS2
PROSTE; PS00154; ATTASE_E; Z
PFAM; PF00122; E1-E2_ATPASE.
Hydrolase; Calcium transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,8%;
33,3%;
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Best Local Similarity 33.39.
The 10; Conservative
RETICULUM CA2+-ATPASE).
DRS2 OR YAL026C OR FUN38.
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1355 AA:
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                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE: 94067151.
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BLA2_BACCE
P04190;
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SEQUENCE
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or send an email to license@isb-sib.ch).
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Lim H.M., Iyer R.K., Pene J.C.:

"Site-directed mutagenesis of dicarboxylic acids near the active site
"Site-directed mutagenesis of dicarboxylic acids near the active site
of Bacillus cereus 5/8/6 beta-lactamase II.";

Biochem. C. 276:401-404(5991).

-: FUNCTION: CAN HYDROLYZE CARBAPENEM COMPOUNDS.

-: CATALYTIC_ACTIVITY: A BETA-LACTAM - H(2)0 * A SUBSTITUTED BETA-
                                                                                                                                                   "Cloning, nuclectide sequence, and expression of the Bacillus cereus 5/8/6 beta-lactamase II structural gene."; J. Bacteriol. 170:2873-2878(1968).
                                                                                                                                                                                                                                                                                      MEDLINE: 89306359.

Lim H.M., Pene J.J.:
"Mutations affecting the catalytic activity of Bacillus cereus 5/B/6
beta-tactamses III.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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P99524:
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NCV-1997 (Rel. 35, Last annotation update)
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC
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-- COFACTOR: BINDS TWC ZINC JONS PER MCLECULE.
-- SIMILARITY: BELONGS TO THE CLASS-B BETA-LACTAMASE FAMILY.
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2.NC 1 (BY SIMILARITY).
2.NC 2 (BY SIMILARITY).
D-NN: NO CHANGE IN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 256;
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PIR: AJ2017: A32017.
PROST PG 490: IBMC.
PROSITE: PS00743: BETA_LACTAMASE_B_1: 1.
PROSITE: PS00744: BETA_LACTAMASE_B_2: 1.
PFGM: PF00753: lactamase_B: 1.
Fydro, ase: Zinc: Actamase_B: 1.
Z9GNAL.
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Pred. No. 1.35e+00;
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     Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D->N, E:
                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 264:11682-11687(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G->E:
                                                                                STRAIN=5/B/6:
MEDLINE: 88227879.
Lim H.W. Perro J.J., Shaw R.W.;
"Cloning, nuclectide sequence, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28038 MW;
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                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS
                                                                                                                                                                                                                                                                MUTACENESIS
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                                                                                                                                                                                                                                                                                                                                                                            [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-S286C / AB972: MEDIINE: 95249563. Bussey H., Kaback D.B., Zho: A., Vo D.T., Clark M.W., Fortin N., Hall J., Ouellette B.F.F., A: 3.1., Barton A.B., Su Y., Davies C.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).

-! FJNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE TRANSPORT OF GALCIUM (BY SIMILARITY). SEEMS TO BE INVOLVED IN RIBOSOME ASSEMBLY.

-! CATALYTIC ACTIVITY: AIP + H(2)0 - ADP + ORTHOPHOSPHATE.

-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
Saccharomyces cerevisiae (Bu. r's yeast).
Eukaryota: Fungi: Asconycota. Saccharomycetes: Saccharomycetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-FEB-2000 (Rel. 39, Last a lotation update)
BETA-LACIAMASE, TYPE II PREC 4SOR (EC 3.5.2.6) (PENICILLINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                Ripmaster T.L., Vaughn G.P., Woolford J.L. Jr.:
"DRSI to DRS7, novel genes: +quired for ribosome assembly and function in Saccharomyces ctr visiae.";
Mol. Cell. Biol. 1337901-7912 1993).
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.smm:c refichium.
.HGSPH.MYLAIION (BY SIMILABHIY).
MW: TEA4G42152A90GA6.CHC84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The nucleotide sequence of chromosome I from Saccharomyces cerevisiae.";
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Pred. No. 1.35e+00;
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                                                                            Saccharomydetadeae; Saccharomydes.
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SEQUENCE
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STATETTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDIANE: 99400945.
Fablane S.M., Sohi M.K., Wan T., Payne D.J., Hateson J.H.,
Mitchell T., Satton B.J.,
"Crystal structure of the zinc-dependent beta-lactamase from Bacillus
crystal structure of the zinc-dependent beta-lactamase from Bacillus
cerous at 1.9-A resolution: binuclear active site with features of a
                                                                                                                                                                                                                                                                                                                                                             Sutton 5.3.. Artymisk P.3.. Cordero-Borboa A.E., Little C., Phillips D.C., Waley S.G., An X-ray-verystallographic study of beta-lactamase II from Bacillus cereas at 0.35 rathographic study of beta-lactamase II from Bacillus Egothem. J. 248:181-188(1987).

    COFACTOR: BINDS TWO ZINC LONS PER MOLECULE. THE ENZYME CAN ALSO
FUNCTION WITH ONLY ONE ZINC ION.
    SUBUNIT: MONOMER.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 96437525.
Cart: A., Duec E., Galleni M., Frere J.-M., Didekerg O.;
*1.85-A resolution structure of the zinc (II) beta-lactamase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The 3-B structure of a zinc metallo-beta-lactamase from Bacilius cereus reveals a new type of protein fold.";
EMBO J. 14:4914-4921(1995).
                                                                                                                                                                   SIGNAIN-569/H.
MEDLINE: 86805446.
Ambler R.P., Dariel M. Fleming J., Hermoso J.M., Fang C., Waley in the mino acid sequence of the zinc-requiring beta-lactamase II the backerium Bachilas cereus 569.1.
FEBS Lett. 189:207-211(1985).
                                       Hussain M., Carlino A., Madonna M.C., Lampen C.O.)
"Cloning and sequencing of the retallochioprotein beta-lactamase of bacilus ceress 569/H in Escherichia coll.";
J. Racteriol. 164:223-229(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caril A., Pares S., Duee E., Galleni M., Ducz C., Frere J.-M.,
Sideberg O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SIMILARITY: BELONGS TO THE CLASS-B BETA-LACTAMASE FAMILY.
                                                                                                                                                SEQUENCE OF 31-18x: 187-210 AND 214-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CHYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE: 96067120.
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                                                                                                                                                                                                                                                                                                                        X-FAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
MEDLINE: 88133841.
Sutton 5.J.: Artymilk P.J.: Cordero-Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 37:12404 12411(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: M11189: AAA22276.1:
PIR: A01006: PNBSU2.
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18ME; 07-JUL-97.
18VT; 23-5EP-98.
18C2; 14-OCT-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus.";
                    MEDLINE: 86008056
Hussain M., Carli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID.
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Bacteria; Firmicutes; Bacili s/Clostridium group: Bactlus/Staphylococcus group: Bacillus/Staphylococcus group:
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-1- SIMILARITY: RELEAST I THE GLANNET FRID. DATAMAKE FARTIN.
                                                                                                   Zinc; Antibiotic reistance; Signal: 30-structure
                                                                                                                                                                                                                                                                                                                                                                          l: Indels
                                                                                                                                                                                                                                                                                                                              Length 257
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ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
W; 23EESBDCO45AE571 CRC64;
                                                                                                                                                            LINC 1, HIGH-AFFINITY.
ZINC 1, HIGH-AFFINITY.
ZINC 2, LOW-AFFINITY.
ZINC 1, HIGH-AFFINITY.
ZINC 2, LOW-AFFINITY.
ZINC 2, LOW-AFFINITY.
W. Z6MEBFB7DDA45431 CRP64-
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PIR: A24993; PNBS2S.
HSSP: P04190: IBMC.
PROSITE: PS00743; BETA_LACTAMASE_B_1; .
PROSITE: PS00744; BETA_LACTAMASE_B_2; 1.
PROSITE: PS0753; lactamase_B; 1.
FAM: PF00753; lactamase_B; 1.
30
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Pred. No. 1.95e-00:
5: Mismatches I
                                                                                                                                             HETA-LACIAMASE
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MEDLINE: 86170399.
                                   PRCSITE: PS00743; BETA_LACTAMASE_B_1: 1.
PROSITE: PS00744; BETA_LACTAMASE_B_2: 1.
PFAM; PF00753; Jactamase_B;
Hydrolase; Zinc; Artibictic '*sistance; %
S10NAL 1 36
CHAIN 31 257 **CITAMASE_B
                                                                                                                                                                                                                                                                                        28092 MW:
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Similarity 57.1%;
8: Conservative
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20-APR-99.
20-APR-99.
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257 AA:
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257 AA;
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(229555:
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
SYTOCHROME P450 19 (AROMATASE) (EC 1.14.14.1) (CYPXIX) (ESTROGEN SYNTHETASE) (P-450AROM).
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Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Mammalia;
Eutheria: Ladomorpha: Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Protecbacteria: gamma subdivision: Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69: DB 1; Length 323; Pred. No. 4.01e+09; 13: Mismatches 3; Indels
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  Score 71: 1 1: Length 257: Pred. No. 1 :Se+00; 5: Mismatches 1: Indels
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PFAM: PFCG545: Glycos_transf_2: 1.
Hypothetical protein: Transferase: Glycosyltransterase.
SEQUENCE = 323 AA; 37680 MW: 7CBC2681039AB5B4 GRC64:
                                                                                                                                                                                                                                                            057287: 005077;
15-71L-1998 (Rei. 36, Created)
15-71L-1998 (Rei. 36, Last sequence update)
15-FB2-2000 (Rei. 39, Last annotation uplate)
PUTATIVE GLYCOSYL TRANSFERASE HI1578 (EC 2....).
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Query Match
Best Local Similarity 57.1%:
Matches 8: Conservative
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                                                                                                                                                                                                                                          SIANDARD;
                                                                                               100 MVEKKFUKRVIDVI 113
                                                                                                                                          18 KVERREIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae
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MEDLINE: 95350630.
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Rad M.R., Luetzenkirchen K., Xu G., Kleinhans U., Hollenberg C.P.:
The complete sequence of a il,953 bp fragment from ClG on chromusome
Ili encompasses four new open reading frames.";
Yeast 7:533-538(1991).
                                                                                                                                                                 Delarue B., Mittre H., Feral C., Benhaim A., Leymarie F.:
"Rapid sequencing of rabbit aromatase cDNA using RACE POR";
C. R. Acad. Sci., III. Sci. Vie 319:663:670(1996).
-: FUNCTION: CAIALYZES THE FORMATION OF AROMATIC C18 ESTROGENS FF-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8459
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01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation)
16-DEC-1998 (Rel. 37, Las
                                                                                                                                                                                                                                                                                                                                                                                             C19 ANDROGENS.

-:- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + C(2) - RUH
OXIDIZED FLAVOPROTEIN + H(2)0.

-:- SUBCELLULAR LOCATION: MEMBRANE-BOUND.

-:- SIMILARITY: BELONGS TO THE CYTOCHROME P456 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron transport; Oxidoreductase: Mondoxygenase; Membrane;
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Pred; No. 4.01e+00;
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEME (BY SIMILARITY).
DE4AD795D635AF3D CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: 270301; CAA94314.1; -. EMBL: 268271; CAA92574.1; -. PROSITE; PSO0086; CYTOCHROWE_P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57401 MW;
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Best Local Similarity 44.0%:
Matches II: Conservative
SEQUENCE FROM N.A.
STRAIN-HY: TISSUE-OVARY;
MEDLINE; 97106641.
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PIR; S17477; S17477.
Hypothetical protein.
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P25370;
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SEQUENCE
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TKT_HUMAN
P29401:
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A CZAKI K., Tanaka K., Imanura H., Hihara T., Kameyama T.,
A Nonaka H., Hinano H., Massura Y., Takai Y.,
A Nonaka H., Hinano H., Massura Y., Takai Y.,
A Nonaka H., Hinano H., Massura Y., Takai Y.,
A Nonaka H., Hinano H., Massura Y., Takai Y.,
A Nonaka H., Hinano H., Massura Y., Takai Y.,
A Nonaka H., Hinano H., Massura Y., Takai Y.,
B Nonaka H., Hinano H., Massura Y., Takai Y.,
B Mondy C., 15:196-2207 (1996).
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01-001-1996 (Rul. 34, Last sequence update)
15-101-1999 (Rel. 38, Last sequence update)
15-101-1999 (Rel. 38, Last annotation update)
RHOI GDP-GIP EXCHANGE PROTEIN 2.
RROM2 OR YERSTIM GR. L8039-3.
SACCHATOMYCES CEREVISIAE (BAKEY'S yeast).
Eukaryota: Fundi: Ascomyrcta: Saccharomyceteles:
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STRAIN-S288C / AB972.
STRAIN-S288C / AB972.
STRAIN-S288C / AB972.
STRAIN-S288C / AB972.
Dobeston M., Addrews S., Brinkman R., Cooper C., Ding H., Du Favelic D., Gattung S., Greco T., Kirsten J., Kuccha T., Railsworth K., Hawkins J., Hillber L., Jier M., Johnson D., Zohnston L., Hawkins Y., Latreille P., Le T., Mards E., Maners C. S., Miller N., Nhan M., Pauley A., Peluso Rifken L., Wilson E., Vigath D., Riken L., Wilson P., Vacadin D., Submitted (JAN-1995) to the EMBL/GenBank/D35J dutabases.
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Score 69: DB 1; Length 566; Pred. No. 4.01e+00; 7: Mismatches 7: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4: Indels
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35 POLY-H.S.
95 POLY-H.S.
152595 MW; SFBC542114E7BC32 CRC64;
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Pred. No. 4.0le+C0;
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                                                                                                   158 DVHAKLEK!VEERRF!KRLSDI! 180
                                                                                                                                    9 MIYNNNEASKVERREIKRVSNVI 31
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SGD: 1.0003182; ROM2.
PFAM: PF06610; DEP: 1.
PFAM: PF00621; RNGGEF: 1.
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Loral Similariny 27.3%;
tes 6: Conservative
93.3%;
Best Local Similarity 39.1%;
Matches 9: Conservative
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329 33
632 63
1356 AA:
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ROM2_YEAST
P51862:
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Abedinta M., Layfield R., Jones S.M., Nixon P.F., Mattick J.S.,
Abedinta M., Layfield R., Jones S.M., Nixon P.F., Mattick J.S.,
Abedinta M., Layfield R., Jones S.M., Nixon P.F., Mattick J.S.,
Action of an operation of the selection of a convenience of a conven
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MCGOOL B.A., Plonk S.G., Martin P.R., Singleton C.K.,

"Cloning of human transketolisse cNAs and comparison of the nordeotide sequence of the coding region in Wernicke-Konsakoff and non-Wernicke-Konsakoff individials.",

J. Riol. Chem. 268:1397-1404(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schenk G., Layfreld R., Candy J.M., Duggleby R.G., Nixon P. B. Submitted (MAY-1996) to the EMBL/GenBack/DDBJ datakasws.
                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa: Chordata: Craniata: Veriebrata; Mammalia
Eutheria; Primates; Catarrhini: Hominidue: Homo.
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ECA-V (IN REF. 1).
LCAFGQ -> AVOINCE (IN REF. 4).
P -> A (IN REF. 1).
THL -> KITM (IN REF. 2).
DRADIAQAVRGLITKA -> TORP:HKL (I
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Jung E.H., Sheu K.F.R.E., SZ MO P., Blass J.P.;
Submitted (SEP-1993) to the MBL/SenBank/MMBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE THANSKET CLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 224-623 FROM N.A., AND PARTIAL SEQUENCE.
                                                             01-05C-1992 (Rel. 24, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
TRANSKETOLASE (EC 2.2.1.1) (TK).
623 AA
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PRCSITE: PS00802: TRANKETCLASE 2: 1.
PFAM: PFC0456: transketclase: 1.
Transferase: Thiamine pyrophosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X67688, CAA47919.1; -. EMBL, L12711, AA51222.1; -. EMBL, U55017, AA49961.1; -. PIR: A45050, A45050, PIR: PH0845; PH0845.
STANDARD;
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230
426
597
623
                                                                                                                                                                                                               TKIL OR TKI.
Homo sapiens (Human).
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426
585
608
623 AA;
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CCNFLICT
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Length 623;

DB 1;

Score 68;

32.98;

Query Match

NIYNY-NEAFKVERRFIKRVSN 29

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RESULT

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649 FKIVRNFISRVVEVF 563
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SEQUENCE
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"Leuconostoc lactis beta-galactosidase is encoded by two overlapping
genes.":
                                                                                                                                                                                                                                                                                                   genos.":
Jacteriol. 174,4475-4481(1992).
-!- CATALYTIC ACTIVITY: HYDRCLYSIS OF TERMINAL. NON-REDUCING BETA-D-CALACTOSIDES.
-!- SUBJUIT: BETESTOUES IN BETA-D-CALACTOSIDES.
-!- SUBJUIT: BETESTOUER CF A LARGE AND A SMALL SUBGUNIT.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                     Saps
                                                                                                                                                                                                            Firmicutes: Bacillus/Clostridium group: Lactobacillaceae;
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091145.
15-371-1998 (Rel. 36, Last sequence update)
15-371-1998 (Rel. 36, Last annotation update)
15-311-1998 (Rel. 36, Last annotation update)
CCLACEN ALPHA 1(XII) CHAIN (FRAGMENI).
Notophihalmus viridescens (Eastern newt). (Iriturus viridescens).
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PROTON DONOR (BY SIMILARITY).
UCLEOPHILE (BY SIMILARITY).
EGCEA1548992CF7D CRC64:
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                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DUC-1998 (Rel. 37, Last annotation update)
BETA-GALACTOSIDASE LARGE SUBUNIT (EC 3.2.1.23) (LACIASE).
                    Indels
Pred. No. 5.72e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68: DB 1;
Pred. No. 5.72e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR: 44.891: A4.2891.
HSSP: P00722: 18GL.
PRINTS: PROG122: GLHYDRLASE2.
PROSITE: PSC0719: GLHYDRLASE2.
PROSITE: PSC0719: GLHYDRLASE2.
PROSITE: PSC0708: GLHYDRLASE2.
PROSITE: PSC0708: GLHYDRLASE2.
HYDROLEFC27: 1.
Hydrolase: Glhycosidase: Plassida.
ACT_SITE: 318 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                           625 AA
                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-6
                                                                                                          PRT;
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38.9%;
        Local Similarity 50.0%;
                                          472 ISRPENALIYNNNEDFQV 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 YHDTAEFKTGSRFIKSLN 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 YNNNEAFKVERRFIKRVS 28
                                                                2 SGKNEGINIYNNNEAFKV 19
                     Conservative
                                                                                                           STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466
534
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534
526 AA:
                                                                                                                                                                                       Leuronostoc lactis.
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                                                                                                                                                                                                                                                      STRAIN=NZ5009:
MEDLINE: 92325034.
                                                                                                                                                                                                 Plasmid pNZ63.
Bacteria: Firm
                                                                                                 ET 13
BGAL_LEULA
Q02603;
                                                                                                                                                                                                                         rencenostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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MEDLINE: 95246925.

MIDLIANDE CONTROL MEDLINE: 1

MEDLINE: 164.503-513(1954).

MEDLINE: 164.503-513(1955).

MEDLINE: 164.503-513(1955).

MEDLINE: 164.503-513(1956).

MEDLINE: 18716.

MED
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SIMILARITY:
SIMILARITY: BELONGS TO THE FAMILY OF FIBRIL-ASSOCIATED COLLAGENS
WITH INTERRUPTED HELICES (FACIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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TO CHONDRCITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
POTENTIAL.
Batrachia, Caudata, Salamandroidea: Salamandridae, Notophthalmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connective tission Repeat, Cell adhesion
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FISACNECTIN TYPE-III.
FISACNECTIN TYPE-III.
FISACNECTIN TYPE-III.
FISACNECTIN TYPE-III.
FISACNECTIN TYPE-III.
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Pred. No. 5.72e+00;
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HSSP: PI1276; IMFN.
PFAM: PF00041; f::3; 7.
PFAM: PF00092; vwa: 1.
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Best Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Saps
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                                                              Query Match 32.4%: Score 67: DB 1: Length 80: Best Local Similarity 32.0%; Pred. No. 8.12e+00: Katches 8: Conservative 10: Mismatches 6: Eddis
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Search completed: Mon Jun 19 16:01:52 2000 Joh time : 21 secs

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(FM)
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Listribution rights by Oxford Molecular Ltd

MPsrch_pp - protein - protein database search, using Smith-Waterman algorithm Run ca:

Mon Jun 19 16:02:08 2000; MasPar time 8 98 Seconds 239.278 Million cell updates/sec Tabular output not generated.

1 SSCKNEGINIYNNEAFKVERRFIKRVSNVI 31 >US-09-142-524A-5 (1-31) from US09142524A.pep 207 litte: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 segs, 69334122 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

sptrembll2 lisp_archea 2:sp_bacteria 3:sp_fungi 4:sp_humar. 5:sp_invertebrate 6:sp_mammal 7:sp_mbc 8:sp_organelle ":sp_bhace 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus Database:

Mean 31,753; Variance 53.908; scale 0.589 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or egual to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Score	Match	Query Match Length DB	DB	CI	Description	Pred. No.
125	60.4	375		096385	CHAOI PRECURSOR.	1.31e-09
108	52.2	367	10	7UN260	POLLEN MAJOR ALLERGEN	2.30e-06
·18	37.7	1308	ሆነ	096129	PREDICTED MEMBRANE ASS	3.97e-01
26	36.7	204	10	C92VG4	T2P11.13 PROTEIN.	8.27e-01
97	36.7	360	:\4	O92CL9	HYPOTHETICAL 41.5 KD P	8.27e-C1
9,6	36.7	548	~	087939		8.27e-0
75	36.2	2380	S	096266	HYPOTHETICAL 283.6 KD	1.19e-00
72	3.00	317	7	09X273	ENDOGLUCANASE.	3.46e-00
7.	34.3	360	œ	O9XPX4	MATURASE (FRAGMENT).	4.91e+00
۲,	34.3	372	ω	C9XPX3	MATURASE (FRAGMENT).	4.91e+00
71	34.3	372	80	OSXPX5	MATURASE (FRAGMENT).	4.91e+00
7.1	34.3	823	7	09Y2E5	KIAA0935 PROTEIN (FRAG	4.91e+00
7.0	33.8	259	13	091964	SENSORY ORGAN HOMEOBOX	6.95e+00
70	33.8	505	00	003561	MATURASE.	6.95e+00
70	33.8	546	~	Q92B23	HYPCTHETICAL 62.3 KD P	6.95e-00
70	33.8	641	~	092JA2	TYPE III DNA MODIFICAT	6.956+00
69	33.3	426	ψ	C28684	CYTCCHROME P450 AROMAT	9.81e+00
69	33.3	433	Ś	001986	C31C9.1 PROTEIN.	9.81e+00
69	33.3	1198	10	C5282	DYNEIN HEAVY CHAIN ISO	9.816+00
99	32.5	290	7	929078	BETA-AGARASE I PRECURS	1 380+03

CZZUJ7 PRELIMINARY; PRT; 367 AA. QGZNUJ7 OQZNUJ7. 002NUJ7. 001NUJ7.1999 (TrEMBLrel: 10, Last sequence update) 01-MAY-1999 (TrEMBLrel: 12, Last annotation update)

RESULT

15 P7 P7 P7

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SECUENCE
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087939
087939;
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Q92GL9
Q92GL9;
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MEDLINE, 99021743,

GARDINER, 99021744,

GARDINER, 99021744,

GARDINER, 99021744,

KRONIN M.J., STATISTIN B., CARUCCI D.J., CUMMINGS L.M., ARAVIND L.,

KRONIN M.J., STATISTIN B., MASON T., YU K., FULLI C., PETERSON J.,

SALEN K., G., GARTIN M., ASTON J., STEPHARIZ D.G., PERFEA M.,

SALENBERG S., ZHOT L., ASTON J., CLANTON R., WHITE G., SMITH B.,

FRASER G.M., ADAMS M.L., VOITER J.G., BYERMAN S. L.),

FRASER G.M., ADAMS M.L., VOITER J.G., BYERMAN S. L.),

FRASER G.M., ADAMS M.L., VOITER J.G., BYERMAN S. L.),

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FRASER G.M., ADAMS M.L., BYERMAN S. L.),

FRASER G.M., ADAMS M.L., BYERMAN S. L.),

FRASER G.M., ADAMS M.L., BYERMAN S. L.),

FRASER G.M., BYERM
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4 PRELIMINARY; PRT: 204 AA.
092V34
092V34
01-MAY-1999 (ITEMBLEE]. 10. Created)
01-MAY-1999 (ITEMBLEE]. 12. Last sequence update)
01-NVY-1999 (ITEMBLEE]. 12. Last annotation update)
172F1.13 PROTEIN.
172F1.13 PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
2018Aryota: Viridiplantae. Streptophyta: Embryophyta: Tracheophyta: Cuphy.iophytes: Spermatophyta: Magnollophyta: eudicotyledons:
0019F1.00phytes: Spermatophyta: Magnollophyta: eudicotyledons:
0019F1.00phytes: Spermatophyta: II: Brassicaies: Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                               "Molecular cicning of mountain cedar (Juniperus ashei) pollen major
POLLEN MAJOR ALLERGEN 1-2.
Juniperus askel (Ozark White cedar).
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
euphy,lophytes: Spermatophyta; Conliferopsida; Conliferales;
Taxodiaceae: Juniperus.
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Eukaryona, Aiveolata: Apicomplexa, Haem: Sporida: Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 upery Match 52.2%: Score 10%: DB 10; Length 367; Best Local Similarity 85.0%: Pred. No. 2.30e-06; Matches 17: Conservative 1; Mismatches 2: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       udery Match 37.7%; Score 78; DB 5: Length: 1308; Best Local Similarity 46.2%; Pred. No. 3.97e-01; Matches 12; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MIDORO-HORIUTI T.M., GOLDBLUM R.M., KURUSKY A., WOOD T.G.,
BROOKS E.G.)
                                                                                                                                                                                                                                                                                                                                                                                                          alteron, Jun a 1.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AFT0665: AAD0036091.: ..
EMBL: AFT0665: AAD036081.: ..
MENDEL: 36544: Junas:1088:36544.
MENDEL: 36545: Junas:1088:36565.
SEQUENCE: 36575: AA: 39824 MM: 4C208630 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61-MAY-1999 (IrEMBLrel. 10, Created)
61-MAY-1999 (IrEMBLrel. 10, Last sequence update)
61-MAY-1999 (IrEMBLRel. 10, Last annotation update)
PREDICTED MEMBRANE ASSOCIATED PROTEIN.
PEB01250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Current (1987).
Science 282:1126-1132(1998).
EMBL: AE001374: AAG71815.: -.
EMBL: AE001374: AAG71815.: -.
EMBL: AE001374: AAG71815.: -.
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096129
096129:
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LECTHNER B., LESTWEIN C., SCHULTZ H., HOERTH P., HAEHNEL W., SCHILTZ E., SCHAEGER H., HEIDER J., "Bloochemical and genetic characterization of benzylsuccinate synthisse from Thauera aromatica: a new glycyl radical enzyme catalysing the first step in anaerobic toluene metabolism.";
MACI. MICTOBIOL 28-515-629 (1998).
EMBL: AJ001848: CAA05048.1:
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Bacteria: Proteobacteria: beta subdivision: Rhodocyclus aroup:
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                                                                                                                                                                                                                                                             Length 204
                                                                                                                                                                                                                                                        Query Match

36.7%: Score 75: DB 10; Length 20;
Best Local Similarity 40.0%: Pred. No. 8.27e-C1;
Matches 8: Conservative 7: Mismatches 5: Indeis
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHERICAL (1.5 KD PROTEIN.
Leptospira borgpetersenii.
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Last annotation update)
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Chloropiast.
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SEQUENCE
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09xqx3
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C9XPX4
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MEDLINE: 99021743.

MEDLINE: 99021743.

RESERVENCE FROM N.A.

RA GARRNER M.C., TETTELIN H., CARUCCI D.J., CUMMINSS L.M., ARAVIND L.,

RA GARRNER M.C., TETTELIN H., CARUCCI D.J., CUMMINSS L.M., ARAVIND L.,

RA KOCNIN E.V., SHALLOM S., MASON T., YU K., FUJII C., PEDERSON J.,

RA SHEN K., JINS J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,

RA SALZBERG S., ZHOJ L., SUTION G.G., CLAYTON R., WHITE O., SMITH H.C.,

RA FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;

Chromosome 2 sequence of the human malaria parasite Plasmodium

RT Chromosome 2 sequence of the human malaria parasite Plasmodium

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MELSON KE. CLAYION R.A., GILL S.R., GWINN W.L., DOLSON R.J.,
NELSON KE. CLAYION R.A., GILL S.R., GWINN W.L., DOLSON R.J.,
MCDONALD L., UTTERBACK I FR., MALEK J.A., LINHER K.O., GARRETI M.M.,
STEWART A.M., COTTON M.D., PRATI M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., STITON G.O., FLEISCHMANN R.D., WHITE C., SALZBERG S.L.,
SMITH H.G. VENTER J.G., FRASER C.M.,
"Evidence for lateral gene transfer between Archaea and bacteria from
Nature 399:223-229(1999).
                                                                                                   Gaps
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BLESON K.E., CLANTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HAFT D.H., HUCKEY E.K., PETERSON J.E., NELSON W.C., KETCHUM K.A.,
MCDONALD L., IGTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.
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                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
Bukaryota: Alveolata: Apicomplexa: Haemosporida: Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Address Similarity 29.2%; Score 75; DB 5; Length 2380; Local Similarity 29.2%; Pred. No. 1.19e-00; Conservative 13; Mismatches 3 Indels nes
                                                            Length 548:
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01-NOV-1999 (TIEMBLEEL 12, Last sequence update)
01-NOV-1999 (TIEMBLEEL 12, Last annotation update)
ENDOGLUCANASE.
                                                                                                                                                                                                                                                                                                     01-MAY-1999 (ITEMBLIEL 10, Created)
01-MAY-1999 (ITEMBLIEL 10, Last sequence update)
01-MAY-1999 (ITEMBLIEL) 10, Last annotation update)
HYPCTHETICAL 283.6 KD PROTEIN.
                                                        Score 76: DB 2: Lu
Pred. No. 8.27e-01;
PFAM: PFC6512: Signal: 1.
SEQUENCE 549 AA; 62441 MW: 4F9768CA CRC32:
                                                                                                   12: Mismatches
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                                                        Ouery Match
Best Local Similarity 34.5%:
Matches 10: Conservative
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Thermotoga maritima
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HARDIS T.M., SOLTIS D.E.;
HARDIS T.M., SOLTIS P.S., SOLTIS D.E.;
*Inversification of the North American shrub genus Ceanothus (Rhamaceae):
*Charmaceae;
*Charm
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HARDIG I.M., SOLTIS D.S., SOLTIS D.E.;
"Diversification of the North American shrub genus Ceanothus
(Rhammareae): conflicting phylogenies from nuclear ribosomal ENA Joud
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STEWART A.M., COTION M.D., PRATT M.S., PHILLIPS C.A., RICHARISON I. HEIDELBERG J., SUITON G.G., FLEISCHMANN R.D., WHITE C., SALZBERG S. SMITH H.O., VENTER J.C., FRASER C.M.:
SUMITH H.O., VENTER J.C., FRASER C.M.:
SUMITH A.O., VENTER J.C., FRASER C.M.:
SEQUENCE 317 AA: 37383 MW: 3EFAIIO8 CRC32;
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euphyllophytes: Spermatophyta: Magnollophyta: eudicotyledons:
core eudicots: Rosidae; eurosids I; Rosales; Rhamnaceae: Adolphia.
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Prod. No. 4.91e-00:
8. Misbarress 3 indels
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7; Miscatches 7; Indels
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Am. J. sot. 0:0-0(1999).
EMBL: AFC49848; AAD30359:1:
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Best Local Similarity 35.3%.
Matches 6: Gooservaline
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Best Local Similarity 40.0%;
Matches 10; Conservative
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MEDITUR: 9544668.3
MEDITUR: 9544668.4
MINAJIMA N., SHYAMA K., SUYAMA M., KIKUNO R., HIRCSAWA M.,
MINAJIMA N., TANAKA A., KOTANI H., NOMORA N., OHARA O.,
"Frediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 10c new cDNA clones from brain which code
for large proteins in viloo.";
DNA Res. 6:63-76(1999).
THE ABOZSIS: BAA7679.1;
SEQUENCE 823 AA: 92710 MW: BF97CB35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spyrdium parvifolium.
Chloroplast.
Exaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
euphyilophyros: Spermatophyta: Magnollophyta: eudicotyledons;
nore endicots: Rusidae: eurosids I: Kosales: Rhamnaceae: Spyridium
[1]
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 372;
                                                                                                                                                                  Score 71; DB 8; Length 372;
Pred. No. 4.91e-00;
8; Mismatches 3; indels
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Pred. No. 4.91e+06;
8: Mismatches 2: Indels
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01-NCV-1999 (ITEMBLrel. 12, Last sequence update)
01-NCV-1999 (IrEMBLrel. 12, Last annotation update)
KIAAQ935 PROTEIN (FRAGMENT).
                                                                 372 AA: 44233 WW: FSAE7E4F CRC32:
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SEQUENCE 372 AA: 44233 MW; F5AE7E4F CRC32;
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EMBL: AFC49847: AAD30358.1: -.
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EMBL: AFC49849; AAD3C360.1;
                                                                                                                                                                         Query Match
Best Local Similarity 55,3%;
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Best Local Similarity 35.3%;
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                           Chloropiast
                                                                 NON_TER
SEQUENCE
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Q9XPX5
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Neognathae, Galliformes, Phasianidae, Phasianinae, Gallus,
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003561 PRELIMINARY: PRT: 5C5 AA.

003561 PRELIMINARY: PRT: 5C5 AA.

1 01-302-1997 (TFEMBLrel. C4. Created)

101-AUG-1999 (TFEMBLrel. D7. Last sequence update)

102-AUG-1999 (TFEMBLrel. D7. Last sequence update)

103-AUG-1999 (TFEMBLrel. D7. Last sequence update)

104-AUG-1999 (TFEMBLrel. D7. Last sequence update)

105-AUG-1999 (TFEMBLrel. D7. Last sequence update)

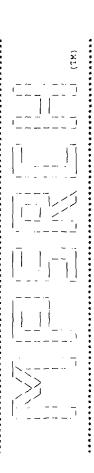
106-AUG-1999 (TFEMBLrel. D7. Last sequence update)

107-AUG-1999 (TFEMBLrel. D7. Last sequence update)

108-AUG-1999 (TFEMBLRel. D7. Last sequence update)

108
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MEDLINE: 94132877.
DELICHER D.L., PEKETE D.M., CEPKU C.L.;
"Asymmetric expression of a novel homeobox gene in veriobrain sension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.159
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ENDRESS M.E., SENNBLAD B., NILSSON S., CIVEYREL I., CHASE M.W.
HUYSMANS S., GRAFSTROEM E., BREMER B.;
CPETA BOL. 1.59-102(1996).
EMBL: 270198; CAA94087.1; ---
MENDE : 23592; Garth:ycf14;23592.
PPAM: FF01348; Introc_matur. S2; 1.
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        Length 8233
                                                                                       4: Indels
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Submitted (SEP-1995) to the EMBL/Genbank/DDBJ databases.
Submitted (SEP-1995) to the EMBL/Genbank/DDBJ databases.
Submitted (SEP-1995) to the EMBL/Genbank/DDBJ databases.
Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
EMBL: 95880: AAA79164.1.
EMBL: 95880: AAA79164.1.
PROSITE: PS00027: HOMEGL :: 1.
PROSITE: PS00027: HOMEGL :: 1.
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091964
091964
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1-NOV-1996 (TEMBLEEL 01, Created)
01-NOV-1996 (TEMBLEEL 02, Last sequence update)
01-NOV-1999 (TEMBLEEL 02, Last annotation update)
sensory ordan Homeobex Protein School
Score 71: DB 4: 13
Pred. No. 4.91e+00:
10: Mismatches 4
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Homeobox; DNA-binding: Nuclear protein.
SEQUENCE 259 AA; 27926 MW: 03819495 CRC32;
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    Ouery Match
Best Local Similarity 34.8%;
Matches 9; Conservative
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STRAIN-II:
MEDILINE: 97176397.
COSCHILANO P.W., YOUNG L.Y.;
"Identification and sequence analysis of two requiatory genes involved
In anaerobic toliene metabolism by strain Ii.";
Appl. Environ. Microbiol. 63:652-660(1997).
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Bacteria: Proteobacteria: beta subdivision: Rhodocyclus group.
Thauera.
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Bost Lonal Similarity 26.1%: Prod. No. 6.95c-00:
Matches 5: Conservative 12: Mismatches 5: Indels
                                        Query Match 33.8%; Score 70; DB 8; Length 505; Best Local Similarity 33.3%; Prod. No. 6.95e+00; Matches 6; Conservative 8; Mismatches 4; Indels Matches
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CCSCH.GANO P.W., YOUNG L.Y.;
CCSCH.GANO P.W., YOUNG L.Y.;
SJEmitted (FER-1999) to the EMBL/GenBank/DDBJ databases.
BMBL: U57950: AADIZ187.1; -.
BYPCTHELICAL Protein.
SSOHENIE 546 AA: 62313 WW: F4484D23 GRC32;
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                                                                                                                                                                     UT 15
092823 FRELIMINARY: PRT: 546 AA.
092823 00-MAY-1999 (TEMBLER): 10, Created)
01-MAY-1999 (TEMBLER): 10, Last sequence update)
01-MAY-1999 (TEMBLER): 10, Last annotation update)
TUTCI:
Chloropiast.
SEGUENCE 505 AA; 60113 MW: EDEB0038 CRC32;
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Job time : 21 secs.
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Release (1A John F. Collins, Biocomputing Research Unit. Copyriah: (c) 1993-1998 University of Edinburgh, U.K. Tistribution rights by Oxford Molecular Ltd.

MPsich_pp protein protein databuse search, using Smith-Waterman algorithm

Mo: Jun 19 16:19:11 2000; MasPar time 2:63 Seconds 81.065 Million cell updates/sec Rus on:

Tabular output not generated.

>US-09-142-524A-14 (1-9) from US09:42524A.pop 57 1 SIXRVSNVI 9

Gescription: Perfect Score: Sequence:

PAM 150 Gap 15

Scoring table:

188963 segs, 29686106 residues Searched:

Minimum Match O% Listing first 45 summaries Post-processing.

ardeneseg35 lidenesegp Dalabase:

Mean 15.426; Variance 44.241; scale 0.349 Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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W11473	W20206	56886W	W20776	W90011	858585	54 847	W55.279	W56301	868668	W19741	W71558	M98793	W20598	W26059	W93941	\$1010X	W79587	W92442	W98912	R80132	W30913
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ALIGNMENTS

Section 1

Cares .. O Score 53: DB 1: Legath 9: Pred. No. 1.87e-01: 6: Mismatches 0: Indels Query Match Best Local Similarity 160.0%; Matches 8; Conservative

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2 IKRVSNVI 9 qq ò

LT 2
WS7750 standard; peptide: 15 AA.
WS7750.
17-SEP-1998 (first entry).
Residues 166-126 of Cry ; ; .
Residues 166-126 of cry ; ; .
Residues 167-13 inmunotherapy:
HLA slass :I nolecuie. RESULT
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Matches
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           Cryptomeria jaronica.

WO9820402-A1.

22-May 1998.

22-May 1997.

32-May 1997.

23-May 1997.

23-May 1998.

R 13-NOV-1996. JP-30205.

R 13-NOV-1996. JP-30205.

R 13-NOV-1996. JP-30205.

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MAIL 96-297617/26.

PROPE CALLY MIX PROD CC LTD.

MPI: 96-297617/26.

PROD CC LTD.

MPI: 96-297617/26.

MPI: 9
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Japanese cedar police alleraen Cry) I derived I-cell epitope peptide.
Japanese cedar: pollen alleraen Cry) I: T-cell epitope: peptides:
prevention: treatment; cryptomeria polle: sis.
Cryptomeria Japonica.
CPYMY-1995
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20-001-1993; JP-262626.
METP : MELLI MILK PROD OC LTD.
MPT: 95-203834/27.
New cryptomeria pollen allorgen incoll epitupe populae - used in: prevention, treatment and investigation of Japanese redai publienesis provention, treatment and investigation of Japanese redai publienesis R75388 is the Japanese redai pollen allergen CTY1 : from which the Incoll optice peptudes R49289 R49295 were derived. The prevention and treatment of cryptomeria pollenosis, and also for the investigation of pollenosis.
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R4552.
13-3052:
Cry : pollen allergen peptide CJI-11.
Cry : pollen allergen peptide CJI-11.
Gryphumeria detection: allergy: treatment: diagnosts: 7 cell epitope: sensitivity.
Cryphumeria Japonica.
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Pred. No. 1.87e-01;
0; Mismatches 0; Indels
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Pred. No. 1.87e+01:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunotherapeutic agent is ineffective.
Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Pest Local Similarity 100.08:
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Owery Match
Best Local Similarity 100.0%:
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ai.ergy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Segmence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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WPIL 95-36591/47.

Wodified Cryptomeria (aponic, City 1) Epotide(s) - users, for treating allergy to (apanese vidar police allerge or minurologically proces reacting allergy to (apanese vidar police allerge or Search Flaure 2) English and processor or city 1) Have been modified as a pain of a product for prediction scheme to develop an optimised drug product for the aponic treatment of humans suffering from allergy to Japanese cedar police allergen or an allerge which is immunologically cross reactive with Japanese cedar pollen allergen. Such modified populdes possess certain characteristics which render them particularly consists of truggment corresponds to amino acids 101-120 of the allergen mature fragment corresponds to amino acids 101-120 of the allergen mature
                                                                                                                                                                                                                                                                                                                   used peptide of the Japanese cedar
acids 101-120. The peptide, Curill,
ad diagnosis of allergies associated
as enhanced therapeutic properties
at containally occurring allerges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1996 (first entry)

(cry) I againese Cedar polien alleraen peptide fragment (CLIOII).

Cry ) I japanese cedar polien allergeen modified: drug production:
allergy: Crytomeria japonica.
                                                                                                                                                                                                    Antigens derived from Japanese cedar poblen allerges {\rm Cry}(j)/i contain at least two T cell epitope(s), used to treat or diamnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
5
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Pred. No. 1.87e+01;
0; Mishatches 0: Indels
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                                                    10-JUL-1992: WO-905661.
01-SEP-1992: US-938990.
URMU-) HWMULDGIC PHARM CCRP.
Bond JF. Garman RD, Griffith II. Nuc M, Pollock J.
WPI: 94-035066/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Franzen BM. Kuc M. Powers SP.
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                                                                                                                                                                                                                                                            allergy
Claim 1. Fig 13, 137pp. Erring
The sequence is that of an iso it
pollen allergen Cry ) I (amin iso
can be used for the treatment of
with Japanese cedar poller
but reduced side effects complications)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LI 6
W44683 standard; peptide: 30 AA.
W44683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R82501 standard: Protein; 20 AA R82501;
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C6-ARP-1995: U04249.

C8-ARP-1995: U3-226248.

06-DEC-1994; U3-350225.

(TMMC-) IMMULOGIC PHARM CCRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 93.0%;
Local Similarity 100.0%;
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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W09527786-Al.
20-JAN-1994.
15-JAN-1993; U00139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans S,
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MASA 1997 JOO740.

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PRINT WAS 1997 JOO740.

C. O. MORE DESCRIPTION OF THE PRINT WAS 1997 JOO740.

C. O. WORLD WAS 1997 JOO740.

C. WORLD WAS 1997 
                                                                                                                                                                                                                                                                                                                                                                                                                    Theel epitope peptides W44682-88 and their derivatives react with sady hollinosis patient peripheral blood 7 lymphorytes A composition prepared by combining at least 2 of the above peptides and/or their derivatives is used for the prevention and treatment of sugil pollinosis.
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Multi-eptiope peptide used as immuotherapeutic agent *4.
Multi-eptiope peptide: immuotherapeutic agent; allergic disease:
T-cnit epticpe realon; allergen: lymphocyte: immuoqiobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                 13-Jan-1996: 161287.
24-JUN-1996: 161287.
24-JUN-1996: LEG1287.
24-JUN-1996: LEG1287.
24-JUN-1996: LPEMIND LID.
(MELL) MELUI SEIKA KAISHA LTD.
(MELL) MELUI SEIKA KAISHA LTD.
(MELL) MELUI SEIKA KAISHA LTD.

WELL: 8-134630/73.
I cell epitope peptide of sugi pollen a Ligen - usofil in the treatment of sugi pollings.
Claim: I: Page 4: 14pp: Japanese.
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Pred. No. 1.87e+01;
0: Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30;
01-May-1998 (first entry)
I-cell epitope poptide #2 of sugi pollen antigen.
I-cell epitope, sugi pollen antigen; sugi politnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59, DB 1; Le
Pred. No. 1.87e+61;
C: Mismatches ();
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Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Juery Match
Best Lond: Similarity 100.0%:
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                                                                                                                 Cryptomeria japonica
310007700-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 AA;
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WO9732660-Al.
                                                                                      Synthetic
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PER 12-581 (1997)
PER 12-581 (1997)
PER 12-581 (1997)
PER 13-581 (1997)
PER 13-582 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 32: Sapp. Japanose.

The present sequence represents a multi-epitope poptide which is used as a new immunotherapeutic adent, it comprises I cell epitope reducins from 2 or more different allorgens freeletably linked via arbithue or lyshing dimers), where the I cell epitope regions: have a positivity index greater than 100 as measured in a patient group responding to the allergen; have at least 70% reactivity with lymphocyres from patients responding to the allergen; and are not reactive with influenced builties (195) antibodies from patients responsive multipodies from patients responsive to the allergen; and are an additional and inservent and treat a wide variety of allergen. The apent can be used to prevent and treat a wide variety of allergen in a capit can be used to prevent and treat a wide variety of allerging liseases, etc. by desensitisation. Side effects, etc. those mediated by 135, are reduced.
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W27369: W27369: (first_entry)
W24-MAR1998 (first_entry)
W121-epicope peptide used as immunotherapeutic agent #1.
W121-epicope peptide: Amminotherapeutic agent: alleranc discass.
W17-ecil epicope region: alleranci lymphocyte; imminoglobulic E.
W97426(0.A).
24.MAR-1998 (first entry)
Mulli-epitope peptide used as immunotherapeutic agent *5.
Multi-epitope peptide: immunotherapeutic agent; allery: discass-
I-cell epitope region: alleryen: lymphocyte; immunoalchilu E.
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide immunostherapeutic agent to treat allerand discusss contains multi-epitope peptide containing T cell epitope regions from different allergens
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Pred. No. 1.87e+01:
Fred. Willes () Indels
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                                                                                                                                                                                                                12-SEP-1997.
10-MAR-1997. JCC740.
10-MAR-1996. JP-380702.
(MEIP.) MEIJI MILK PROD CO LTH.
Dairiki K. Iwama A. Kino K. Kur
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Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 9; Conservative
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                                                                                                                                       Synthetic.
WC9732600-Al.
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Best Local &
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L1 8 W27373 standard: peptide: 31 AA. W27373;

RESULI ID W2 AC W2

24 IKPVSNVI 31

2 :KRVSNV: 9

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Cedar polien allergen B.
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09-MAY-1995.
20-OCT-1993: 262626.
20-OCT-1993: JP-262626.
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EP-700929-A2.
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134 AA;
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Dairkix M. Wamma A. Kino K. Mume A. Sone T:

MPI: 97-47695/43.

Peptida immuno: phrapeutic agent to treat allergic diseases -
contains rulti-epitope peptide containing T cell epitope regions

from different allergens

Claim 6: 1496-31: Septe: Japanese.

The present sequence represents a multi-epitope peptide which is used as

The present sequence represents a multi-epitope peptide which is used as

The present sequence represents a multi-epitope peptide which is used as

The present sequence represents a multi-epitope peptide with is used as

The present allergens of petide regions: have a positivity index

Greater than 100 as measured in a patient group responding to the

Allergen: have at least 70% reactivity with lymphocytes from patients

The sponding to the allergen; and are not reactive with immunoglobilin E

(19E) antibodus from patients responsive to the allergen. The agent can

Class antibodus from patients responsive to the allergen and treat a wide variety of allergic diseases.

Sequence 105 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5: Page 42: 58pp: Laganese.

Claim 5: Page 42: 58pp: Laganese and the processor sequence represents a multi-epitope peptide which is used as a new immunotherapeutic agent. It comprises I cell epitope regions from 2 or none different allervens (preferably linked via arginine or lysine dimens), where the I cell epitope regions: have a spositivity index greater than 100 as measured in a patient group responding to the allervens and are not reactive with immunoslobulin E (igb) untipodies irom patients responding to the allergen and are not reactive with immunoslobulin E (igb) untipodies irom patients responsive to the alleratem. The about once the used to prevent and treat a wide variety of alleratic diseases, e.g. by desensitisation, side effects, e.g. those mediate; ly 102, are reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
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                                                                                                                                                                                                                                                                                                       24-MAR-1998 (first enity)
Multi-epitope peptide isad as immunotherapeutic agent #2.
Multi-epitope peptide immunotherapeutic agent; allergic disease;
The peptide region: allergen: lymphocyte; immunoglobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MMR-1998 (lirst entry)
Multi-epitope peptide used as immunotherapeutic agent #5.
Multi-epitope peptides in motherapeutic agent; allerand disease
T-cell epitope regions alleraem: lymphonyte, immunoalabulin E.
Synthetic.
W0973250C-Ai.
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contains multi-epitope peptide containing I cell epitope regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 105:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409/35.00
12-826-1997.
10-MARK-1997. JU0740.
10-MARK-1996. JF-060702.
10-MAR-1996. JF-060702.
(MEIP.) MEIT MILK PROD CO LID.
TELY K, LWAMA A, KIND K, KUME A, SOBE T:
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10-MAR-1997. 160740.
10-MAR-1995. JE-980762.
(MEIP.) MEJJI MILK PROD CO LITE.
MAJI 97-470495/43.
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W2737: standard: peptido: 134 AA.
W2737:
                                                                                                                                                                                                                     standurd; peptide: 105 AA
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Local Similarity 100.0%:
es 8: Conservative
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                                                  2 :KRVSNVI 9
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M27370:
DE W27370:
DE W27370:
DE MULLI-EPLODE
KW 7-0-81 ePLODE
K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
WC9732600-Al.
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FY5388 is the Japanese cedar pollen alleraen Cryj I., trom which the Troll epitope peptides R89289-R89295 were derived. The peptides can be used for the prevention and treatment of cryptomeria pollenosis, and also for the investigation of pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sign
                                                             Gaps
                                                                                                                                                                                                                                                                                                    Japanese cedar pollen allergen Cryl I.
Japanese cedar: pollen allergen: Cryl I: T-cell epitope: peptides
prevention: treatment; cryptomeria pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pollen, allergen, imm neglobulin E, 19E, Treel, epitupe:
ly: pollinosis: therapy: immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         School 527 198 10 Denuth 553,
Pred No. 1.87e+01;
Score 53: DB 1: Length 134: Pred. No. 1.67e-01:
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106, 120
/note="T-cell epitope peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "T-cell epitope peptide"
91, .105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "-cell epitope peptide"
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/note= "I-cell epitope
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08-SEP-1995; 306295.

10-SEP-1994: JP-242137.

14-JUL-1995: JP-200264.

14-JUL-1995: JP-200264.

(HAYE.) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
61. .75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K81567 standard: Protein: 353 AA.
R81567:
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R75388 standard; protein; 353 AA.
R75388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MEIP.) MEIJI MILK PROD CO LID. WPI; 95-203834/27.
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326
                Query Match
Best Local Similarity 106.0%;
Matches 8; Conservative
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Local Similarity 10:104:
es 8: Conservative
                                                                                                                                                                                                                                                                                      12-MAR-1996 (first entry)
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              Hinc K. Saito S. Taniquebi Y.

WPI: #-140976/15.

When periodics derived from cedar pollen allergens - activate allergen-specific Teells, but not allergen-specific Igs antibodies.

Jaim El page 3132: 56pp; English.

Synthetic peptides base on portions of cedar pollen allergens A (RB199) and B (RB199) were tested for their doubley to activate a specific Ircells, but not allergen-specific Igs antibodies. 6 Peptides (RB189) were 1dentilied as Treell epitodes. 1 hase peptides, 10 Ns subsequences (RB19179) essential epitodes. 1 hase peptides in subsequences (RB19179) essential confront as immittation, and horologous peptides (RB189 96) can be useful as immittation, and horologous peptides (RB189 96) can be useful as immittation, and horologous peptides (RB188 96) can be useful as immittation and horologous peptides (RB188 96) can be useful as immittation and horologous analysis.
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23 July 1993 (first entry)
Cry Japanese cedar pollen; allorgen; antigen; allergy: B cell; T cell.
Cryptomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-44x-1995 (first entry)
Japannes cedar pollen antiqen Gryji.
Japannes cedar: pollen antiqen: allergen: Gryji: sigi: pollinosis.
Gryptumeria japonica.
Key.
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Pred. No. 1.87e-01:
U: Mismatches 0
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1. 21
/note= "signal peptide"
22. 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               760166 standard: Protein: 374 AA.
860166:
24-488-1995 (first entry)
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R31937 standard: Protein: 374 AA
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19-711-1997
107-2AN-1993: G01116.
67-JAN-1993: JP-UCITI6.
(MELT.) MELUI SEIKA KAISHA.
MPI: 94-269689/33.
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PER 13-13-A.

21-JAN-1993.
PP 21-JAN-1993.
PP 10-D1-1992; U05651.
PP 10-D1-1991; US-730452.
PP 10-D1-1991; US-730452.
PP 15-JUL-1991; US-730452.
PP 15-JUL-1991; US-730452.
PP 16-JUL-1991; US-730452.
PP 17-JUL-1991; US-730452.
PP 18-JUL-1991; US-730452.
PP 18-JUL-1991; US-730452.
PP 18-JUL-1991; US-730462.
PP 18-JUL-1991; US-73046.
PP 18-JUL-1991; US-73046.
PP 18-JUL-1991; US-73046.
PP 18-JUL-1991; US-73046.
PP 18-JUL-1991; US-JUL-1991; US-JUL-
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Best Local Similarity 100.0%: Pred. No. 1.87e+61:
Matches 8: Conservative 0: Mishatches 0: Indeis
/note+ "mature Gry ) I*
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MPsrch_pp = protein - protein database search, using Smith-Waterman algorithm

Tue Jun 20 13:37:46 2000; MasPar time 2.17 Seconds 59.945 Million cell updates/sec Kun on:

Tabular output not generated.

>US-09-142-524A-14 (1-9) from US09142524A.pep 57 1 SIKRVSNVI 9 Title: Description: Perfect Score: Sequence:

2ak 150 3ap 15 Scoring table:

145341 seqs, 14437480 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Mean 14.393; Variance 44.473; scale 0.324 Database

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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77.2 564 2 US-08-865 - Sequence 1, Application 1. 27.2 51 0.5-08-865 - Sequence 4, Application 1. 25.5 1 0S-08-459 - Sequence 4, Application 2. 25.5 1 0S-08-459 - Sequence 4, Application 2. 25.5 1 0S-08-459 - Sequence 4, Application 2. 25.5 1 0S-08-516 - Sequence 4, Application 2. 25.6 1 0S-08-516 - Sequence 4, Application 2. 25.6 1 0S-08-516 - Sequence 3, Application 2. 25.4 2 0S-08-576 - Sequence 3, Application 2. 25.4 2 0S-08-576 - Sequence 3, Application 2. 25.4 2 0S-08-672 - Sequence 3, Application 3. 2 0S-08-842 - Sequence 6, Application 3. 2 0S-08-842 - Sequence 6, Application 3. 2 0S-08-842 - Sequence 6, Application 3. 2 0S-08-842 - Sequence 7, Application 3. 2 0S-08-842 - Sequence 2, Application 3. 2 0S-08-310 - Sequence 2, Application 3. 2 0S-08-310 - Sequence 2, Application 3. 2 0S-08-310 - Sequence 97, Application 4. 3. 4 PCT-0855-0 Sequence 97, Application 4. 227 1 0S-08-310 - Sequence 6, Application 4. 227 1 0S-08-310 - Sequence 6, Application 4.	a :	Match	Cenati	Ē.	0 1	Description		Fred. No.
77.2 510 US-08-655 Sequence 6, Application 1. US-08-459 Sequence 4, Application 2. 255 1 US-08-459 Sequence 4, Application 2. 255 1 US-08-459 Sequence 2, Application 2. 255 1 US-08-56 Sequence 4, Application 2. 257 1 US-08-576 Sequence 4, Application 2. 257 1 US-08-576 Sequence 3, Application 2. 254 2 US-08-576 Sequence 3, Application 2. 254 2 US-08-576 Sequence 8, Application 2. 252 1 US-08-672 Sequence 9, Application 3. 2 US-08-672 Sequence 9, Application 3. 2 US-08-842 Sequence 142, Application 3. 2 US-08-310 Sequence 2, Application 3. 2 US-08-310 Sequence 142, Application 3. 2 US-08-310 Sequence 142, Application 3. 2 US-08-310 Sequence 97, Application 4. 227 1 US-08-310 Sequence 97, Application 4. 227 1 US-08-310 Sequence 6, Application 4.	7	77.2	564	7	US-08-865-	Sequence 1.	Application	1.39e-02
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71.9 401 2 US-08-576- Sequence 45, Applicati 2 US-08-679- Sequence 3, Applicatio 2 US-08-679- Sequence 3, Applicatio 2 US-08-672- Sequence 9, Applicatio 3 US-08-672- Sequence 9, Applicatio 3 US-08-672- Sequence 9, Applicatio 3 US-08-842- Sequence 9, Applicatio 3 US-08-871- Sequence 2, Applicatio 3 US-08-816- Sequence 12, Applicatio 3 US-08-916- Sequence 12, Applicatio 3 US-08-916- Sequence 12, Applicatio 3 US-08-916- Sequence 142, Applicatio 3 US-08-916- Sequence 97, Applicatio 4 US-08-917- Sequence 97, Applicatio 4 US-08-110- US-08-110- Sequence 97, Applicatio 4 US-08-110-	٠, 4	5.5		(7	US-08-031-	Sequence 4,	Applicatio	2.90e+02
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71.9 2544 2 US-08-576- Sequence 32, Applicati 2. 10.2 332 1 US-08-672- Sequence 8, Application 3. 10.2 332 2 US-08-872- Sequence 9, Application 3. 10.2 332 2 US-08-842- Sequence 9, Application 3. 10.2 332 2 US-08-842- Sequence 9, Application 3. 10.2 885 4 PCT-US95-0 Sequence 2, Application 3. 10.2 885 4 PCT-US95-0 Sequence 2, Application 3. 10.2 885 4 PCT-US95-0 Sequence 2, Application 3. 10.2 909 2 US-08-310- Sequence 142, Application 3. 10.2 909 2 US-08-310- Sequence 142, Application 3. 10.2 909 2 US-08-310- Sequence 97, Application 4. 10	4 1	5. 5.		7	US-08-679-	Sequence 3.	Applicatio	2.90e-02
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76.2 332 2 US-08-780- Sequence 2, Applicatio 3.76.2 332 2 US-08-842- Sequence 8, Applicatio 3.76.2 332 1 US-08-842- Sequence 8, Applicatio 3.76.2 332 1 US-08-811- Sequence 9, Applicatio 3.70.2 885 4 PCT-US95-0 Sequence 2, Applicatio 3.70.2 885 4 PCT-US95-0 Sequence 2, Applicatio 3.70.2 959 4 PCT-US95-0 Sequence 142, Applicatio 3.70.2 959 4 PCT-US95-0 Sequence 142, Applicatio 3.70.2 959 4 PCT-US95-0 Sequence 97, Application 4.84 33 4 PCT-US95-0 Sequence 97, Application 4.884 33 4 PCT-US95-0 Sequence 97, Application 4.884 33 4 US-08-310- Sequence 97, Application 4.884 227 1 US-08-745- Sequence 6, Application 4.	4 0	70.2		. 1	US-08-672-		Applicatio	3.59e+02
76.2 332 2 US-C8-842- Sequence 8, Applicatio 3.76.2 332 2 US-O8-842- Sequence 8, Applicatio 3.76.2 332 1 US-O8-671- Sequence 9, Applicatio 3.70.2 885 4 PCT-US95-0 Sequence 2, Applicatio 3.70.2 885 4 PCT-US95-6 Sequence 2, Applicatio 3.70.2 885 4 PCT-US95-0 Sequence 142, Applicatio 3.70.2 909 2 US-O8-310- Sequence 142, Applicatio 3.70.2 909 2 US-O8-310- Sequence 97, Applicatio 4.88.4 33 2 US-O8-310- Sequence 97, Applicatio 4.88.4 33 2 US-O8-310- Sequence 97, Applicatio 4.27 1 US-O8-310- Sequence 67, Applicatio 4.27 1 US-O8-310- US-O8-31	0	70.2		ď	US-08-780-		Applicatio	3.69e+02
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70.2 885 4 PCT-US95-6 Sequence 2, Applicatio 3 70.2 885 2 US-08-316- Sequence 142, Applicatio 3 70.2 909 2 US-08-310- Sequence 142, Applicat 3 68.4 33 4 PCT-US95-0 Sequence 97, Applicat 4 68.4 33 2 US-08-310- Sequence 97, Applicat 4 68.4 227 1 US-08-310- Sequence 6, Applicati 4 68.4 227 1 US-08-346- Sequence 6, Applicati 4	40	70.2		4	PCT-US95-0	Sequence 2,	Applicatio	3.69e+02
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227 1 US-08-745- Sequence 5, Applicatio 4	65	68.4	~	(7	US-08-310-			4.68e+02
	G)	68.4	22	-1	13-08-345-	Sequence 6,	Applicatio	4.68e+02

4 39 68.4 227 1 NS-08-597- Sequence 2. Application 4.68±-62 3 68.4 317 2 08-518- Sequence 2. Application 4.68±-02 3 68.4 317 3 08-951- Sequence 2. Application 4.68±-02 8 68.4 346 1 07-761- Sequence 2. Application 4.68±-02 9 39 68.4 503 1 05-68-50 Sequence 6. Application 4.68±-02 1 39 68.4 503 1 05-68-47 Sequence 6. Application 4.68±-02 1 39 68.4 1019 2 05-68-47 Sequence 2. Application 4.68±-02 3 68.4 1019 2 05-68-47 Sequence 2. Application 4.68±-02 4 39 68.4 1019 1 05-08-22 Sequence 2. Application 4.68±-02 5 38 66.7 1 05-08-22 Sequence 3. Application 4.68±-02 6 38 66.7 1 05-08-22 Seque	T 1 CS-08-865-337A-1 STANDARD PRI: 564 AA. XXXXXX	03 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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Post Local Similarity 62.5%: Pred. No. 1.39c-02:
Matches 5: Conservative 3: Mismatches 0: Indels
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COMPUTER CARA
COMPUTER READABLE FORM:
MEDDING THE COMPUTER.
COMPUTER. DISKETTO
COMPUTER. SWITTER
COMPUTER.
                                          STRANS

CPROJACE SOURCE:

LIBRARY BRAINOTIA

CLONE: Consensus

TWO 564 AA: 62110 MW: 1662460 CN:

TWO 564 AA: 62110 MW: 1662460 CN:

TWO 73 NO. 177
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08865337A Patent No. 5972649
SENERAL INFORMATION:
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SEQUENCE CHARACIERISTIGS:
LENGIR: 564 amino acids
TYPE: umino acid
STRANDENESS: siggle
TOPOLOGY: linear
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Sequence 4, Application US/ H59264
Patent No. 570320
Patent No. 570320
GENEAL INFORMATION:
GENEAL INFORMATION:
GENEAL INFORMATION:
APPLICANT: TALLY Frances P
APPLICANT: GLUZZANN, B-(L) A
APP
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MEDIUM TYPE: Floppy disk
COMPUTER: Parentin Release #1.0, Version #1.46
COMPUTER: Parentin Release #1.0, Version #1.46
COMPUTER: Parentin Release #1.0, Version #1.46
COMPUTER: COMPUT
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                                                                                                                                                                        Query Match 77.2%; Soure 44; DB 2; Lendth 610-Best Local Similarity 62.5%; Frod. No. 1.396-02;
Matches 5; Conservative 4; Misratches 0. Indels
CLONE: 1945387
SEQUENCE 610 AA: 67466 MW; 1878916 CN:
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IMMEDIATE SCERCE:
CLONE: B-LACTARASE
JENCE 255 AA: 27847 MW: 349604 CN:
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MCLECULE TYPE: peptide
ORIGINAL SOURCE:
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1D US-08-459-264-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXX
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GENERAL INFORMATION:
APPLICANT: Anlaixy, No. 580769;rdine
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Hen, Rene
APPLICANT: Hen, Rene
ITILE OF INVENTION: Polypeptides Having Serotonin Receptor
ITILE OF INVENTION: Polypeptides Having Serotonin Receptor
ITILE OF INVENTION: Polypeptides and Uses Thereo:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sdro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.6. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/356.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.9%; Score 41; DB 1; Let Best Local Similarity 85.7%; Pred. No. 2.90e-02; Matches 5; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATE: 29-JUN-1992
PRIOR APPLICATION DATE: 40-JUN-1992
APPLICATION DATE: 01-JUN-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 99-519
REFERENCE/DOCKET NUMBER: 89-519
REFERENCE/DOCKET NUMBER: 89-519
RECOMMUNICATION INFORMATION:
INCOMMUNICATION INFORMATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 A.A.
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rhone-Poulenc Morer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE 1YPE: protect.
JENCE 357 AA: 40804 WW: 741967 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCOMTR: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08031538 Patent No. 5968817
                                                                                                             Sequence 2, Application US/08356405
Patent No. 5807691
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                                                                Sequence 2, Application US/08356405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (610)454-38*9
TELEPAX: (610)454-3808
INFORMATION FOR SE0 10 No: 2: SEQUENCE CHARACIEH:STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 357 amino acids
amino anid
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US-08-031-538-4
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                                                                                                                                                                                                                                                                                   Sequence 4. Application US/08459263
Patent No. 574242
GENERAL INFORMATION:
APPLICANT: RASMUSSEN. Beth A
APPLICANT: GLUZMAN, Yakov
ITILE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCES
ITILE OF INVENTION: DV CLASS B BETA-LACTAMASE ENZYMES FROM BACTERCIDES
ITILE OF INVENTION: FRAGILIS
ON THE OF INVENTION: PRAGILIS
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COMPTER 19022
COMPTINE FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CORRESTING SYSTEM: PC-DGS/MS-DGS
SOFTWARS: Partentin Release #1.0, Version #1.30
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,263
FILING LATE: 02-02N-1995
FILING LATE: 02-02N-1995
TACKETE/CATION: 1335108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42: DB 1: Length 255: Pred. No. 2.27e+92; 2: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING HAIE: V. C.C.
CORNEY ACTION: 435
ALTORNEY ACENT INCRAATION:
NAME: Rebinson. Joseph R
REGISTRATION NUMBER: 33.448
REEDSCOMMUNICATION INFORMATION:
TELEPHIAE: 212-527-7700
TELEPHIAE: 212-753-6337
TELEX: 226-687
INFORMATION FOR SEC ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEUKTH: 255 Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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IMMEDIATE SOURCE:
CLONE: B-LACIAMASE
SENCE 255 AA: 27647 MM: 349664 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                               PRT:
                                                                                                                                                                                                                                                     Sequence 4, Application US/08459263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSES: Darby PC
STREET: 865 Ihird Avenue
CITY: Now York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANCARD:
                                                                                                               SIANDARD;
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ORIGINAL SOURCE:
ORGANISM: Bacillus ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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ID US-C8-356-405-2
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AC xxxxxx
                                                                                                             US-38-459-263-4
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3 KRVSNVI 9
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SENERAL INFORMATION:
APPLICANT: SUCCLIFE, U Gregor
APPLICANT: Extender, Mark G
APPLICANT: LOVELDER: Timothy W
TITLE OF INVENTION: HIMAN SEROTON:N REMEPTORS. DNA ENCODING
TITLE OF INVENTION: HE RUCEPTORS, AND USES THEREOF
NUMBER OF SUCURES: 73
CORRESPONDENCE ADDRESS:
ADDRESSED: The SCRIPPS Research Institute: Himce of
ADDRESSED: The Sourieps Research Institute: Himce of
ADDRESSED: The Sourieps Research Institute: Himce of
STREET: 10566 No. 5958817th Toriey Plues Road, TPC B
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                                                                                                                                                                                                                                                                                                                                                                                                           CWOLLER REARABLE FORM:

CWOTER REARABLE FORM:

WEDION THEE FORM:

WEDION THEE FORM:

WEDION THEE FORM:

POLDOSAMS:

SOFTWARE:

FILLING SYSTEM:

POLDOSAMS:

SOFTWARE:

FILLING SYSTEM:

POLDOSAMS:

FILLING SYSTEM:

FILLING SYSTEM
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Patent No. 54-8194
GENERAL INN: RAMATION: US/08576526A
AFFLICANT: RAIZ. L
APPLICANT: R
APPLI
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                                                                                                                                                                                                                                                                                                 STREET: 10666 N
                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 9977-925-80-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISS KRVSNVM 161
                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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MEDIUM TYPE: Floppy disk
COMBUTER: EN PC compatible
COMBUTER: EN PC compatible
COMBUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATORNEY/ACENI INFORMATION:
NAME: Diamed Casion
REGISTRATION NUMBER: P-40.94 (
REFUENCE/COCKET NUMBER: G-57.US.U)
TELECOMMUTCATION INFORMATION:
TELECHONE: (847) 936-317
COMPUTER REAABLE FORM:
MEDIUW TYPE: DISKELE
COMPUTER: IBM COMPATIE:
COMPUTER: IBM COMPATIE:
COMPUTER: IBM COMPATIE:
COMPATING SYSTEM: DIS
SOFTIMENE: REALESU VERSION 2 U
COMPATION NUMBER: US/18/574.626A
FILLING DATE: 21-DEC-1995
CLASSIFICATION 1435
PROCR APPLICATION 1435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
MOLECULE TYPE: No. 5998194e
SEQUENCE 401 AA: 43347 WW: 755260 CN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEG 10 NO. 45:
SEQUENCE CHARACTERISTICS:
I DNOTH: 401 amino acids
1:ee: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD
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US-08-579-635A-3
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   SEQUENCE CHARACTERIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COPERATING SYSTEM:
                                                                                                                                1833 IRRVCD11 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 TVKRVGIII 170
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                                                                                                                                              2 IKRVSNVI 9
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              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
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ID US
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                                                                                                                                                                                                                                                                                                                                                                Sequence 32. Application US/08576626A
Parent No. 5998194
GENERAL INFORMATION:
APPLICANI: Summers, R.G.
APPLICANI: Summers, R.G.
APPLICANI: Donadio, S.
APPLICANI: Donadio, S.
APPLICANI: Staver, M.J.
ITLE OF INVENTION: 9105VNTHESIS GENES
NUMBER OF SEQUENCES:
ADDRESSE: ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISACLE
                                                                                                                                                                                  Overy Match
Best Local Similarity 55.6%; Pred. No. 2.90e+02:
Matches 5; Conservative 2: Mismatches 2: Indels
ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600.1-141
IELECOMMUNICATION INFORMATION:
TELECHONE: 201-48-5800
TELEFAX: 201-343-1684
INFORMATION FOR ESQ IS NO: 3:
SECURCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast660 Version
CURRENT APPLICATION UNBER: US/08/576,626A
FILING DATE: 2: DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuo.
REGISTRATION NOMBER: P+40,943
REFERENCE/DOCKET NUMBER: 5857.US.OI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-2623
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                    HYPOTHETICAL: NO
SEQUENCE 445 AA: 49222 MW: 983134 CN:
                                                                                                                                                                                                                                                                                                                                                           Segmence 32, Application US/08575526A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                             148 SAKRIDDVI 156
                                                                                                                                                                                                                                                                                          US-C8-576-626A-32
                                                                                                                                                                                                                                                SIKRVSNVI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yamada, Tad., ka
APPLICANT: Yamada, Tad., ka
TILE OF INVENTION: Gene Encoding Melanocortin Receptors
NUMBER OF SECURSES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         0
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                                                                                                                                                               Query Match
71.9%; Score 41: DB 2; Length 2544,
Best Local Similarity 50.0%; Pred, No. 2.90e+02:
Matches 4; Conservative 3; Miscratches 1: Indols
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Local Similarity 44.4%; Pred. No. 3.69e+02;
Nes 4; Conservative 4; Mismatches 1; Indels
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SCHWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 'CQ/672,109B
FILLING DATE: June 27, 1596
CLASSITICATION: S36
ATTRANSY AGENT INFORMATION:
NAME: SMILE, DEADN F.
RECISTATION NUMBER: 36693
REFERENCE/DOCKET NUMBER: 21.5-000853DVC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Harress, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hill.
                                                                                                                                                                                                                                                                                                                                                                                                                     332 AA
                                                                    TOPOLOGY: linear | MOLECULE TYPE: No. 5998194e | SEQUENCE 2544 AA: 279108 FM; 3:031572 CN:
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MOLECULE TYPE: protein
SEQUENCE 332 AA; 36956 MW; 598933 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/C8672109B
Patent No. 5710265
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08 721098
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (810)641-1600
2544 amino acids
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amino acid
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ZIP: 48303
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AC XXXXX

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DI XX SEQUENCE 8 AFFINCE SEQUENCE SE
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 2. Application 05/08769749A
Patent No. 543279
GENERAL INFORMATION:
APPLICANT Leo, Frank
APPLICANT Leo, Rei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
FITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT WIMBER OF SEQUENCES: 10
CORRESPONDED ADDRESS:
APPRESSORDED ADDRESS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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Pred. No. 3.69e-02:
4: Mismatches 1: Indels
                                                   332 AA
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STREET: 1155 Avenue of the Americas
CIIY: New York
STAIE: New York
                                                   PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10.66/271;
COMPUTER FEALMALE FURM:
NEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DCS
SOFTWARE: FEASESU VEYSION 2.0
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SEQUENCE 332 AA: 35987 MW: 998934 ON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7. E. C.
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Paront No. 5869257
GENERAL INFORMATION:
APPLICANT: Yanada, Tadataka
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08780749A
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                                                   STANDARD:
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Rest Local Similarity 44.4%:
Matches 4: Consorvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKROWE
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ACCONTRACTOR SECULARY

ACCONTRACTOR SEQUENCE 2, Application of the process of the
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US-08-842-238-8
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Parcet No. 5817797
CENERAL INFORMATION
APPLICANI: Vanada, Tadataka
APPLICANI: Vanada, Tadataka
APPLICANI: Vanada, Tadataka
APPLICANI: Genes Encoding Melanocortin Receptors
UNMBER OF SEQUENCES: 23
CORRESPONDENCE ADURESS:
ADDRESSEE: Harress, Dickey & Pierce, P.L.C.
STREET: P.O. Box R28
CITY: Bloomfield Hills
STATE: M.
APPLICANT: Gantz, Ira
FILLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Match 70.2%: Shore 40; DB 4; Length 42; Local Similarity 44.4%: Fr 4; No. 3 696-62; Res 4; Conservative Mismatches 1; Indels Res
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,045
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATION:
OPERATING SYSTEM: PC-DOS/MS-DNS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/842.236
                                                                                                       ADDRESSEE: Harness, Dickey & Fierce, P.L.C. STREET: P.O. Box 828
STREET: P.O. Box 828
STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILLING DATE:
CLASSIFICATION: A 45
AIONEY/AGET. INFORMATION:
NAME: SMITCH, DEADN F.
REGISTRATION NUMBER: 34683
REFERENCE/POCKET NUMBER: 2115-600854DVE
IELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 6:
SECUENCE CRARACTERISTICS:
LENGIH: 332 amino acids:
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MCLECULE TYPE: prote:n
UENCE 332 AA: 36956 MW: 596933 CN:
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Length 332

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Score 40: DB 1; Li
Pred. No. 3.69e+02;
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TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 885 amino acids TYPE: amino acid STRANDEDNESS: not releva
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Best Local Similarity 44.4%;
Matches 4; Conservative
Ouery Match
Best Local Similarity 44.4%;
Matches 4; Conservative
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CITY: Boston
STATE: MA
                                                              162 IVKRVGIII 170
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                                                                                        1 SIKRVSNVI 3
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PCT-US95-04589-2
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Patent No. 5703220
GENERAL INFORMATION:
APPLICANT: Yamadd, Tadataka
APPLICANT: Santz, Ira
APPLICANT: Santz, Ira
APPLICANT: SANTS, Ira
APPLICANT: SANTS IN Receptors
NUMBER OF SEQUENCES: 23
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Pred. No. 3.69e+02;
4: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: CARRESPONDENCE ADDRESS: AADDRESSE: Harness. Dickey & Pierce, P.L.C. STREET: P.C. Box 828
C.TY: Booffield Hills
STATE: MI
           CLASSIPICATION: 536
ATORNIY/ASAFITATION:
NAME: SELIC, DEAGES: 36693
REGISTRATION NUMBER: 36693
RECISTRATION NUMBER: 2115-C00853DVE
IELECHMUNICATION INFERMATION:
TELEPHONE: (810)641-1650
INFERMATION FOR SEQ ID NO: 8109541 N
                                                                                                                                                                                                                                                                                                                                                                                                                 332 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCLECULE TYPE: protein
SEQUENCE 332 AA: 36956 MW: 598933 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/086715258
                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 332 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 44.4%;
Matches 4: Conservative
                                                                                                                                                                                                                                                                                                                       162 TVKRVGIII 170
                                                                                                                                                                                                                                                                                                                                                   SIKRVSNVI 9
                                                                                                                                                                                                                                                                                                                                                                                                  LT 14
US-08-671-5258-8
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1: Indels
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ZIP: 02110-2994
COMPUTER READBLE FORM:
MEDININ TYPE: Floppy disk
COMPUTER: 19M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SCFTWARE: PATENTIN RC-BASE #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2. Application PC/IUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel: Fraderick M.
APPLICANT: Stackwicz, wien J.
APPLICANT: Brent, Andr. F.
APPLICANT: Brent, Andr. F.
APPLICANT: Margiri, F. Jiaki
APPLICANT: Karagiri, F. Jiaki
APPLICANT: Karagiri, F. Jiaki
APPLICANT: Middinos, Muchael M.
APPLICANT: Widdinos, Muchael M.
APPLICANT: You Guo-Liun
APPLICANT: Yo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PROR APPLICATION DATA:
PROR APPLICATION DATA:
APPLICATION NUMBER: US 06/227.3f.
FILING DATE: 13-APP-1944
AITORNEY/AGENT INFORMATION:
NAME: CLATK, Faul 1
REJESTRATION NUMBER: 31.162
REFERENCE/ZOCKET NUMBER: 00746/23000)
TELECOMMUNICATION INFORMATION:
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 885 AA; 102110 MM: 4152599 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                       FRT
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (*) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:28:52 2000: MasPar time 14:36 Seconds 63:146 Million cell updates/sec Tabular output not generated.

Run on:

>US-09-142-524A-14 (1-9) from USO9142524A.pep 57 Description: Perfect Score: sednense:

1 SIKRVSNVI 9

PAM 150 3ap 15 Scoring table:

721208 segs, 100765575 residues

Searched

Minimum Match 0% Listing first 45 summaries Post-processing:

Catabase

a-pending lient 2:06 3:050 4:07 5:080 6:081 7:082 8:083 9:084A lo:0648 11:085 12:086 13:067 14:088 15:089 16:090 17:091 18:092 19:093 20:094 21:095 22:NEWP 23:NEWD50 24:NEWD8 25:NEWD9

Nean 17,247; Variance 40,530; scal 0.426 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4.33e-01 4.33e-01 4.33e-01 4.33e-01 4.33e-01 4.33e+01 4.33e+01 Sequence 36, Applicati Sequence 4, Applicati Sequence 5, Applicati Sequence 5, Application Sequence 5, Application Sequence 62, Applications Sequence 1, Application Sequence 2, Application Sequence 3, Application Sequence 15, Application Applicati Applicati Applicati Applicati Applicati Sequence 5, A Sequence 52, Sequence 62, lescription Sequence 62 Sequence 62 Seguence 62 Seguence 62 CS-C8-46G-CS-C8-46G-CS-C8-25G-US-08-226-US-08-35C-US-08-35C-US-09-142-US-09-142-US-08-468-US-08-468-US-08-467-US-08-467-US-08-467-US-08-467-US-08-467-US-08-142-US-09-142-US-09-142-US-09-142-US-09-142-US-09-142-US-09-142-US-09-142-US-09-142-US-09-142-US-09-142-Score Result No.

```
Sequence 36, Application US/J79389vCA
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Pollock, Joanne
APPLICANT: Bond Julian
TILLE OF INVENTION: Allergenic Proteins And Peptides From
TILLE OF INVENTION: Allergenic Codar Pollen
CORRESPONDENCES:
CORRESPONDENCE AUGRESS
ADDRESSED: Lahive & Cocxfield
SIREH: Sixty State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCUMING THE CONTROL OF THE CONTROL O
                                                                                                                                                                                                                                                                                                                                              Cuery Match 93.0%: Soure 54: LB lot Lougth 200
Best Local Similarity 100.0%: Pred. No. 4.33e+61;
Matches 8: Conservative 0: Mismatches 0: Indeis
  REGISTRATION NUMBER: 38.872
REFERENCE/DOCKET NUMBER: 025.6 USD6 (IMI-028CPD6)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.A. O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36. Application US/07938990A
                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA; 2080 MW: 2304 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARL
                                                                                                                                                                              : 20 amine acids amine acids
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                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
ID US-57-938-990A-36
                                                                                                                                                                                                                          TOPOLOGY:
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APPLICANT Griffeth. Irwin J.,
APPLICANT Bollock. Joanne:
APPLICANT Bond, Jalian F.:
APPLICANT Garman. Richard D.,
APPLICANT Ruo, Mei-Chang,
APPLICANT Ruo, Mei-Chang,
APPLICANT Brauer, Andrew,
APPLICANT Brauer, Andrew,
APPLICANT Bracks, Sturmen H.:
APPLICANT Bracks, Sturmen H.:
APPLICANT Bracks, Sturmen H.:
APPLICANT Bracks, Sturmen H.:
APPLICANT Bracks, Sturmen APPLICANT Bracks, Sturmen MUMBRR OF SEUJENCES.
IIILE OF INVENTION LAPACES. 26:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immutogic Pharmaceutical Corporation. Inc.
STREET GOUTRY USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :
ن
                                                                                    NAME: Carlene A. Vanstone
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-0280P2)
TELECOMMINICATION INFORMATION:
TELEPRONE (617) 466-6000
TELEFAX: (617) 466-6000
TELEFAX: (617) 466-6000
SEQUENCE OFARACIERITICS:
SEQUENCE CHARACIERITICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cuery March 93.0%, Score 53, DB 10: Length 20: Best Local Similarity 100.0%; Pred, No. 4.33e-01; Matches 8: Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARDINE VAION
CARTIEN VAION
CARDINE FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CYMPUTER: BEN PC compatible
CYMPUTER: PATENT: PC-DCS/MS-DCS
SOFTWARE: PATENT: Release #1.0, Version #1.25
COMPUTER: PATENT: No. 910:
CAPPLICATION NOMBER: US/08/467,006
FILING DATE: June 6, 1995
CLASSIFICATION DATA
PRIOR APPLICATION DATA
PRIOR APPLICATION DATA
FILING DATE: December 6, 1994
ALTONEY/AGENT INFOMMATION:
CALLING DATE: DECEMBER 6, 1994
ALTONEY/AGENT INFOMMATION:
CALLING DATE: DECEMBER 7, 1994
ALTONEY/AGENT INFOMMATION:
CALLING DATE: DECEMBER 7, 1994
ALTONEY/AGENT INFOMMATION:
CALLING DATE: DECEMBER 10, 1994
ALTONEY/AGENT INFOMMATION:
CALLING DATE: DATE
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/08467006 GENERAL INFORMATION:
                                                                          FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Darlene A. Vanstone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36. Application US/08467006
                                                                                                                                                                                                                                                                                                                                           TYPE: amino actd
TOPOLOGY: licear
M. LECULE TYPE: peptido
ERAGMENT TYPE: interial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1P: 02154
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IL US-08-467-006-36
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Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOINFUL INFORMATION:
APPLICANT: Bond, Julian F.:
APPLICANT: Gorman, Fichard C:
APPLICANT: Gorman, Fichard C:
APPLICANT: Young, Siurnei H.:
APPLICANT: Young, Siurnei H.:
APPLICANT: Exaley, Mark A.:
APPLICANT: Exaley, Mark A.:
APPLICANT: Exaley, Mark A.:
APPLICANT: Dowers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From ITILE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 26:
APPLICANT: SEQUENCES: 26:
APPLI
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SIREET: 610 Lincoin S'
SIATE: Waltham
SIATE: MA
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Best Local Similarity 100.0%; Pred. No. 4.33e-01;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 38,872
RECOMMUNICATION NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 227-7400
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACIERISTICS:
              Score 53: DB 7: Length 20:
Pred. No. 4.33e-01;
C: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Foliase #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18/08/467.029
FILLING DATE: Jone 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
APPLICATION NUMBER: 16/550.225
FILLING DATE: December: 4/, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     23 AA
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./MS-DOS
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FRAGMENT TYPE: inter...1
SEQUENCE 20 AA; 2085 MW; 2364 CN;
                                                                                                                                                                                                                                                     STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy (COMPUTER: 1BM PC COM; OPERATING SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                 Query Match 93.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                             10 IKRVSNVI 17
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                                                                                                                                        2 IKRVSNVI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH
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APPLICANT FOLLOCK, Joanne:
APPLICANT FOLLOCK, Joanne:
APPLICANT GAIRAN, Richard D.
APPLICANT GAIRAN, Richard D.
APPLICANT GAIRAN, Richard D.
APPLICANT STU-mei H.)
APPLICANT Brauer, Andrew.
APPLICANT Brauer, Andrew.
APPLICANT Brauer, Steven P.
IIILE OF INVENTION: Alierquenic Proteins and Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEDJEMENS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: Immulogic Pharmaceutical Corporation, Inc.
SITEET: 610 Lincoin St
CITY: Waltham
SIATE: MA
CONTRY: USA
CONTRY: USA
ZIP: 70154
COMPUTER: EDAR: FORM:
MEDIJWITPE: FIDOPY disk
COMPUTER: EDAREE FORM:
MEDIJWITPE: FORM: DE-GASE 4.00. Version 41.25
COMPUTER: EDAREE FORM: DE-GASE
SOFTWARE: PREVIOUS AND ADTA:
APPLICATION NUMBER: US/08/226,246A
FILING DATE: SEPTEMBER: DT/VS93/00139
FILING DATE: SEPTEMBER: DT/VS93/00139
FILING DATE: SEPTEMBER: DT/VS93/00139
FILING DATE: SALUMBER: DT/VS93/00139
FILING DATE: ADALMATION:
MAMME: DATE-CANANICATION NUMBER: DS.725
REFERENCE/DOCKET NUMBER: DS.725
REPREVIEW DS.725
REFERENCE/DOCKET NUMBER: DS.725
REPREVIEW DS.725
REFERENCE/DOCKET NUMBER: DS.725
REPREVIEW D
                                                                                                                                                           ;;
O
                                                                                                                                                         C; Indels
                                                                                                             Score 53; DB 4; Length 20; Pred. No. 4.33e+01: 0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                               20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/08226248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36. Application US/08225248A
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FRAGMENT TYPE: internal
FNCE 20 AA: 2080 MW: 2304 CN:
                   MCLECULE TYPE: peptide
FRAGMENT TYPE: internal
UENCE 20 AA: 2080 MW: 2304 CN:
                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                             Juery Match
Best Local Similarity 100.5%;
Matches 8; Conservative
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  RESULT 4
ID US-08-226-248A-36
                                                                                                                                                                                                  10 IKRVSNVI 17
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                                                                    SECTENCE
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RESULT 7
ID US-08-467-697-36
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                                                                    ó
                                                                                                                                                                                                                                                                         APPLICANT No. Mel-Chang:
APPLICANT Yeung Siu-mei H.;
APPLICANT Braier, Andre H.;
APPLICANT Braier, Andre H.;
APPLICANT Braier, Andre H.;
APPLICANT Braier, Andre H.;
APPLICANT Braier, Sieven P.
APPLICANT POWERTS, Steven P.
TILE OF INVENTION: Japanese Cedar Pollen
CTRES PROBRESS: 26
ADDRESSEE, ImmuLogic Pharmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                       E: ImmuLogic Pharmaceutical Corporation, Inc. 610 Lincoln St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDION TYPE: Floppy disk
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/35C,225
FILIN: DATE: December 6, 1994
CLASS:FICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,246
APPLICATION NUMBER: 07/938,90
FILING DATE: September: 1992
APPLICATION NUMBER: PCT/35%3/U01%4
FILING DATE: September: 1992
APPLICATION NUMBER: PCT/35%3/U01%4
FILING DATE: September: 1992
APPLICATION NUMBER: PCT/35%3/U01%4
FILING DATE: January 18, 1963
ATIONEV/ASSN: INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53: DB 8: Length 20: Pred, No. 4.33e+01;
C: Mismatches C: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Darluge A. Vanstone
REGISTATION NUMBER: 35.729
REFERENTE/DOCUMBER: 025.6 US (IMI-028GP2)
TELECOMMUNICATION INFRAMATION:
TELEPHONE: (617) 466-6000
                                                                    20 AA
                                                                                                                                                                                    Sequence 36. Application US/38350225
GENERAL INFUSRATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Boldox, Joanne:
APPLICANT: Bond, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Nuc, Mai-Chang,
APPLICANT: Nuc, Mai-Chang,
APPLICANT: Pung, Sturmel H.;
APPLICANT: Brauer, Andrew:
                                                                     PRT:
                                                                                                                                                            Sequence 36. Application US/08350225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Inear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
UENCE 20 AA; 2080 MW; 2364 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 15 NO. 36: SEQUENCE CHARACTERISTICS: LENTH: 20 amin 1705.
                                                                     STANCARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: C2154
CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaery Match 93.0%;
Rest Local Similarity 105.0%;
Matches 8; Conservative
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                                                         LT 6
CS-08-350-225-36
1:1': : : 2 1KRVSNVI 9
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STATE:
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                                                                                                                                                                                                                      APPLICANT SILICAL AND APPLICANT POLICACY, JOSE APPLICANT BOND, JULIAN APPLICANT GALTAIN, Richa D. APPLICANT KUO, Mei-Cha: APPLICANT KUO, Mei-Cha: APPLICANT YOUNG SIU THE APPLICANT POWERS AND APPLICANT POWERS. Stewn P. TILLE OF INVENTION: Albergacic Proteins And Peptidos From TILLE OF INVENTION: Albergacic Proteins And Peptidos From TILLE OF SEQUENCES: Stewn P. TILLE OF SEQUENCES: Stewn P. TILLE OF SEQUENCES: 2511 CORRESPONDENCE ADDRESS: ADDRESSE: Immulogic Planmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53: DB 10: Length 20:
Pred. No. 4.33e+01:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER 0.55.6 USD4 (IMI-CZROPIG)
TELECOMMUNICATION INF RMA (IMI-CZROPIG)
TELECHIONE (617) 2.27 % (17)
TELECHIONE (617) 2.27 % (17)
TELECHIONE (617) 2.27 % (17)
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.697
FILING DATE: June 6, 1995
20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 087-50-225
FILING DATE: December 6, 1594
ATIONEX/AGENT INFORMATION
NAME: 3 are E. Remillar
REGISTRATION NUMBER: 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-OOS/MS-DIS
                                                                                                                                                          Sequence 36, Application US/18167697
SENERAL INFORMATION:
APPLICANT: Griffeth, INC. J.
                                                                                                                         Sequence 36, Application US/08467697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA; 2080 MM: 2364 CN;
                                                                                                                                                                                                      Gritfeth, irw. J.,
Pollock, Joan
Bond, Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 610 Lincoln st
CITY: Walthar
STATE: MA
COUNTRY: USA
ZIP: 02154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 amino acids
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Local Similarity 100.0%;
es 9; Conservative
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Best Local S
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Score 53: DB 17: Length 31: Pred. No. 4.33e+01: 0: Mismatches 0: Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
                                                                                                                                                                                                                                                                  Sequence 62, Application US/07938990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 60 Aa; 6644 MW: 19464 CN;
31 AA; 3585 KW; 4902 CN;
                                                                                                                                                                             STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                             Ouery Match
Best Local Similarity 105.0%;
Matches 8; Conservative
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ID US-C7-938-990A-62
                                                                                    24 IKRVSNVI 31
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                                                                                                       2 IKRVSNVI 9
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 SEQUENCE
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SENERAL INFORMATION:
APPLICANT: Some, Toshio
APPLICANT: Kume, Akinori
APPLICANT: Karnixi, Kazuo
APPLICANT: Mama, Akiso
APPLICANT: Lama, Akiso
APPLICANT: Monsuke
IIILE OF INVENTION: Peptide-based Immunotherapeutic Agent For Treating
IIILE OF INVENTION: Allergic Diseases
FILE REFERENCE: Docket No. SPO-103
CURRENT FILING DATE: 1999-31-04
EARLIER APPLICATION NUMBER: US/09/142.524
CURRENT FILING DATE: 1996-03-10
EARLIER FILING DATE: 1996-03-10
EARLIER FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE PATENTIN VOY: 2.0
SEQ ID NOS: 5
                                                                Sequence 4, Application US/03142524

GENERAL INFORMATION:
APPLICANT: Sone, Toshio
APPLICANT: Kariki. Kazuo
APPLICANT: Wame, Akiso
APPLICANT: Non-SP-103
CURRENT APPLICATION NUMBER: US/09/142,524
CURRENT APPLICATION NUMBER: 9/80/702
EARLIER FILING DATE: 1996-03-10
EARLIER FILING DATE: 1997-03-10
NUMBER CF SEQ ID NOS: 5
SCHARRE: PALENTIN Ver. 2.0
SEQ ID NOS: 3
SEQ ID NOS: 3
SEG ID NOS: 3
SEG ID NOS: 3
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                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism:peptide SEQUENCE 31 AA; 3661 MW; 4960 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Unknown Crganism:peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53: DB 17: Length 31;
Pred. No. 4.33e+01;
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AA
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                                           Sequence 4, Application US/09142524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match
Local Similarity 100.0%;
Nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                 IYPE: PRI
ORGANISM: Unknown
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ORGANISM: Unknown
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 IKRVSNVI 31
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                                                                                                                                                                                                              Sequence 62. Application US/U7+38990A
GENERAL INFORMATION:
APPLICANT: GILIfit, Irw.n J.
APPLICANT: Pollock, Joanne
APPLICANT: Bond Julian
TITLE OF INVENTION: Albergenic Proteins And Peptidus Ficm
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive 6 Cockfield
STREET: Sixty State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 19920901

CLASSIFICATION: 435

PRICK APPLICATION: 435

APPLICATION NUMBER: 15, 191

APPLICATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

RECISTRATION NUMBER: 36,207

RECISTRATION NUMBER: 36,207

RELEPHONE: (617) 227-5941

INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHRRACEERISTICS:
LENGTH: 60 Aming acids

LENGTH: 60 Aming acids
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                                                                                                                                 Sequence 62. Application US/C8466940
SEREAL INFERMATION:
APPLICANT: Gilloth Irwin US/B8468940
APPLICANT: Golloth Irwin US/B8468940
APPLICANT: Golloth Ulian F.)
APPLICANT: Goldoth Ulian F.)
APPLICANT: Garman, Richard D.
APPLICANT: Brown, Sturmel H.)
APPLICANT: Existy, Marchard D.
APPLICANT: Existy Marchard D.
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARED: PATENTIN Release #1.0. Version #1.25
CURRENT APPLICATION LATA:
APPLICATION NUMBER: US/06/468,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Darlene A. Vanstoro
REGISTRATION NUMBER: 35,729
REFERENCE/GOCKET NUMBER: C25.6 US (IMI-U2NCH2)
TELEPHONE: (617) 466-600
TELEPHONE: (617) 466-600
INFORMATION FOR SEQ 15 NO: 62:
SEQUENCE CHARACTERISTICS:
                          50 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER (8/226,248 FILLNS DATE: AFFIL 9, 1948 APPLICATION NUMBER: 07/938,990 FILLNG DATE: SOFTEMBER: 1, 1992 APPLICATION NUMBER: PCIVCE93/001/09 FILLNG DATE: 0.01.017 15, 1993 ATTORNEY/AGENT INFORMATION:
                             9.8.1
1.4
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350.225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: December 6, 1994 APPLICATION NUMBER: 08/226,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 60 AA: 6644 MW: 19464 CN;
                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02154
OCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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best Local Similarity 100.08;
Matches 8; Conservative
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GY: linear
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RESULT 11
ID US-08-468-940-62
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OBMERAL INFORMATION

APPLICANT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Immulogic Pharmaceutical Corporation, 610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-5'8/MS-1'S
SOFTWARE: Pate:tin Felease #1.0. Version #1.25
CURRENT APPLICATION DAIA:
                     60 AA
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                                                                                                                                           Sequence 52, Application US/08225248A
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FRAGMENT TYPE: internal
JENCE 60 As; 6644 MW; 19464 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 466-5100
TELEFAX: (617) 466-6.41
INFORMATION FOR SEQ ID NO: 62.
                     STANDARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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LENGTH: 60 amino acids
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Best Local Similarity 100,0%;
Matches 8; Conservative
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                   US-08-226-248A-62
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US-08-467-697-62
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ZIP: 02154
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US-08-350-225-62
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                                                                    Sequence 62, Application US/08467697
GENERAL INSTRUCTION.
APPLICANT Griffeth, Irwin J.,
APPLICANT Bollock, Joanne,
APPLICANT Bollock, Joanne,
APPLICANT Garman, Richard D.,
APPLICANT Garman, Richard D.,
APPLICANT FORG STITME H.,
APPLICANT FORG STITME! H.,
APPLICANT STAGE STITME! H.,
APPLICANT Brauer Andrew.
APPLICANT POWERS STITME! H.,
APPLICANT Brauer Andrew.
ITLE OF INVENTION: Albergenic Proteins And Peptides From UNTARR OF SEQUENCES: 261
CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ć.
                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: MA
COUNTRY: MA
COUNTRY: MA
COMPUTER: READABLE FORM:
MEDITY TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCATION DATA:
APPLICATION NUMBER: US/08/467,697
FILMS DATE: WS/08/467,697
FILMS DATE: WS/08/410N: WS/08/467,697
FILMS DATE: WS/08/410N: TELEPHYNE: (617) 227-7440
INFORMATION FOR SEQ 15 NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 aming deids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%: Pred. No. 4.33e+01,
Matches 8: Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      ADDRESSEE: Immulogic Pharmaceutical Corporation.
SIREET: 610 Lincoln St
CIIY: Waltham
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 60 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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                                                         62. Application US/08467697
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US-08-467-023-62
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APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Suu-mei H.;
APPLICANT: Yeung, Suu-mei H.;
APPLICANT: Extey, Mark A.;
APPLICANT: Extey, Mark A.;
APPLICANT: Powers, Steven P.
IIILE OF INVENTION: Allorgenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESSONDENCE ADDRESS:
ADDRESSEE: Immittogic Pharmaceutical Corporation, Inc.
STREET: Hullouic Pharmaceutical Corporation, Inc.
STREET: Maltinan
STREET: Waltinan
                                                                                                                                                                               Guery Match 93.0%; Score 53: DB-8: Length 66: Best Local Similarity 100.0%; Pred. No. 4.336-01; Matches 6: Conservative 0: Mismatches 1: Indels
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REGISCHAIN FOR SEQ 10.73
SEQUENCE CHARACIERISTICS:
LENGTH: 60 aming acids
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TOPCLGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 60 AA: 6644 MW: 19454 CN;
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Sourch completed: Mon Jun 19 16:29:08 2600 Job time: 16 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm WPsrch_pp

Mon Jun 19 16:18:47 2000; MasPar time 4.95 Seconds 85.758 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-14 (1-9) from US09142524A.pep 57 : SIKRVSNVI 9

Title: Description: Perfect Score: Sequence:

PAM 150 Cap 15 Scoring table:

142080 seqs. 47172405 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir62 1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 22.352; Variance 25.242; scale 0.886 Statistics: Pred. No. is the number of results pred.cted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 20 0	3,770-01	3.776-01		9	2.32e+01	2.32e+01	۲.	ř.	3.76e-01	.76	3.76e+01	3.76e-01	3.76e+01	3.76e+01	3.76e+01		3.76e+01	6.02e+C1	٥.	6.02e+01	0.	6.02e+01	6.02e+C1
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75.4 318 2 537225 ribose-phosphate pyro 6.022-01 75.4 377 2 66937 hypothetical protein 6.22-01 75.4 439 2 3 .24 probable aspatrokinas 6.22-01 75.4 459 2 1 .08 probable aspatrokinas 6.22-01 75.4 459 2 1 .08 probable aspatrokinas 6.22-01 75.4 788 1 .00728 APPORTER Protein 6.02-01 75.4 785 1 .00728 APPORTER Protein 6.02-01 75.4 785 1 .00728 APPORTER Protein 6.02-01 75.4 785 2 .00728 APPORTER Protein 6.02-01 75.4 792 2 .00728 APPORTER Protein 6.02-01 75.4 792 2 .00728 APPORTER Protein 6.02-01 75.4 75.3 APPORTER Protein 6.02-01 75.4 75.3 APPORTER Protein 7.07-01 75.4 75.3 APPORTER Protein 7.07-01 75.4 75.4 75.4 75.4 75.4 75.4 75.4 75.4	ALICNMENTS #ty, complete rgen Cry) I pree	Komiyamd, N.: Shimizu, K.: Kusakabe. : K. K. S. Sequencing of commun. (1994) 199:619-62 d sequencing of conv. coding for Cry 3 of Japanese cedar polien. 4183234 **Habe! Sch **D25545: NID:4493633; PID:d1006087; PI polit uthors inscribed carbohydrate binding idne. 2	y pectors (yase 18159) In Front Standard Sequence Establish predict major allergen (IV) () I (cloudicted elabel MATA (Sex) (coving site carbohydrate (Asn) (covincted elabel mata) I mmolecular weight 40702 mebt	93.0%; Score 53; DB 2: Length 374; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; NVI 138 NVI 9	JC2123 #type omplete major allergen Cr j I precursor (clone pCCI-2-2) - Japanese cedar #formal_name Cryptomeria japonica #common_name Japanese cedar 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
40000000000000000000000000000000000000	RESULT ENTRY TITLE ORGANISM	CONS NOTE THOUS TITLED TO SOSS - TEFER SOSS - TEFER TO SOSS - TEFER THE SO	CLASSIFICATION KEYWORDS FEATURE 1-21 22-374 158.191,293,3	Query Match Best Local Sim Matches 8; Db 131 IKRVSN OY 2 IKRVSN	RESULT 2 ENTRY TITLE ORGANISM DATE

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ACCESSIONS REFERENCE

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##FESIGUES 1958 ##Jabe: HIM ##CTOSS-Teferences EMBL:AE00044; GB:U00089; NID:q1674140; PID:q1674156 ##DOTOSS-Teferences EMBL:AE00044; GB:U00089; NID:q1674140; PID:q1674156 ##DOTE the nucleotide sequence was submitted to the LMHL Lata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ###COSSITECTURINGS GEORGES GEORGES NIT (####77:31 PID)QZ##3745. GB:AEUGH457
###XPerimental_source strain VE5
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Lenox, A.L.: Graham, D.E.: Overboek, R.; Scead, M.A.;
Keller, M.; Anjay, M.; Buter, R.; Feldman, R.A.;
J.M.: Obsen, G.G.: Swarson, R.V.
Nature (1998) 392:453-358
The complete genome of the hyperthermophilic pacterium
                                                                                                                                        of the barretim
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type II secretion system protein (gspE-3) homolog -
Archaecglobus fulgidus
formal_name Alchaecglobus fulgidus
55-Dec-1997 *sequence_revision 05-Dec-1997 *text_change
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Pred. No. 2,32e+01;
2; Mismatches 1; Indels
*sequence_revision 25-Apr-1997
                                                                                                                                          inalysis of the genome criae.
                                                                          Himmelreich, R.: Hilbert, H.: Plagens, B.C.: Herrmann, K.:
Nucleic Acids Res (1996) 24:4420-4449
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#length 192 #molecular-weight 22076
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#Cross-references MUID:981966*6
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Mycoplasma preu
#cross-references MUID:97:05885
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Best Local Similarity 66.7%;
Matches 6: Conservative
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27-Feb-1997 #se
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                                                                                                                                                                                                                                                                                    *accession PC165
##molecule_Lype protein
##residues 22-13158+81,219-232,236-158,299-307,346-372 ##label SG2
##molecules 22-13158-81,219-232,236-158,299-307,346-372 ##label SG2
##mole testidue 279
residue 279
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                                  ERENCE 17.123
FRUIDOUS SCHOOL TIL KOMINGMMA, N.) Shimizu, K.; Kusakabe, T.; Morikubo, Fauthors School TIL Komingma, N.) Shimizu, K.; Kusakabe, T.; Morikubo, Fauthors British Brothers Brothers Brothers Brothers Brothers Brothers Brothers Brothers of Charles and Sequencing of CDNA coding for Cry j 1, a rajor efficiency Millorgen of Capanese cedar pollen.

**Cross-reference* Millorgen of Capanese cedar pollen.
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                                                                                                                                                                                ##Cross-references GB:025.44; NID:q493631; PID:d1906086; PID:q493632
##experimental_source pollen
rocks.nn PC2665
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Matches 7: Conservative 1; Mismatches 0: Indels
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Matches 8; Conservative
    26-Aug-1999
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#authors
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TITLE ORGANISM PATE

RESOLT ENT RY SUMMARY

ORGANISM

RESULT UNIRY TITLE

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22-374

SUEMARY

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Gaps

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                                                                      Fauthors Klenk, H.P.; Clayton, R.A.; omb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc, R.J.; Owlnon, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyrpides, N.C.; Eleischmann, R.D.; Ouackenbush, J.; Loc, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Ouackenbush, J.; Peterson, S.; Reich, C.I.; McNeal, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kanne, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujil, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.D.; Woese, C.R.; Venter, J.C.

**Pipural Nature (1997) 390:364-370

##Cross-references Wuldergenome sequence of the hyperthermophilic, Sulfate-reducing archaeon Archaeogicbus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoside-diphosphate kinase (EC 2.7.4.6) - Aquifex aeolicus #formal_name Aquifex aeolicus 10-sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *region ATP binding *status predicted\
*active_site His (phosphohistidine intermediate) *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Deckert, G.: Warren, P.V.; Gaasterland, T.: Young, W.G.: Lenox, A.L.; Graham, D.E.; Overbeex, R.: Snead, M.A.; Keller, M.: Aday, M.: Huber, R.: Feldman, R.A.: Stort, J.M.: O.Esn. G.J.: Swanson, R.V.

#journal Nature (1999) 392:353-358
#tile The Complete genome of the hyperthermophilic bacterium Aquifex acolicus.
#cross-references WIID:98-96666
#accession F70437
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ATP binding: hexamer: phosphohistidine; phosphoprotein;
phosphotransferase; pyrimidine nucleotide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **cross-references GB:AE001035; GB:AE000782: NID:92689358;
PID:AAB90245:: FID:9264959; ISOR:AF0996
FICATION *superfamily conserved hypothetical protein MJ0930
RY *length 569 *mclecular-weight 66520 *checksum 121:
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PID:q2983932; GB:AE000657
**experimental_source strain VF5
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translation not shown
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Pred. No. 2.32e+01;
2; Mismatches 0; Indels
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Best Local Similarity 75.0%:
Matches 6: Conservative
29-Sep-1999
569374
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*#molecule_type_DNA
##residues 1-159 ##label MIG
##cross-references GB:M30487: NID:g336645: PIDN:AAA67629 1: PID:g336655
RNCE 215840 Stirewalt, V.L.: Michalcwski, C.B.: Luffelhardt, W.: Buhnert,
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                                                                                                                                                                                                                                                                                                                                                Michalowski, C.B.: Pianzagl, B.: Loeffelhardt, W.: Bohnert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal protein SS - Synechocystis sp. (strain PCT 6803) protein $11812 | Formal_name Synechocystis sp. pcc 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, July 1995
Nucleotide sequence of the cyanelle genome from Cyanophara
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                                                                                                                                                                                       ribosomal protein S5 - Cyanophora paradoxa cyanelle
ribosomal protein S5 - Cyanophora paradoxa
#formal_name cyanelle Cyanophora paradoxa
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_chanave
22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                 *journal Mol. Gen. Genet. (1990) 224-222-231
*Litle The cyanelle SIO spc ribosonal protein Gene Uperon Hiom Cyanophora paradoxa.
*Cross:references.MUID:91117189
                                             Gaps
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Esuperfamily Escherichia coli ribosomal protein SS
cyanelle: protein biosynthesis: ribosome
Flength 169 - #molecular-weight 17980 - #checksum 755
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**cross-references EMBLU30 21; NID:q1016683; PIDN.AAA81219
**experimental_source strait Pringsheim L8555
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Sest Local Similarity, 62.5%; Fred. Nr. 5.7%+51;
Matchys., 5. Conservative. J. Mismatches. G. Lochs.
    Length 142:
                                         1: Indels
Score 44; DB 1; L
Pred. No. 3.75e+01;
                                           3: Mismatches
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  Ouery Match 77.2%;
Best Local Similarity 55.6%;
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                                             Conservative
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T06876
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R.A.; Gocayne, C.D.; Keriavdge, A.R.; Dougherty, P.A.; Tomb, J.F.; Adams, M.D.; Reich, C.L.; Overbeek, R.; Khrhess, E.F.; Weinstock, K.G.; Merrick, J.W.; Gillek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Sadow, P.W.; Hanna, M.C.; Cotton, M.C.; Fuhrmann, C.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.C.; Fuhrmann, M.C.; Fuhrmann, M.C.; Cotton, M.C.; Fuhrmann, M.C.; Fuhrmannn, M.C.; Fuhrmann, M.C.; Fuhr
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##cross-references GB:AE000743: NID:G2983875: PID:G298384: UB:AE00557
##experimental_source strain VFS
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iron-dependent tartrate debydratase beta chain homilody
carbon-oxyden lyase; bydro-lyase
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homology # abel TIDE
#length 195 #molecular-welcht 21868 #checksim 6962
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1-195 ##label BUL
##cross-references GB:U67510: OR:177117: NID:q1591325: PIDM.AAR~M412.
##cross-references GB:U67510: OR:177117: NID:q1591699
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Pred. No. 3.76e+01;
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Fordw. A.L.: Chart, E. E.: Worbeek, P.: S
Milber, M.: A.: An. N.: W. H.: F.: Bullen,
J. M.: Jases, D.: Watton, V.
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Matches 4; Conservative
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Bult, C.J.: White, C.: Olsen, G.J.: Zhou, L.; Fleischmann,
R.D.: Sutton, G.G.: Blake, J.A.: FitzGerald, L.M.: Clayton,
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                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence not shown: translation not shown
    #journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium Synechocysis sp. PCD6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MUD:97061201
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Submitted to the EMBL Data Library, April 1998
The sequence of A. thallana FUN23.
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Pred. No. 3.75e+01:
4: Mismatches 0: Indels
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Best Local Similarity 62.5%:
Matches 5: Conservative
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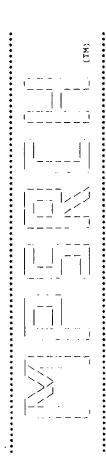
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                                                                                                                                                                                     Tan, J.; d'Agostaro, G.A.F.; Bendiak, B.; Reck, F.; Sarkar, M.; Squire, J.A.; Leong, P.; Schachter, H. Blochem. (1995) 231:37-328 The human UD-N-acetylqlucosamine:alpha-6-D-mannoside-beta-1, 2- N-acetylqlucosaminy.transferase II qene (MGAT2). Cloning of genomic DNA, localization to chromosome 14q21, expression in insect cells and purification of the
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alpha-1,6-mannosyl-qlycoprotein beta-1,
2-N-acetylqlucosaminyltransferase (EC 2.4.1.143) - human
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KEYWORDS alycoprotein: alvor
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Babyichuk, E.; Cottrill, P.; Storozhenko, S.; Fuangtiona, M.; O'Farrell, M.; Van Montagu, M.; Inze, D.; Kushnit, S. submitted to the FiBL Data Library, November 1997
Higher plants po poss two poly(ADP-ribose) polymerasus.
**residues 1-457 **)>bel KLE
**cross-references GB:AE '125; GB:AE000783; NID:q2688021;
PIDN:AA.:66531.1; PID:q2688030; TIGR:BB0135
**experimental_source strain B31
**EXPERIMENTAL_source strain B31
**ECATION **superfamily histidine--tRNA ligase; amino acid--tRNA ligase
repeat homology; histidine--tRNA ligase homology
                                                                                                                                                                                                                                                                                                                                                                                          :.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA binding: glycosyltransferase: NAD: pentosyltransferase
*length 653 *molecular-weight 72995 *checksum 7074
                                                                                                                                                                                    aminoacyl-tRNA synthetase: liquase: protein biosynthesis
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*length 457 *molecular-weight 52848 *checksur 4898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 2; Length 653:
Pred. No. 3.76e+61;
3: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Query Match 77.2%: Score 44; DB 1; Length 457; Best Local Similarity 56.7%: Pred. No. 3.76e-01; Matches 5; Conservative 2; Mismatches 1; Indels
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Best Local Similarity 62.5%;
Matches 5: Conservative
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                                                                                                                         CLASSIFICATION
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edimburgh, J.K. Distribution rights by Oxford Molecular Ltd

protein * protein database search, using Smith-Waterman algorithm MPsrch_pr

Mon Jun 19 16:17:57 2000; MasPar time 3.44 Seconds 79.741 Million cell updates/sec Rutt on:

Tabular output not generated.

>CS-09-142-524A-14 (1-9) from USC9142524A.pep 57 Description: Perfect Score:

SIKRVSNVI 9 sedneuce: 83857 seqs, 30454973 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38

Mean 22.858; Variance 21.70%; scale 1.053 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUGI BASHI FRITEIN PPE 4
PUTATE LIASS PECURSO
HYPOTHELICAL PROTEIN M
NUCLEOSIDE DIPHOSPHATE
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30S RIBOSOMAL PROTEIN
PUTATIVE FUMRATE HYDR I HYPOTHETICAL 42.0 KD P ASPARTOKINASE (EC 2.7. DIACYLGLYCEROL KINASE, ATP-DEPENDENT PROTEASE RIBOSE-PHOSPHATE PYROP HYPOTHETICAL 82.1 KD PHYPOTHETICAL PROTEIN M HISTONE H4. CHLOROPLASI 30S RIBOSO ALPHA-1,6-MANNOSYL-GLY HISTIDYL-TRNA SYNTHETA 30S RIBOSCMAL PROTEIN 30S RIBOSCMAL PROTEIN THIAMINE BIOSYNTHESIS Description SBP_TRYJA PEL_EMEN: Y269_MYCPN NDK_AQUAE RRS_CYAPA RSS_SYNY3 FUMBAN SYH-BOREC SYH-BOREC SYH-BOREC MENI MOUSE MENI HUMAN YMS2 YEAST Y682_METJA H4_PHYPO RRS_PORPU RSS_MYCLE RSS_MYCTU KPR2_YEAST APBE_SALIY YPJH_BACSU AK_CHLIR KDGA_MOUSE LON_RICPR SUMMARIES 2 Query Matob Leagth Score Result No.

1.356-61	10-056	1,756-01	2, 986-51	I 2 996-01	1 2 980-01	1 2.98e-01	1 2.980-01	4	A 2, 98+01	: 1	~	?	.7	2.48e-	Y 2.98+-01	2.986-01	1 5.01++01	0 5.014+21	เก	5.010+01	50,000
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VD05_VACCV	VD05_VARV	VD05_VACCC	RS5_SYNP5	BLAB_BACCE	BLA2_BACSP	BLA BACCE	F. B_HAEIN	Fr. BRAT	E:PB_MOUSE	K 'S_XENLA	DNAA MYCGE	DNAA_MYCPN	SUIZ YEAST	XYLG_HAEIN	PPOL_ARATH	YAH8_SCHPC	YGG4_YEAST	APGI_YEAST	MML2_MYCTU	YHK3_YEAST	TOREN CHAN
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0.1	(Rel. 32, Last se
0.1	15-DEC-1998 (Rel. 37, Last am Station update)
DE	SUGI BASIC PROTEIN PRECURSOR SBP) (MAJOR ALLERGEN GRY 3 1) (CRY 3 1).
SO	
8	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
8	euphyllophytes, Spermatophyth, Confidencesida, Confidences,
8	Taxodiaceae: Cryptomeria.
Z.	
RP	SEQUENCE FROM N.A., AND PARTIAL SECUENCE.
S,	TISSUE*POLLEN
×	MEDITINE: 94183234
RA	Sone T., Komivama N., Shimizu K., Kusakabe T., Morik Do K.
RA	
RT	"Cloning and sequencing of CDNA coding for Cry 3 1, a major allergen
RI	•
RL	Biochem Biophys. Res. Commun 199:619-625(1994).
S.	[2]
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эг Эг	SEQUENCE OF 22-41.
S.	TISSUE-POLLEN;
×	MEDIINE; 89031257.
RA	Taniai M., Ando S., Usui M., Karimoto M., Sakaquchi M., Inouve S.,
ΚX	
RT	"N-terminal amino acid sequence of a major allergen of Japanese cedur
RT	
RL	FEBS Lett. 239:329-332(1988).
γ. ∝	[7]
RP	CARBOHYDRATES.
×	MEDLINE; 95003748.
RA	Hijikata A., Matsumoto I., Kojima K., Ogawa H.;
RT	"Antigenicity of the oligosaccharide molety of the Japanese cedar
RT	
RL	Int. Arch. Alleray Immunol. 105:198-202(1994).
ပ္ပ	-!- PTM: CONTAINS FUCOSE/XYLOSE-CONTAINING N-LINKED OLISOSACCHARIDES.
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36	- I SIMILADITA' BETONG TO THE BOLVENCHABINE TAKED DAMITY I
)	CARLEAUTIC BELOWGO TO THE FOLISACCHARIDE LIASE FARILL I.

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EMBL: U05592; AAA80568.1;
PFAM: PF00544: pec_lyase;
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Best Local Similarity
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P75395;
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     SOFFE
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                 This SKISS-PROT ectry is copyright. It is produced through a collaboration the EMBL cutstitute of Bioinformatics and the EMBL cutstation the Employment of Bioinformatics in Stitute. There are no restrictions on its use my non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ist-sib.ch).
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MEDLINE: PSTUBS56.

"New Co., Whitehead M.P., Cleveland I.E., Dean R.A.;

"Sequence analysis of the Aspergillus miduians postate lyase pelA
gene and evidence for binding of promoter regions to CREA, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1: Length 374;
Pred. No. 4.96e-02;
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1 -> F (IN CRY J 1-B).

4 -> Y (IN CRY J 1-B).

5 -> T (IN CRY J 1-B).

L -> S (IN CRY J 1-B).

L -> S (IN CRY J 1-B).

K -> O (IN CRY J 1-B).

K -> O (IN CRY J 1-B).

POTENTIAL.

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W: 74AB25950248F56F CRC64:
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Eukaryota: Ponii: Ascomycoa: Pieciom, cetes: Ei: 1.u ms
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EMBL: 026545: BAA0520.1: --
EMBL: 034639: BAA0520.1: --
EMBL: 034639: BAA0520.1: --
EMBL: 034639: BAA0520.1: --
EMBL: 034639: BAA0520.1: --
PRINTS: PRC0607: AMBALLEGEN.
Allergen: Giynoprotein: Wiltigene family: Signal.
SIGNAL.
22 374 SGS: BASIC PROTEIN.
VARIAN: 12 12 1. -> F (IN CRY J.1-B).
VARIAN: 22 202 1. -> 7 (IN CRY J.1-B).
VARIAN: 22 22 1. -> 7 (IN CRY J.1-B).
VARIAN: 22 22 1. -> 7 (IN CRY J.1-B).
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15-DEC-1998 (Rel. 37, Last sequence updat;)
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15-DECATE LYARE PRECURSOR (EN. 4.2.2.2).
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This SWISS-PROI entry is copyright. It is produced through a pollab ration between the Swiss Institute of Biointormatics and the EMBL bulktation the European Bioinformatics institute. There are no restrict possess its use by non-profit institutions as long as its content; is in way modified and this statement is not removed. Usaye by and for comparing entities requires a license agreement (See http://www.ish.chb.ch/announce/or send an email to licenseitsb-ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete sequence analysis of the genome of the bacterium Mycophasma
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L..
Graham D.E., Overbeek R., Sneud M.A., Keller M., Aujay M., Huber B.,
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15-DEC-1998 (Rel. 37, Last sequence update).
15-FEB-2000 (Rel. 39, Last annutation update).
NOCHECSIDE DIPHOSPHATE KINASE (EC 2.7.4.5) (NDF KINASE).
NDK OR AQ_1590.
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Bacteria: Firmicutes: Bacillus/Clostridium aroup: Mollicutes.
Mycoplasmataceae; Mycoplasma.
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Manches 7: "Chegarative L. Mismanthas Or India.
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tical protein.
El 358 AA: 42417 NW: Albhhofaz44fffch hanska
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Prof. No. 3.17e-51;
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01-NCV-1997 (Rel. 35, Last Sections update)
10-NCV-1997 (Rel. 35, Last annotation update)
HYPOTHELICAL PROTEIN MGZ69 HOM.LOG.
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Similarity 87.5%:
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MEDLINE: 97105885.
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usave by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       ..
                                     Nature 392:353-358(1996).
-!- FUNCTION: MAJOR ROLE IN THE SYNTHESIS OF NUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-UTEX 5550.
MEDLINE: 91117183.
Michalowski C.B.: Pfanzagl B., Loctielhardt W., Robnert H.J.:
The cyanglic S.O spc r.bosonal protesn gene operon from Cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SSP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-LB555 / PRINGSHEIM:
Stirewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.":
                                                                                                                                                                                                                                                                                                                                                                       ó
                                                           Eŭkaryota: Glascocystophyceae: Cyanophoraceae: Cyanophora.
                                                                                                                                                                                                                                                                                                                                           Ouery Match 77.2%; Score 44: DR 1; Length 142: Best Local Similarity 55.6%; Pred. No. 1.02e+01: Matches 5: Conservative 3: Mismatches 1: Indels Matches
                                                                                                                                                                                                                                                                                                         120 120 BY SIMILARITY.
142 AA: 15942 MW: 18985DFA0317E998 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRS_CVAPA STANDARD: PRT; 169 AA. P23402: 01-NV-1991 (Rel. 20, Created) 01-NV-1991 (Rel. 2), Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) CYANELLE 30S RIBOSOMAL PROTEIN S5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              paradoxa.":
Mol. Gen. Genet. 224:222-231(1990).
                                                                                                                                                                                                                                                    EMBL: AEOCU746: AACO7481.1: -. PROSITE: PSCG469; NDP_KINASES; 1. PFAM: PFOC334: NDK: 1. Transferase: Kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: M20487: AAA63629.1; -.
EMBL: U30821: AAA81219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyanophora puradoxa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 82 AIKRVREII 90
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SEQUENCE
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                                                                                                                                                                                                           Query Match 77.2%; Score 44: 58.1; Length 169: Best Local Similarity 62.5%; Pred. No. 1.02e-01; Matches 5: Conservative 7: Mismatches 0: Indels Matches
                                                                                                                                                           17980 MW: 7053390669812A9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AA: 18241 MW: A93COF86E88475B1 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synecholystis sp. (strain PCT 6803).
Bacteria: Cyanobacteria: Chr. Gooddles: Synechodystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
30S RIBOSOMAL PROTEIN S5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NCV-1997 (Rel. 35, Last sequence update)
01-NCV-1997 (Rel. 35, Last annotation update)
PIR: $12220; R3KT5.
HSSP; P02357; IPKP.
MENDEL; P727; CXPpa:rps5:1.
PROSITE: PS00585; R:RDCSCMAL_S5: 1.
PFAM; PF00333; Riboscomal_S5: 1.
PENDSCOMAL PF0033; Riboscomal_S5: 1.
SEQUENCE 169 AA: 17980 WW; 70533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PSC0085: RIBOSOMAL_S5: 1. PFAM: PF0033; Ribosomal_S5: 1. Ribosomal_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: D90905: BAA17333.1; +
BSSP: P02357; 1PKP.
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64 SIRRVSNV 70
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262
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HISS OR BB0135.
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                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SIRAIN-JALI / DSM 2661 / AICC 43067);
MEDLINE: 96337499.
MEDLINE: 96337499.
Suite Coll White Coll State St
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"The human UDP-N-acetylq.ucosamine: alpha-6-D-mannoside-beta-1,2-N-acetylqlucosaminyltransferase II gene (MGAI2). Cioning of genomic nNA, localization to chromosome 14q21, expression in insect cells and purification of the reconficient protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNT2_BUMAN STANDARD: PRT: 447 AA.

O10469:
01-04-1994 (Rel. 34, Last sequence update)
02-051-1996 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALPHA-1.6-MANNISYLE/GUNCOPROTEIN BETA-1,2-N-
ACETYLGUOCSAMINYLRANSFERSE (EC. 2.4.1.14); (N-GLYCOSYL-
OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGUUCOSAMINYLTRANSFERASE II)
(BETA-1,2-N-ACETYLGUUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
PUTATIVE FUMARATE HYDRATASE BETA SUBUNIT (EC 4.2.1.2) (FUMARASE)
MJ0617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Motazoa, Chordata, Craniata, Vertebrata, Mammalia,
                                                        Methanococcus jannaschii.
Archaea: Euryarchaeota: Methanococcales: Methanococcaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 1; Length 195;
Pred. No. 1.02e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CARBOXYL GROUP (POTENTIAL).
: ASFDEB0E77D00992 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996).
-!- CATALYTIC ACTIVITY: L-MALATE - FUMARATE + H(2)0.
-!- PATHWAY: TRICARBOXYLIT ACID CYCLE.
-! SIMILARITY: TO THE C-TERMINAL OF CLASS I FUMARASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Lyase; Iricarboxylic acid cycle; ACT_SITE 36 36 POTENTIAL; BINDING 164 104 CARBOXYL GROUP (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 1-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AA: 21868 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: U67510: AAH98612.1: -.
IIGR: MJ0617: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.2%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95361854.
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MEDLINE: 95361854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SIKRVSNV 8
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                                                                                                                                                                                                                                    FUNCTION CATALYZES AN ESSENTIAL STEP IN THE CONVERSION F CLIS CANNAISE TO COMPLEX N-62NYANS.

MANNOSE TO COMPLEX N-62NYANS.

1.6-(N-ACETYL-BETA-D-GLUGOSAMINE + ALPHA-LOKANN SYL-1.6-(N-ACETYL-BETA-D-GLUGOSAMINYL-1.2-ALPHA-D-MANNOSYL-1.4) BETA-D-GLUGOSAMINYL-1.2-ALPHA-D-MANNOSYL-1.4) BETA-D-GLUGOSAMINYL-1.2-ALPHA-D-MANNOSYL-1.6-(N-ACETYL-BETA-D-GLUGOSAMINYL-1.2-ALPHA-D-MANN SYL-1.3)-BETA-D-MANNOSYL-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein: Golgi stack: Disease mutation:
DOMAIN 1 9 CYTOPLANIC (FOTENTIAL).
TRANSMEM 10 29 SIGNAL-ANGHCK (TYPE-11 MENBRANE PH (EIN)
DOMAIN 30 447 LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: GLYCOSYLATION.
SUBCELLOULAR LOCATION: TYPE 11 MEMBRANE PROTEIN. GOLGT.
DISEASE: CONGENITAL DEFICIENCY OF MOATZ IS ASSOCIATED WITH SEVERAL INFRAMENT OF NORMAL EMBRYGENESTS. PARTICULARLY IN THE NEW TS SYSTEM IN PATIENTS WITH CARBOHYDRATE-DEFICIENT GLYCOPROTEIN SYSTEM IN PATIENTS WITH CARBOHYDRATE-DEFICIENT GLYCOPROTEIN THE ETIOLOGY OF A VARIANT FORM OF CONSENITAL DYSENYTHMORDELIC ANDMINATAL DYSENYTHMORDELIC
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051160.
15.DEC-1996 (Rel. 37, Last sequence update)
15.DEC-1998 (Rel. 37, Last sequence update)
15.DEC-1998 (Rel. 37, Last ann tation update)
HISTIDYL-TRNA SYNTHETASE (EC 6 1.1.21) (HISTIDINE--THNA LIGASE)
                                            MEDIUME: 96404413.
MEDIUME: 96404413.
Tan J., Dunn J., Jaeken J., Schachter H.;
Tan J., Dunn J., Jaeken J., Schachter H.;
Mutations in the MGAT2 gene controlling complex N-91your Syntheause carbohydrate-deficient glycoprotein syndrome type II, an autosomal recessive disease with defective brain development autosomal recessive disease with defective brain development.
Am. J. Hum. Genet. 59-810-87(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM: 212066: -.
MIM: 212066: -.
Transferase: Glycosyllransferase: Transfembrane: Signal-anchor.
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STRAIN-ATCC 35210 / B31;
MEDLINE: 98065943.
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Store 44: DB Is Length 447: Ited. No. 1,72e-11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOTENTIAL,
H -> R (IN CDG2),
/FIId-VAR C03415,
S -> F (IN CDG2),
/FIId-VAR C03416,
K) 533076DC68BC6A572 CRC64,
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Bacteria: Spirochaetales: Spirochaetaceae: Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOLO TRESTM
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[2]
VARIANTS CDG2 ARG-262 AND PHE-290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 AA: 51550 MW:
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Best Loral Similarity 75.0%:
Matches 6: Conservative
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447
69
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262
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CONFLICT
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Lathigra R., White C., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischrann R.D., Richardson D., Peterson J., Kerlavage A.R., Oucakenbush J., Salzberg S., Hanson M., van Vugt R., Paliner N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garlack S., Flail C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Verter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
MEDLINE, 99,039765.
Stewart C., Parente F., Piehl F., Farnebo F., Quincey D., Silins G.,
Stewart C., Carle G.F., Lemmens I., Grimmond S., Xian C.2., Khodel S.
Bergman L., Carle G.F., Lemmens I., Grimmond S., Xian C.2., Khodel S.
Teh B.T., Lagercrantz J., Siggers P., Calender A., van de Vem V.,
Kas K., Weber G., Hayward N., Gaudray P., Larsson C.;
"Characterization of the mouse Meni gene and its expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncoyene 17:2485-2493(1998).
--- FUCTION: NOT KNOWN.
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
---- TISSUE SPECIFICITY: UBIQUITOUS. EXPRESSED AT HIGH LEVEL IN TESTIS
                                                                                                                                          PROSITE: PS00.179: AA_TRNA_LIGASE_II_1: 1.
PROSITE: PS00.339: AA_TRNA_LIGASE_II_2: FALSE_NEG.
PFAN, PF00.537: LNA-Synt_2D.
Aminoacyl-tRNA_synthetase: Protein biosynthesis: Ligase: ATP-binding.
SEQUENCE 457 AA: 52849 WW; 106E9D5F8EF04988 CRC64:
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Eutheria, Rodentia, Sciurognathi, Moridae, Muricae, Mis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Pest Local Similarity 55.7%: Pred. No. 1.02e+01:
Matches 6: Conservative 2: Mismatches 1: Indels
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Submitted (JCN-1998) to the EMBL/GenBank/CDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            EMBL: AE001125; AAC66531.1: -.
TIGR: BB0135; -.
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Bassett J.H.D., Thakker R.V.:
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15-DEC-1998
15-FEB-2000
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Nature 390:5
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088559;
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This SWISS-PROT entry is copyright. It is produced through a cullaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by add tor corrested entities requires a license agreement (See http://www.isb-sib.ch.cannounce/or send an email to licenseisb-sib.ch).
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Collins F.S., Emmert-Buck M. Debelenko L.V., Zhuang Z.,
Lubensky I.A., Liotta L.A., Ortree J.S., Wang Y., Roe B.A.,
Helsemann J., Boguski M.S., Wal S.K., Kester M.B., Kim Y.S.,
"Pepper C., Dong O., Spiege, v. M., Burns A.D., Marx S.J.,
"Positional cloning of the ene for multiple endocrine neoplasia-type
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Heppner C., Kester M.B., Agarwal S.K., Debelenko L.V.,
Emmert Buck M.R., Guru S.C., Manickam P., Olufemi S.-E.,
Skarulis M.C., Doppman J.L., Alexander R.H., KIM Y.S., Saggar S.K.,
Lubensky I.A., Zhuang Z., otta L.A., Chandrasekharappa S.C.,
Collins F.S., Spiegel A.M., Burns A.L., Marx S.J.;
"Somatic mutation of the Meni gene in parathyroid tumours.";
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Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Marmalia;
Eutheria; Primates; Catarrhin: Hominidae: Homo.
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Pred. No. 1.02e-01;
"...marches 0; InJels
                                                                                                                                                                                                                                                                                                                                                                                                                                              M -> I (IN REF. 2).
G -> E (IN REF. 2).
I. -> S (IN REF. 2).
J. C3FBB3A5695244E9 CRC64).
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466 G
512 I.
67472 MW.
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Best Local Similarity 62.5%:
Matches 5: Conservative
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512 5
611 AA;
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CONFLICT 457
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Giraud S., Zhand C.X., Serova-Sinilnikova D., Wautot V., Salandre J., Buisson N., Waterlot C., Batters C., Forchet N., Aubert J. P., Eny P., Cadiot G., Delemer B., Chabre C., Niccoli P., Leprat F., Duron F., Emperager B., Couquid F., Gouder P., Sarfati E., Rhou J.-P., Guichard S., Routor W., Meyier P., Caron P., Variygher W., Caron P., Variygher M., Lenoir G., Assaya M., Peix J.-L., Puceat M., Rohmer V., Valiotton M., Lenoir G., Goudray P., Proye C., Conte-Devolx B., Chanson P., Shugart Y.Y., Goldgar D., Murat A., Calcher A., Gord Tine mutation analysis in patients with muitiple endocrine Am. J. Hum. Genet. 65:455-467(1998).
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"Analysis of recurrent germline mutations in the MENI gone encountered
in apparently unrelated families.";
Hum. Mutat. 12:75-82(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT FIHP SLU-189.
MEDLINE: 9957776
PETITORINE: 957776
PETITORINE: SHITTANEME S., Sakurai A., Hashizume K., Hama Y., Ito K.,
Shingu K., Kobayashi S., Amano J., Fukushima Y.,
"Novol Videk MNN germilise mutation in a Japanese kindred with
familial hyperpararhyroidism".
Am. -1 Med. Gover. 851221-222(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "identification of five novel germline mutations of the MEN1 gene in Japanese multiple endocrine neoplasia type 1 (MEN1) families.";
I. Med. Genet. 35:915-919(1998).
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Kobayashi S., Amano J., Fukushima Y., Hashizume K.,
*Novel MENI gene mutations in familial multiple endocrine neoplasia
Bassett J.H.D., Forbes S.A., Pannett A.A.J., Lloyd S.E., Christie P.T., Wooding C., Harding B., Besser G.M., Edwards C.R., Monson J.P., Sampson J., Wass J.A.H., Wheeler M.H., Thaxker R.V.: "Characterization of mutations in patients with multiple endocrine neoplasia type 1.":
Am. J. Hum. Genet. 62:232-244(1998).
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Darling I., Lictia L., Zhiang Z./
"Somatic mulations of the MENI timor suppressor dene detected
sporadic anglotibroms."
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MEDLINE: 99011276.
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MEDLINE: 99048878.
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between the Swiss Institute of Bicinforraties and the EMBL edistation the European Bioinformatics Institute. There are no restrictions on its modelised by non-profit institutions as long as its content is in ma way modified and this statement is not removed. Usage by and for connercial entities requires a license arrement (See http://www.isureib.ch/announce/or send an email to license@isb-sib.ch).
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A Mutch M.G., Dilley W.G., Sanjutjo F., Debenddetti M.K., Coherty F.M., Mutch M.G., Dilley W.G., Sanjutjo F., Debenddetti M.K., Coherty F.M., Mutch M.G., Dilley W.G., Sanjutjo F., Debenddetti M.K., Coherty F.M., Germine metations in the Full ple endocrine neoplasia type: Lence at Federations in the Full ple endocrine neoplasia type: Lence at Federations in the Full ple endocrine neoplasia type: Lence at Federations in the Full Ple endocrine neoplasia type: Lence at Federations in the Full Ple endocrine neoplasia type: Lence at Federations in the Full Ple endocrine neoplasia type: Lence at Federations in the Full Ple endocrine neoplasia type: Lence at Federations in the Full Ple endocrine neoplasia type: Lence at Federations in the Federation in the Callings of Hyperbard Federation in the Callings in the Calse of Federation in the Callings in the Calse of Hyperbard Federation in the Calse of 
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                                                                                             Belgian patients with mouniple
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EMENI TRP-39; TYR-177; ASP-184; PRO-269 AND PRO-272.
99103464.
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H -> Y (IN SPCRADIC MEN1).

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F -> V (IN FMEN1).
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Flated diseases.
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(IN FMEN1).
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H -> Y (IN FMENI)
/FIId-VAR_005433.
K -> I (IN FMENI).
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CEG VAR_CC5425
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D (IN FMEN1)
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H -> D (IN
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                                                                                                                  endocrine neoplasia type 1 and
Hum. Mutat. 13:54-50(1999).
                                                                                                                                                                      VARIANTS MENI ASP-161 AND ANG
MEDLINE: 99166881.
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EMBL: 093237: AAC51229.1; -.
EMBL: 093237: AAC51230.1: -.
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VARSPLIC 149 153
VARIANT 12 12
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/FTId-VAR_005436

US-09-142-524A-14.rsp

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CHAIN
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     DE:
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                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycetes: Saccharomycetales:
Saccharomycetaceae: Saccharomyces.
                                                                                                                                                                                                                                                   FM52_YEAST STANDARD: PHI; 720 AA. Q04322.
Q04322.
G1-NCV-1997 (Rel. 35, Last sequence update)
O1-NCV-1997 (Rel. 35, Last sequence update)
O1-NCY-1997 (Rel. 35, Last annotation update)
HPFOTHELICAL 82. KD PROTEIN IN SOSI-MRPL24 INTERGENIC REGION.
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Methanococcus jannaschii.
Ardhaea: Euryarchaeota: Methanococcales: Methanococcaceae;
                                                                                                                                Score 44: DB 1: Length 615: Pred. No. 1.02e+01:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44: DB 1: Length 720:
Pred. No. 1.02e+01:
3: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-S288C / AB972:
Pearson D. Bowman S., Harrell B.G., Rajandream M.A.:
Submitted (JAN-1995) to the EMBL/GenBank/DDB2 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               821+1 MW: E1423DB4F1557267 (Prit4
G -> D (IN MEN1).
/FIId-VAR (08017.
A -> P (IN FMEN1).
/FIId-VAR_005437.
A -> D (IN FMEN1).
/FIId-VAR_005438.
/FIId-VAR_005439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL PROTEIN MJ0882.
                                                                                                                                                        3; Mismatches
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                   Note: remainder of annotations omitted.
                                                                                                                                77.2%;
:larity 62.5%;
Conservative
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Best Local Similarity 62.5%;
Matches 5: Conservative
                                                159
   161
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SECUENCE 720 AA: 8
                                                                                                                                             Local Similarity
                                                                                                                                                                                118 VKKVSDV: 125
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                                                                    14
   161
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Q58095:
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                                                                                                                                  Query Match
                          VARIANT
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                                                                                                                                                                                                                      Jannaschil.", Science 273:1058-1073(1996)
Science 273:1058-1073(1996)
-!- PIM: THIS PROTEIN UNDERGUES A PROTEIN SELF SPLICING THAT INV.LVES
A POST-THORAL EXCISION OF THE THE INTERVENING HESLIN
(INTER) POLICAMED BY PEFTIDE LIGATION (POTENTIAL)
-!- SIMILARITY: BELONGS TO THE UPFO027 (RTCB) FAMILY.
Mail Col., White 0., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gorayne J.D., Kertavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Kerch J.L., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nowiger R., Cutterback R., Kelley J.M., Fetcrson J.D., Sadow P.W., Harist W.A., Kaine B.P., Hordovsky R., Klenk H.-P., Fraser C.M., Smith H.C., Woesen C.R., Vertex J.C., "Complete genome sequence of no methanogenic archaeon, Methan...vvvvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 87260013.
Wilhelm M.L., Wilhelm F.-X.;
"Both histone H4 genes of Physarum polycephalum are interrupted by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 89279930.
Wilhelm M.L., Wilhelm F.-X.:
Wilhelm M.L., Wilhelm F.-X.:
"Histone genes in Physarum polycephalum: transcription and analysis of the flanking regions of the two H4 genes.";
J. Mol. Evol. 28:322-326(1989).
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HYPOTHETICAL PROTEIN MOUGEL.
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MJA HYPZ INTEIN (POTENTIAL).
HYPOTHETICAL PROTEIN MJ0682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44: DB N: Length 968: Pred. No. 1.02e+0N: 3: Miscatches 0: Infels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39A2A55280456130 CRC64:
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13-A06-1987 (Rel. 65, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Myxodastria; Physarida: Physarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR, MC0682: -.
PROSITE: PSOGBBL, PROTEIN_SPLICING: 1.
PROSITE: PSO1286: UPF0627: 1.
PFAM: PF01139: UPF0627: 1.
Hypothetical protein; Protein splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intervening sequence.";
Nucleic Acids Res. 15:5478-5478(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physarum polycephalum (Sline mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110206 MW:
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Local Similarity 62.5%;
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968
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IKRVSNVI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (So http://www.isb-sib.ch/announce/or send an email to licenselist-sib.ch).
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Chicroplast.
Eukaryota: Rhodophyta: Banglophyceae: Banglales: Banglaceae: Porphyra.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Mol. Blot. Reg. 13:533-335(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43: DB 1: Length 102:
Pred. No. 1.756+01:
3: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N -> K (IN H42).
- 82237908E72841FC CR064;
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01-007-1996 (Rel. 34, Last sell-cone apdate)
01-007-1996 (Rel. 34, Last uncoration update)
04/08-08-08-1898 RIBOSCHAL (RELIEIN SS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X0C449; CAA2514C.]; ...
EMBL; X15141; CAA31229.]; ...
EMBL; X15141; CAA3124C.]; ...
EMBL; Y0036; CAA68442.]; ...
PTR; A22859; A27859; PTR; A21075; S10075; PTR; S10076; S10076; PROSELE; PROGEA! HISTONEH4.
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48 48 N
102 AA: 11311 MW:
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Sest Local Similarity 55.6%;
Matches 5: Conservative
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SEQUENCE FROM N.A.
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DR EMBL U38804: AACC8184.1: -.
DR HSSP P02357: DRKP.
DR HSSP P02357: DRKP.
DR PROBLE: 10355: PORPULES511.
DR PROSITE: PS00585: RIBOSOMAL_S5. 1.
DR PROSITE: PS00585: RIBOSOMAL_S5. 1.
DR PROSITE: PS00585: RIBOSOMAL_S5. 1.
KW Ribosomal protein: Chloroplast
SQ SEQUENCE 174 AA: 18294 MW; 902.HDA332624600 CR064:
CQUETY MATCH
BEST LOCAL SIMILATITY 56.0%; Pred. No. 1.75e-01:
MATCHES 4: CONSERVATIVE 4: MISFALCHES 0; Indeis 1.0;
DD 24 VKRVTKVV 3:
II ::!:
OY 2 IKRVSNVI 9
Search Completed: Mon Jon 19 16.18:03 2005
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:18:20 2000: MasPar time 8:41 Seconds 74:216 Million cell updates/sec Run co:

Tabular cutput not generated.

>US-09-142-524A-14 (1-9) from US09142524A.pep 57 1 SIKRVSNVI 9 Title: Description: Perfect Score: Sequence:

PAM 150 Cap 15 Scoring table:

225878 segs, 69334122 residues Searched:

Minimum Match OW Listing first 45 summaries Post-processing:

spirembil2 lisp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelie 9:sp_phage 10:sp_plant 1::sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus Database:

Mean 21.880; Variance 21.726; scale 1.007 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO.	Score	Cherry	psery Match Length DH	ī.	0	Descrip: .m	Pred. No.
	6.7	86.0	8668	v.	073636	PHEROMONE RECEPTOR.	1.C4e+30
7	48	84.2	326	~	0924E5	PARA PROTEIN.	1.87e+00
m	46	80.7	4:1	10	046322	PLASMID GRO4970, COMPL	5.90e+00
4	46	80.7	465	S	023157	WO4D2.3 PROTEIN.	5.906-00
Ś	4.5	80.7	783	~	092H39	BETA-N-ACETYLGLUCOSAMI	5.90e+00
ω	4.5	78.9	192	7	067344	HYPOTHETICAL 22.1 KD P	1.036+01
7	ς. *	78.3	293	~	09X546		1.03e+01
ထ	5.5	78.	360	~	09ZGT6		1.030+01
6	45	78.9		٦	029266	TYPE II SECRETION SYST	1.63e+01
10	ιΩ * *	78.9	683	~	013331	ACETOLACIATE SYNTHASE.	1.036+01
11	45	78.9	682	~	001154	ACETOLACIATE SYNTHASE.	1.03e+01
12	44	77.2	175	10	O6526C	F6N23.2 PROTEIN.	1.80e-01
13	44	77.2	256	~	067471	HYPOTHETICAL 29 KD P	1.80e+01
14	44	77.2	433	10	Q92VS4	F15k9.17 PROTEIN.	1.80e+01
15	44	77.2	434	7	092VS5	F15K9.16 PROTEIN.	1.800+01
7,6	44	77.2	512	7	044486	DINITROGENASE BETA SUB	1.800+01
۲٠ ۲۰۱	77	77.2	610	Ξ	O9WVR8	MENIN	1.80e+01
8,1	44	77.2	653	10	050017	POLY (ADP-RIBOSE) POLYM	1.806+01
19	44	77.2	1098	4	015050	KIAAC342.	1.80e+01
20	43	7.5	170	ĸ	217690	***************************************	

3.096-01	3.098+01	3.09001	3.09e+31	3,099-01	3.09e-01	3.096+31	3.090+01	3,090-01	3,095+03	3 090.01			5.250+01					5.250001	5.250001		\$.250+01	5.25e+01		F.25e+01
24CAA LONG HYPOTHETICA	GALACTOSE-1-PHCSPHATE	ABC TRANSPORTER ATP-BI	POPULUS TRICHOCARPA :S	COS46.2.	HYPOTHETICAL 43.0 KD P	ASPARTOKINASE III.	SIMILAR TO CYTOCHROME	ATP-DEPENDENT 21NC MET	PUTATIVE 90.4K PROTEIN	PUTATIVE POTASSIUM TRA	HOXW AND ORF2 GENES	MAP KINASE MEST.	PXU1-45.	PUTATIVE FLIPPASE.	GEYCOPROTEIN B.	104K PROTEIN.	1064AA LONG HYPOTHELLS		CRF MSV043 PUTATIVE RN	SODIUM CHANNEL ALPHA-S	POLYPROTEIN.	CALO PROTEIN (FRAGMENT	PUSHOVER.	PUSHOVER.
074080	09×484	069156	055881	P91568	055916	084367	027472	092GE1	093119	064769	044025	013352	09X315	©9XER3	035362	P87544	09YF67	059462	05%350	028644	630M60	096958	Q9XYD1	Q9XYD2
-1	7	7	10	Ŋ	7	7	S	~	<u>,</u>	10	7	,~,	~	7	7	14	-	~	7	ç	7	S	2	2
240	251	293	308	347	390	431	583	601	785	792	167	ur) • ∢ • 3	100 PT	511	854	931	1064	1179	1319	1984	2858	4116	4120	5322
75.4	75.4	75.4	75.4	75.4	75.4	75.4	75.4	75.4	75.4	75.4	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	\sim	73.7	m	73.7
43	43	43	43	43	43	43	43	€	₩	43	42	4.5	42	4.2	42	42	45	42	42	42	42	42	42	42
21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	36		4 1	42	43	4	4.5

ALIGNMENTS

868 AA.	Created) Last sequence update) Last annotation update)	Fugu rubripes (Japanese pufferfish) (Takiffugu rubripes). Eukaryota: Metazoa: Chordara: Craniata: Vertebrata: Actinople:your: Eukaryota: Teleostel: E leostel: Acanthopteryqui: Percomorpha: Terracdontifoxmes: Tetrac loudel: Tetracdontidue: Fugu. [1] [2] MEDULNE: 98226788. MEDULNE: 98226788. MATIO Y., YAMAMOTO J., NOZAKI Y., TOKURA K., HAZAMA M.,	MARANIZED S.C. BRENNES S.C. FUGLALIVE performer solutions related to the Ca2+-sensing ledeptor in Fugu. 1. Fugu. 1. Fugu. 2. Fugu. 3. Fugu	Score 49: DB 13: Length 868: Pred. No. 1.046-00; 2: Mismatches 0: Indels 0: Gaps 0:	PRT; 326 AA. Created) Last sequence update) Last annotation update)
PRT	07, Created) 07, Last seg 12, Last ann	oufferfish (a*a, Cran (e*a) (c*a) (c*a) (c*a) (c*a) (c*a) (c*a)	receptors relations to the control of the control o		PRT; 10, Created) 10, Last seq 10, Last ann
PRELIMINARY;	(TrEMBLrel, (TrEMBLrel, (TrEMBLrel, CEPTOR,	Fugu rubripes (Japanese pufferfish) (Takifua Bukaryota: Metazoa: Chorda'a: Craniata: Vert Neopterygii: Teleostei: E. Heostei: Acantho Tetraodontiformes: Tetrao. Toldei: Tetraodo [1] SEQUENCE FROM N.A. MEDLINE: 98226788.	PARAMETER DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PERSON OF T	Query Match Best Local Similarity 75.0%; Matches 6: Conservative 282 IKRVADVI 289 1111:11	PRELIMINARY; TrEMBLrel. TrEMBLrel.
LT 1 073636 073635;	01-AUG-1998 (IFEMBL 01-AUG-1998 (IFEMBL 01-NOV-1999 (IFEMBL PHEROMONE RECEPTOR.	Fugu rubripes (Jap Eukaryota: Metazoa Neopterygii: Teleo Terrandontiformes: [1] SSOJENCE FROM N.A. MEDLINE: 98226788.	Putation of Fugural Proc. Nat. Proc. Nat. Proc. Nat. Proc. Nat. Proc. Pram. Proc. Pram. Proc. Pram. Proc. Presoner Proc. Presoner Proc. Presoner Proc. Proc. Presoner Proc. Pr	Ouery Match Best Local Simil Matches 6: 282 IKRVADVI 2 IKRVADVI 2 IKRVSNVI	0924E5 0924E5; 0924E5; 01-MAY-1999 01-MAY-1999 01-MAY-1999 PARA PROTEIN
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092H39:
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Gracilaria.
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MEDLINE: 94150718.
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GRANDER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa: Nematoda; Secernentea: Rhabditia; Rhabditida;
Rhabditina: Rhabditoidea; Rhabditidae: Peloderinae; Caenorhabditis.
Escherichia coli.
Plasmid Incil Colib-P9.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
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Pred: No. 1.87e-00;
2: Mismatches 0: Indels
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                             SAMPE: G., MIZOBUCHI K.:
"Organization and diversification of plasmid genomes: co-
nuclectide sequence of the Tollb-P9 genome.";
Submitted (EEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABD21078: EAA75111.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
GOFF L.J., MCKN D.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF034718; AACC4724.1; '...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 3 O4652 ORECOMINARY; PRI: 411 AA. O46522 O46522 CI-30N-1998 (TrEMBLIE). 06. Created) CI-30N-1998 (TrEMBLIE). 06. Last sequence update) CI-30N-1998 (TREMBLIE). 07. Last annotation update) PLASMID GRO4970, COMPLETE SEQUENCE.
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Last annotation update)
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Pred. No. 5.90e+60:
                                                                                                                                                                                                                                       326 AA: 36227 MW: 92469414 CRC32;
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Rest Local Similarity 62.5%;
                                                                                                                                                                                                                                                                               84.2%:
75.0%:
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Best Local Similarity 75.0%
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5: Conservative
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Plasmid Gro4970.
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                                                                                  (1)
SEQUENCE FROM N.A
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This is
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                                                             Escherichia.
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"Cloning, sequence analysis and characterisation of genes innulved in
chitic degradation of a marine bacterium. Pseudoalteromonds sp. strain
59.";
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MEDECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V., "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.":
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JONES M., KERSHAW J., KIRSTEN J., LAISIER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCI. 'RAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKE. .., ROOPRA A., SAUNDERS D., SHCWNKHEN
MALDON N., SMITH A., SONHAWHER E., STADEN R., SJLSION J.,
THIERRY-MIEG J., THOMAS K., VADIN M., VAUGHAN K., WATERSTON R.,
WAISON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome iii of C.
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01-AUG-1998 (IrEMBLrel. 07. Created)
01-AUG-1998 (IYEMBLrel. 07. Last sequence update)
01-NOV-1998 (IYEMBLrel. 08. Last annotation update)
HYPOTHETICAL 22.1 KD PROTEIN.
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01-MAY-1999 (TrEMBLrel. 10, Jast sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Best Local Similarity 75:0%: Prod. No. 5:90e+60:
                                                                                                                                                                           Microbiology C:0-0(1999).
EMBL: AEC72234, AAC83237.1; -.
EMSP: P06965: 1028
SEQUENCE 783 AA: 88856 MW; FF87EDF8 CRC32;
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Bacteria: Proteobacteria: qam.
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CHIQ.
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360 AA:
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KALANBARET T. W. BULACH D.M., RAJAKUMAR K., ADLER B.,

"Genetic Organization of the Lipopolysaccharide O-antigen Biosynthetic
Locus of Leptospira borgeterseni Serovar Hardjebovis.",

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL: AF078.35: AD12950.1;

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                           DECKERT G. WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., ADRAKHAM D.E., OVERBEEK R., SNRAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLLSON G.J., SWANSON R.V.; SUDMILLED (JUL-1997) to the EMBL/GenBank/DDBJ databases. Hypothetical frotein. TACO7306.1: TACO7306.1: ARCO7306.1: SEQUENCE 192 AA: 722076 MW: 7528ADDD CRC32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45: DB 2; Length 192: Pred. No. 1.03e+01: 2; Mismatches 1: Indels
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Plasmid R.plasmid pAG1.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycetales: Corynebacterineae: Corynebacteriaceae;
Corynebacterium.
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OI-NoV-1999 (ITEMBLED. 12. Last sequence update)
CI-NoV-1999 (ITEMBLED. 12. Last annotation update)
IETRACYCLINE REPRESSOR PROTEIN HOMOLOG TRH.
THH.
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Best Local Similarity 66.7%;
Matches 6: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY
Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AIKRVKNVL 119
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                                                                                    SEQUENCE FROM N.A.
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STRAIN-VC-16 / JSM 4304 / ATCC 49558;

RM MEDLINE: 9604933.

RECHUM K.A., DODSON R.A., TOMB J.-F., WHITE C., NELSON K.E.,

RA KECHCHW K.A., DODSON R.A., GWINN M., HICKEY E.K. PETERSON J. D.,

RA RICHARDSON D.L., KER-AVAGE G.R., GRAHAM D.E., KYRPIDES N.C.

RA RICHARDSON D.L., KER-AVAGE G.R., GRAHAM D.E., KYRPIDES N.C.

RA RICHARDSON D.L., MCHENNEY K., ADAMS M.D., LOFIUS S.,

RA PETERSON S., RECH C.L., MCNEIL L.K., BADGER J.H., GLODEK A., ZBGC J.,

RA PETERSON S., RECH C.L., MCHENNA J.F., MCDONALD L., UTERSACK T.,

RA OVERBERK R., GOCAYNE J.D., MREDMAN J.F., MCDONALD L., UTERSACK T.,

RA SADOW P.M., JANDREA K.P., BOWMAN C., FULLI C., GARLAND S.A.,

RASON T.M., OLSEN G.J., FRASER C.M., SMITH H.G., WCESE C.R.,

RANSON T.M., SELEN G.J., FRASER C.M., SMITH H.G., WCESE C.R.,

RANSON T.M., SELEN G.J., FRASER C.M., SMITH H.G., WCESE C.R.,
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ш
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-!- SIMILARITY: WITH OTHER ENYMES WHICH REQUIRE TPP.
EMBL, AF013601; AAB81248.1; -.
PROSITE; PS00187; TPP_ENZYMES: 1.
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Phyllachorales: Magnaporthaceae: Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Archa : lobules: Archaeoglobuceue;
Archaeoglobus.
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                                                  Query Match 78.9%; Shire 45: DB 2: Length 36C: Best Local Similarity 75.0%; P. J. No. 1.03e+01: Matches 6: Conservative Mismatches 1: Indeis
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01333: PRELIMINARY; PRT; 682 AA.
01333: 015334
015.2AN-1998 (TEMBLEEL: 05, Crivated)
015.2AN-1998 (TEMBLEEL: 05, Last sequence update)
015.0V-1999 (TEMBLEEL: 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05. 3. ited)
01-JAN-1998 (TrEMBLrel. 05. La.; sequence update)
01-NOV-1998 (TrEMBLrel. 08. L. i annotation update)
TYPE_I SECRETION SYSTEM PROT '4 (GSPE-3).
822C1EE3 CRC32;
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569 AA: 56520 MW: 6FBF77DB CRC32:
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41546 MW;
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Hypothetical protein.
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STRAIN-4091-5-8;
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Budaryota, Viridiplantae: Stroptophyta: Embryophyta: Iracheuphyta.
euphy:cphytes: Spernatophyta: Magnoliuphyta: eudicotylodoms:
core eudicots: Rosidae: eurosids II: Brassicales: Brassicaceae:
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Eukaryota: Findi: Ascomyrota: Euascomycetes: Pyrenomycetes:
Phyllachorales: Magnaporthaceme: Magnaporthe.
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                                                                                                                            Score 45, DB 3, Length 682;
Pred. No. 1.03e-01;
4; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N A.
STRAILH-6043:
SWENGARG J. FARKALL I., VALENI B.S.;
SWENITED (UCT.1995) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY. WITH OTHER ENZYMES WHICH REQUIRE IPP.
EMBL: U39201, AA81669.1:
PROSITE: FSOURT TPP_ENZYMES: 1.
PROSITE: FSOURT TPP_ENZYMES: 1.
SPEM: PF00255: TPP_ENZYMES: 1.
SEQUENCE 682 As: 73873 MW: BESANDUR CROX:
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AFC58919: AAC13612.1; -.
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01-A0G-1996 (fremBLre), 07. Created)
01-MOV-1999 (fremBLre), 07. Last sequence update)
01-MOV-1999 (fremBLre), 02. Last annotation (pdate)
F6N23.2 PB(1EIN
                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM: PRO0205: IPP_enzymes: 1.
Flavoprotein: Lyase: Thiamine pyrophosphate.
SEQUENCE 682 AA: 73949 WW: 82F28861 CR732:
                                                                                                                               Query Match
Best Local Similarity 55.5%;
Matches 5; Conservative
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Hest Local Similarity 55.6%,
Matches 5: Conservative
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STRAIN=CV. COLUMBIA;
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STRAINFOV. COLUMBIA:
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STRAIN-CV. COLUMBIA:
GEISEL C.;
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GRAHAM DIEL, OVERBEEK R., SNEA M.A., KELLER M., AUCAY M., HORER P.
FELDMAN R.A., SHORT J.M., GLSH, G.D., SWANSON R.V.;
SMEALKER (JUL-1997) to the EMBL/FORBER databases.
EMBL: ACC00743: AAC07436.1; Hypothatical protein.
SEQUENCE 256 AA: 29913 MW: EMBERBAR CHC32.
                                                                                                                              3.200
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyliophytes: Spermatophyta: Magnoliophyta: eudicotyledons:
core eudicots: Rosidae: eurosids II; Brassicales: Brassicalese:
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STRAIN-CV. COLUMBIA;
VYSOISRAIA V.S., SCHWARTZ J.R., TORIUMI M., YU G., LI J., LIU S.,
KREMENETSKAIA I., LUROS J., ARAUJO R., BUEHLER E., CONWAY A.B.,
DEWER K., FENG J., KIM C., LI Y., SHINN P., SUN H., DAVIS R.W.,
ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
"Arabidopsis thallaca chromosome I BAC F15K9 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 98196666.
DECKERT G., WARREN P.V., GAASTEKCAND T., VICTNO W.D., LENK A D.L.
DECKERT G., WARREN P.V., GAASTEKCAND T., VICTNO W.D., ADJAY W., BUDER
MARAM D.E., OVERBEEK R., SN'AD M.A., KELLER M., ADJAY W., BUDER
FELDMAN R.A., SHORT J.M., OLL, WARNSON R.V.,
The complete genome of the D. Itbermophilic barnering Aquitex
                                                   Score 44: DB 2/ Legath 256: Pred: No. 1,80e+61; F: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                             01-A06-1998 (TrEMBLrel, C7, Created)
01-A06-1998 (TrEMBLrel, C7, Tast Sequence update)
01-NOV-1996 (TrEMBLrel, C8, Last annotation update)
HYPOTHETICAL 29.9 KD PROTEIN.
AQ.1501.
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01-MAY-1999 (TrEMBLrel. 10, Last Sequence update)
01-MOY-1999 (TrEMBLrel. 12, Last annotation update)
F15K9-17 PROTEIN.
                     478978F9 CRC32:
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Bacteria: Aquificales: Aquificuedae: Aquifex
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2.
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PF00027: CNMP_binding: 1
NCE 175 AA: 19898 MW:
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Best Local Similarity 44.4%:
Matches 4: Conservative
                                                                     77.2%;
Similarity 55.6%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aeclicus.";
Nature 392:353-358(1998).
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                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                           23 SUKRISEVV 31
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PFAM; PFO
SEQUENCE
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067471
067471;
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01-MAY-1999 (TEMBLrel. 10, Created)
01-MAY-1999 (TEMBLrel. 12, Last annotation update)
01-NV-1999 (TEMBLrel. 12, Last annotation update)
F15K9.16 PROFEIN
F15K9.16.
F15K
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SYNAN-COLUMNIA.
VYSOTSKAIA V.S. SCHARIZ J.R., TORIUMI M., YU G., LT J., LIU S.,
VYSOTSKAIA V.S., SCHARIZ J.R., TORIUMI M., YU G., LT J., LIU S.,
KREMENETSKAIA I., LJROS J., ARAJOO R., BUEHLER E., CONNAY A.B.,
DEWES K., FENG J., KIM C., LI Y., SHINN P., SUN H., DAVIS R.W.,
ECKEH J.R., FENGESPIEL N.A., THECLOGIS A.
"Arabijdopsis in indiiana chromosome i BAC FISKS sey, ence.";
Submitted (JJL-1998) to the EMH./Genhank/DDBJ JJJAbasses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.2%; Score 44; DB 10; Length 433; Best Local Similarity 75.0%; Pred. No. 1.80e+51; Matches 6; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1998) to the EMBL/GenBank/EDBJ databases.
EMBL: AC005278; AAC72119.1: ...
MENDEL: 33845: Arath/3000/33845.
SEQUENCE 433 AA: 45717 MM: D931B22E CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A.
STRAINLEV. COLUMBIA:
THEOLOGIS A.:
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA:
THEOLOGIS A.:
Submitted (CCT-1998) to the EMBL/Genbank/DDBL databases.
                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
THEOLOGIS A.:
Sylmitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL: AC005278; AAC722201; '...'Harth:3000;38844. SEQUENCE 434 AA: 46148 MM: 5ED90252 CRC32;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA:
THEOLOGIS A.:
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQTENCE FROM N.A.
STRAIN-CV. COLUMBIA;
THEOLOGIS:
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STRAIN-CV. COLUMBIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA;
THEOLOGIS;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIKRVSNV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis.
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Gaps

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318 SIKRVASV 325
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            1 SIKRVSNV
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Search completed: Mon Jun 19 16:18:30 2000 Job time : 10 secs.

3

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protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:11:57 2000; MasPar time 3.71 Seconds 57.500 Million cell updates/sec Run on:

Tabular output not yenerated.

(1-9) from USC9142524A.pep 57 >US-09-142-524A-14 1 SIKRVSNVI 9 Description: Perfect Score: Sequence:

Search completed: Mon Jun 19 16:12:04 2000 Job time : 7 secs.

2 IKRVSNVI 9

ç

PAM 150 Gap 15 Scoring table:

188963 segs, 23686106 residues Seurched:

Minimum Match 08 Cisting Post-processing:

first 45 summaries Maximum DB seq length 9

a-denesed35 Setabase:

dbasadop:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 15.426; Variance 44.241; scale 0.349

Statistics

SULMANACIS

Residues 139-117 of Cr 1.87e-01 Pred. No. | Score March Length DB | 15 | Description | Pre | No. | Score | No. | N Result

AL IGNMENTS

Note: Postigrocessia runoved 44 summaries from list due to search parameters Chosen

```
17-SEP-1996 (first entry)
Residies 109-117 of Cry ) 1.
Cry ) 1: Ilpanese cedar pollen antides: allergy: immunotherapy:
HLA class II molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1997; JU4129,
13-NOV-1996; JP-302053,
(MEIP) MEIDT KILK PRCD CO LTD.
MEILIKL K. KIND K. KUMP A. SOGE T:
WPIP 98-297617/25.
                                                                   W57751 standurd: peptide: 9 AA.
W57751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryptomeria japonica.
WO9825962-Al.
22-MAY-1998.
SOLI
PACKER
PACK
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Peptides derived from Japanese cedar pollen antigens are minumoncherapeutic agents. useful for allergy treatment and typing HLA class II molecules in allergy sufferers
Claim 12. Page 26, 50pp; Japanese.
This sequence represents rest use 109-117 of the Cry j i protein, and is a peptide of the invention. The peptides are derived from Japanese cedar pollen antigens, and are used as immunocherapeutic agents in the treatment of allergy. The peptides can be used for identification and typing of the particular HLA class II molecules in an allerdy sitterer, and also for peptide immunotherapy of an allergy. Using these peptides the immunotherapy can be targeted more specifically to the requirements of the individual patient, allowing more effective treatment of an allergy, including those patients for whom treatment with a conventional immunotherapeutic agent is ineffective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347.5
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53: DB 1: Length 5:
Pred. No. 1.87e+01:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%:
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IKRVSNVI 9
                                                                                                                                                                                                                                                                                                                                                                             Seguence
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C
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Tue Jun 20 13:39:35 2000; MasPar time 2.16 Seconds 60.035 Million cell updates/sec 3450 On :

Misrch_pp = protein + protein database search, using Smith-Waterman algorithm

Tabular cutput not generated.

708-09-142-524A-14 (1-9) from USC9142524A.pep istle: Description: Perfect Score: Sequence:

1 SIKRVSNVI 9

PAM 150 Gap 15 Scoring table:

145341 segs, 14437480 residues Scarched:

Post-processing:

Minimum Match Of Listing first 45 summaries Maximum DB seg length 9

alissued 1:5A_COMB 2:5B_COMB 3:5_CUM 4:PCT_CUMB 5:backfiles1 Dalabase:

scale 0.324 Mean 14,393, Variance 44,418. Statistics:

Prod. No. is the number of results predicted by chance to have a score greater than of equal to the store of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No Rosalt No. Score Match Length DB 1D

Pred. No.

No matches tound

Search completed: The Jun 20 13:39:38 2000 Job time : 3 secs.

US-09-142-524A-14a.rap

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protein : profein database search, using Smith-Waterman algorithm MPsrch_pp Run on:

Mot. Jun 19 1(:12:21 2000; MasPar time 14:17 Seconds 63.988 Million cell updates/sec Tabular output sot generated.

>0S-09-142-524A-14 (1-9) trom US09142524A.pep 5-1 SIRRVSNV: 9

Title: Description: Perfect Smore: Sequence:

721208 segs, 100765575 residues PAM 150 Searched:

Scoring table:

Minimum Match Olimstins Insting first 45 summaries Maximum OB seq length 9 Post-processing:

a-pending liect 2:06 3:060 4:07 5:080 6:081 7:082 8:083 9:084A 10:0848 11:085 12:086 13:087 14:088 15:089 16:090 17:091 18:092 19:093 20:094 21:095 22:08FF 23:08FF06 24:NEWU8 25:NEWU9

Database:

Mean 17,247; Variance 40.530; scale 0.426

Statistics:

Pred. No. is the number of results predicted by charce to have a score grouper than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description esult Query No. Score Match Length DB Result

Pred. No

No matches found

Search completed: Mon Jun 19 16:12:44 2000 Job time: 23 secs.

* * * * * *	(MT)

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MPsrch_pp | protein | protein database search, using Smith-Materman algorithm

Mon Jun 19 15:11:24 2000; MasPar time 3.89 Seconds 109:175 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-14 (1-9) from USO9142524A.pep 57

SIKRVSNVI 9 Title: Description: Perfect Score: Sequence:

142080 segs, 47172406 residres PAM 150 34P 15 Searched:

Scoring table:

Minimum Match O% Listing first 45 summaries Maximum DB seq length 3 Post-processing:

Uatabase:

Mean 22.352; Variance 25.242; scale 0.886 pir62 lipiri 2:pir2 3:pir3 4:pi 4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Ourly No. Score Match Length 38 ID Description Pred. No.

Scarch completed: Mon Jun 19 16:11:40 2000 Job time : 16 secs.

:

No matches found.

	(TR)	
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Reloase 3.1A John F. Collins, Biocomputing Research Calt. Copyright (c) 1993-1998 Universit of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp = protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:10:20 2000; MasPar time 2.50 Seconds 109:525 Million cell updates/sec Run od:

Tabular output not generated.

>38-09-142-524A-14 (1-9) from US09142524A.pep 57

Title: Description: Perfect Score: Sequence:

1 SIKRVSNVI 9

PAM 150 Gap 15

Scoring table:

83857 segs, 30454973 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 9 Fost-processing:

swiss-prot38 1:swissprot Database:

Mean 22,858: Variance 21,701: scale 1.053 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. No. Score Match Lenath (9-15) Descriptorn Pred. No Result Guorg No. Score Match Length FB 15

No matches found.

Search completed: Mon Jun 19 16:10:32 2000 Job time: 12 secs.

US-09-142-524A-14a.rspt

******	(HL)

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:10:49 2000; MasPar time 5.97 Seconds 104.457 Million ceil updates/sec Run on:

>08-09-142-524A-14 (2-9) from C809142524A.pep 57 1 SIKRVSNVI 9

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

225878 segs, 69334122 residues Searched:

Post-processing:

Minnum Match 0% Listing first 45 summaries Maximum DB seg length 9

Catabase:

spirembil2 lisp_archea 2:sp_bacter.a 3:sp_fungl 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant ll:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 21.880; Variance 21.726; scale 1.007 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or what to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description CI Result Ouery No. Score Match Length DB

Pred. No.

No matches found.

Search completed: Mon Jun 19 16:11:08 2000 Jub time : 19 secs.

: : :
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protein : protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:06:50 2000: MasPar time 3.66 Seconds 58.202 Million cell updates/sec Run ca:

not denerated. Tabular output

.US-09-142-524A-7 (1-9) from USC9142524A.Pep 64 Description: Perfect Score:

1 FIKRVSNVI 9

Sequence:

PAM 150 Gap 15 Scoring table:

188963 segs, 23585105 residues Searched:

Summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseq35 l:deneseqp Database

Pred. No. is the number of results pred cted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Variance 46.25 : scale 0.362

Mean 16.765;

Statistics

SUMMARIES

Result		šianč Š	,				
2	Score	March	Match Length	ž :	91	Description	Pred. No.
	64	100.0		r-1	W57751	Residues 109-117 of Cr	1.25e+00
7	54	100.0	1	-1	W57750		1.25e+00
m	64	100.0	7	~ 4	R89291	Japanese cedar pollen	1.25e+30
4	64	100.0	7	- 1	R45552	14	1.25e+00
υn	64	100.0	~	. 1	R82501		5 5
9	64	100.0		r-4	W44683	T-cell epitope peptide	1.25e+00
7	64	100.0		٠.,	W27372	Multi-epitope peptide	1.25e+00
80	64	100.0			W27373		1.25e+00
σ	64	100.0		٠.	W27369	Multi-epitope peptide	1.25e+00
10	\$ 9	100.0	105		W27370	Multi-epitope peptide	1.25e+00
11	99	100.0		-	W27371		1.25e+00
1.2	54	100.0		_	R75388	Japanese cedar poilen	1.25e-00
13	64	100.0		-	R81587	Cedar pollen allergen	1.25e-00
14	54	100.0		-	R60166	Japanese cedar pollen	1.25e+00
15	9	100.0		-	R31537		1.25e-00
16	64	100.0		~	882490	Ţ	1.25e+00
17	64	100.0		-	845541	Cry j I pollen allerge	1.25e+00
18	64	36.6		-	R04895	LCill	3
19	78	75.0		~	R45577	Jun s I.	1.05e-02
20	8	75.0		-	'n	Jun v I.	5e-0
27	r:	73.4		1	Θ	Human growth-related C	6e+0
22	46	72.9	20	٠,	w	**	77e-02
23	9 *0	71.9	20	~	R82502	j I Japanese Ceda	1.77e-02

1,77e+02	1,770-02	1.77-6-02	1.770.02	1.77e-02	2.290-02	2 276-02	2.296-02	2.29e-02	2. 490-32	2,296-02	2.296-02	2 29e-02	2.29e-02	20-867.7	2.250-02	2 236-02	2.290+02	2 290+02	2.966+02	2.96-02	2 96e+02
Streptococcus preumoni	_	Bankia qouldi endealue	Hexosaminidase enzyme	Staphylococcus aureus	Hepatitis C virus enve	Hepatitis C virus 180.	Mouse synaptosomal ass	Mouse SNAP-25 polypept	Synaptosomal associate	Human thoracic aprta 5	Human thoracic acrta G	PsbF (WbpF) protein in	Human multiple endocri	Thermostable pyruvic a	Tumor suppressor prote	Staphylococcus aureus	Staphylococcus aureus	Adenyiate cyclase pro:	Synthetic anti-neoplas	Peptide enhancer of 1:	Amphipathic peptide #2
W60982	W49856	W3:562	W6.503	W97702	R69562	RF 9533	W : 3426	8516 3	W30103	W02727	R48755	W37356	W86348	R41889	W29749	M99657	95956M	W64518	R77068	R84155	R64795
н	7		-	-	-	-	-	-	-4	-1	- 1			٠-۱	٦		۲,	-	~	7	٦
	537	537	847	857	192	192	206	206	5 06	258	258	316	566	587	610	r-	866	1874	27	32	33
71.9	71.9	71.9	71.9	71.9	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.3	76.3	68.8	8.89	8.89
46	46	46	46	46	4.5	4 5	4	45	₹	4.5	5.5	-4	4	4 5	4 5	45	45	45	4	7	4 4
24	25	26	27	28	29	30	31	3.2	33	34	35	36	3.7	38	36	40	. ,	42	£ 3	*	4. O

ALIGNMENTS

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PD 22-MAY 1998.
22-MAY 1998.
23-MOV-1997; J04129.
PR 12-NOV-1997; J04129.
PR 13-NOV-1997; J04129.
PR 13-NOV-1997; J04129.
PR 13-NOV-1997; JP-12-MOV-1997; JP-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MOV-12-MO
                                        W5751;
17-SEP-1998 (first entry)
Residues 109-117 of Cry j 1
Cry j 1; Japanese cedar polien antigen; allergy; immunotherapy;
HLA class II molecule.
Cryptomeria japonica
W5775î standard: peptide; 9 AA.
```

ç, Query Match 100.0%; Score 64: DB 1: Length 9; Best Local Similarity 100.0%; Pred. No. 1.25e+00; Matches 9; Conservative 0; Mismatches 0; Indeis FIKRVSNVI 9 ô

0:

Gaps

W57750: 17-SEP-1998 (first entry) Residues 105-120 of Cry 1. Cry 1 1: Japanese cedar pollen antigen: allergy: immunotherapy: HLA class II molecule. JI 2 W57750 standard; peptide; 15 AA. RESULT TD W5 AC W5 OT 17 OE RE KW Cr

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ULT 6
W44683 standard: peptide: 30 AA.
W44683:
                                                                                                                                                                                                                                                                                                                                                                                                                                              R82501 standard; Protein; 20 AA R82501;
15-APR-1996 (first entry)
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 9: Conservative
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                  20-JAN-1994.
15-JAN-1993; U00139
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                                                                                                                                                                                                                                                                                                                                                      9 FIKRVSNVI 17
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MO9401560-A.
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Best Local S
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                                                                                                                                                        allergy
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                                                                                                                      Peptides delived from Japanese cedar pollen antigens are peptides delived from Japanese cedar pollen antigens are immunocherapeutic agents - useful for allergy treatment and typing HLA class II molecules in allergy sufferers claim 12, page 26: 06pp; Japanese.

This sequence represents residues 106-120 of the Cry iI protein, and its a peptide of the invention. The peptides a derived from Japanese cedar pollen antigens, and are used as immuno herapeutic agents in the treatment of allergy. The peptides can be used for identification and typing of the farticular H.A class II molecules in an allergy sufferer, and also for peptide immunocherapy of an allergy. Using these peptides the immunocher py can be targeted more specifically to the requirements of the individing those patients for whom treatment of an immunocherapeutic agent is ineffective.
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20-0CT-1993: 25.2626.
20-0CT-1993: 25.2626.
20-0CT-1993: 25.2626.
20-0CT-1993: 25.2626.
20-0CT-1993: 25.2626.
NEUL WILL WILK PROD CO LITE.
NPW CYPEROMERIA police allerate in coll epitope peut. 3c - used for herecardion, treatment and investigation of Japanese cedar pollen allerace Cryl I. from which the T-cell epitope peptides R89289-R89295 were derived. The peptides can be used for the prevention and treatment of cryptomeria pollencisis, and also for the investigation of pollenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1996 (:1rs: entry)
Japanese cedar pollen alleruen Cryj I derived T-cell epitope peptide.
Sapanese cedar: pollen allergen: Cryj I: T-cell epitope: peptides;
prevention: treatment: cryptomeria pollenosis.
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Pred. No. 1.25e+00;
0; Mismatches 0; indels
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 64: DB 1: Length 15: Pred. No. 1.25e+00: 0: Mismatches 0: Indels
                                               12-NOV-1997; JG4129.
13-NOV-1996; JP 302053.
13-NOV-1996; JP 302053.
MEREP | MELLY MICK PROD CO LTD.
Dalliki K, KIDO K, Kume A, Sone T;
WPI: 98-297617/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R89291 standard: peptide: 15 AA
                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity 100.0%;
Matches 9: Conference
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Rest Local Similarity 100.0%;
Matches 9: Conservative
      japonica
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     Cryptomeria ja
WO9820902-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R89291;
12-MAR-1996
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WPIT 95-366391/47.

WPIT 95-366391/47.

Wolfied Cryptomeria japonica (Cry j): peptide(s) - useful for interacting allergy to japanese cedar follen allergen or immunologically cross reartive allerances.

Sisclosure: Fluury 2: 51pp; Enalish.

Novel peptides of cry j have been mudified as a part of a preformulation scheme to develop an optimised drug product for preformulation scheme to develop an optimised drug product for therapeutic treatment of humans sufferling from alleray to Japanese cedar pollen allergen which is immunologically cross reaction characteristics which render them particularly possess certain characteristics which render them particularly cuitable for drug product formulation. Peptide fragments of Cry j: modified and unmodified, are given in R82491-R82255. This peptide fragment corresponds to amino acids 101-120 of the allergen mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ġ
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O
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He sequence is that of an isolated peptide of the Japanese cedar polite atlergen Cry 1 (amito acids 101-120). The peptide. CJI-13, can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens. Sequence 20 AA:
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Cry 1 I: Japanèse Cedar pollen allergen: modified: drug production:
allergy: Crytpomeria japonica.
Crytpomeria japonica.
w09527786-A1.
                                                                                                                                                                             Antigens derived from Japanese cedar polier allergen Cry j l\cdotcontain at least two T cell epitope(s), used to treat or diagnose
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10-JUL-1992; WO-U05661.
01-SEP-1992: US-938990.
(IMMU-) IMMULOGIC PHARM CORP.
Bond JF, Garman RD, Griffith IJ, Kuo M. Pollock 2;
WPI: 94-035066/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 1; I.6
Pred. No. 1.25e+00;
0; Mismatches 0
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Pr d. No. 1.25e+00;
0 Mismatches 0
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Query Match
Best Local Similarity 100.0%:
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9: Conservative
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WO9732600-Al.
                                                                                                                                                                W09732600-A1.
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from different allerges of the property of the present allerges of the present allerges of the present allerges of the present sequence represents a multi-epitope supplies which is used as a new immunotherapeutic agent. It comprises T ceil epitope regions from 2 or more different allergens (preterably linked via arginine or lysine dimers), where the T ceil epitope regions have a positivity index greater than 100 as measured in a patient group responding to the allergen; and are not reactive with immunoglobulin E (igh) antibodies from patients responsive with immonoglobulin E (igh) antibodies from patients responsive to the allergen. The agent can be used to prevent and treat a wide variety of allergic diseases, e.g. by desensitisation. Side effects, e.g. those mediated by igt, are reduced.
                                                                                                                                                                                         13-Jan.1996. 163287.
24-JUN.1996. 163287.
24-JUN.1996. JP-153287.
24-JUN.1996. JP-153287.
24-JUN.1996. JP-153287.
(MELT ) MELLI SEIKA KAISHA LID.
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Pred. No. 1.25e+00;
001-MAY-1998 (first entry)
--cell epicopy peptide #2 of sudi pollen antigen.
T-cell epicope: sugi pollen antigen; sugi pollinoxis.
Synthetic:
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Pred. No. 1.25e+00:
0: Mismatches 0:
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Dairiki K. Iwama A, Kino K. Kume A. Sone T:
WPI: 97-470495/43.
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W27373 standard: peptide: 31 AA.
W27373:
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Best Local Similarity 100.0%:
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Best Local Similarity 100.0%;
Matches 9; Conservative
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10-MAR-1997; 300740.
10-MAR-1996: 3P-080702.
                                                                                                                             Cryptomeria japonica.
Jiooba7700-A.
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ID W2
AC W2
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The Mark 1996; JCC140.

MARK 1996; JP-680722.

MARK 1997; JCC140.

MARK 1997; JCC160.

MARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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24.MAR-1998 (first entry)
Mulli-epitope peptide used as immunotherapeutic agent #5.
Mulli-epitope peptide: immunotherapeutic agent; allergic disease.
Theeli epitope region; allered; lymphocyte; immunoalobalin E.
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Multi-epitope peptide: immunoth..apeutic agent; allergic disease:
T-cell epitope region: allerge... ymphocyte: immunogiobuli: E.
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10-MAR-1995, J00740.
10-MAR-1996, JP-080702.
(MEIP ) MEIGH MILK PROD CO LID.
Dalriki K, Iwama A, Kino K, Kume A, Sone T;
PPI 97-470495/43.
Peptide immunoitherapeutic agent to treat allergic diseases
contains multi-epitope peptide containing T cell epitope regions
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Pred. No. 1.25e-00:
3: Mismatches 6: Indels
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Claim 9; Page 32: 58pp: Japanese.
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Local Similarity 100.0%:
                                     / Match 100.0%;
Local Similarity 100.0%;
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                                                                            9; Conservative
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C8-SEP-1995: 306295.

10-SEP-1994: JP-242137.

14-JUL-1995: JP-200222.

14-JUL-1995: JP-200222.
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09-MAY-1995.
20-OCT-1993: 262626.
20-OCT-1993: JP-262626.
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134 AA:
                                                                                                               17 FIKRVSNVI 25
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Sedneuce
                                     Query Match
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Claim 5: Page 32: 58pp: Japanese.
The present sequence represents a multi-epitope peptide which is used as a new immunocherapeutic agent. It comprises I cell epitope regions from 2 or more different allerens (preferably linked val aranine or lysine different allerens (preferably linked val aranine or lysine different s), where the T cell epitope regions: have a positivity index greater than 100 as measured in a patient group responding to the allerent seconding to the allerent and are not reactive with immunoglobilin E responding to the allerents responsive to the allergen. The agent can be used to prevent and treat a wide variety of allergic diseases, e.g. by desentitisation. Side effects, e.g. those mediated by 19E, are reduced.
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Multi-epitope peptide used as immunotherapeutic auent *5.
Multi-epitope peptide: immunotherapeutic agent: allergic disease:
I-cell epitope region: allergen: lymphocyte; immunoglobulin E.
Synthetic.
                                                                                                                                                  Multi-epitope peptide used as immunotherapeutic agent #2.
Multi-epitope peptide: immunotherapeutic agent; allergic disease:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-WRR-1996: JP-080722.
[MRIP ) MILK PROD CO LID.
Dairliki K, Iwama A, Kinc K, Kume A, Sone T;
WPI; 97-476495/43.
Peptide immunoritherapeutic agent to treat allergic diseases -
contains multi-replice protide containing I celi epitope regions
from different allergens
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                                                                                                                                                                                             I-cell epitope region; allergen; lymphocyte; immunoglobulin E.
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W27371;
                                                                        RESULT 10
10 W27370 standard: poptido: 105 AA
AC W27370;
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Best Local Similarity 160.0%:
Matches 9; Conservative
                                                                                                                                   (lirst entry)
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10-MAR-1997; J30740.
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              1 FIKRVSNVI
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                                                                                                                               24 - MAR - 1998
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                                                                       3.100
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                                                                                                                                                                                                                                                                                                                    12-MAR-1996 (first entry)
Japanese cedar polien allergen Cryj :
Japanese cedar: polien allergen: Cryj I: T-cell epitope: peptides
prevention: treatment: cryptomeria pollinosis.
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Cedar polien allergen B.
Cedar pollen: allergen: immunoglobulin E: IgE: T-cell epitope;
antibody; pollinosis: therapy: immunotherapy.
Cryptomerla japonica.
EP-700929-A2.
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Score 64: DB 1: Length 134:
Pred. No. 1.25e+00;
Fred. No. 1.25e+00; 1ndels
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/note= "T-cell epitope peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "I-cell epitope peptide"
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91. .105
/note* "T-cell apitope
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R75388 standard; protein; 263 AA.
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WPI: 95-203834/27,
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Job time : 5 secs
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F 8 (MEI) 94-26860/33.
F 94-26
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Hino K. Salto S. Taniguchi Y:

WPI: 96-14/976/15.

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Spacese redar pollen antigen Cryji.
Japanese redar pollen antigen: allerden; Cryji: sugi: pollinosis.
Cryptemeria japonica.
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Japanese cedar pollen: allergen: antigen: alleray: B cell: T ceil.
Cryptomeria japonica.
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22. .374
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R31937:
03-JCN-1993 (first entry)
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R60166 standard: Protein: 374 AA.
R60166:
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Best Loral Similarity 100.0%;
Matches 9: Conservative
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Best Local Similarity 100.5%;
Matches 9; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 Universit: of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

protein - protein database search, using Smith-Waterman algorithm MPSrch_pp

Tue Jun 20 13:35:10 2000: MasPar time 2.16 Seconds 60.125 Million cell updates/sec Run on:

Tabular output not generated

>US-09-142-524A-7 (1-9) from US09142524A.pep 64 Description: Perfect Score: Sequence:

I FIKRVSNVI 9

PAM 150 Gap 15 Scoring table:

145341 segs, 14437480 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-issued
1:5A_COMB 2:5B_COMB 3:5_COMB 4:PCT_COMB 5:backfiles1 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 15,775; Variance 46,625; scale 0.338 Statistics:

SUMMARIES

4.45e-C1 4.45e-C1 5.46e-C1 5.76e-C1 5.76e-C1 5.76e-C1 5.76e-C1 5.76e-C1 1.58e-C2 2.03e-C2 2.03e-C2 2.03e-C2 2.03e-C2 2.03e-C2 2.03e-C2 2.03e-C2 2. Application 4. Application 4. Application 4. Application 1. App Sequence 75, Sequence 9, A Sequence 1, A Sequence 2. Sequence 2, Sequence 2, Sequence 4, Sequence 1, Sequence 80, Sequence 80, Description. Sequence 80 Sequence 80 Sequence 18 Sequence 76 Sequence 6 Sequence 1 Sequence 2 Sequence 2 Sequence Sequence S Sedneuce Sequence 0.05 - 0.8 - 5.18 - 0.05 - 0.8 - 5.18 - 0.05 - 0.5 - 0 Query Match Length DB Score \(\oldsymbol{0} 8220084052008409 Result ò.

4 68.8 27 4 PCT-US94.1 Sequence 27. Application 68.8 27 4 PCT-US95.0 Sequence 21. Application 68.8 27 4 PCT-US95.0 Sequence 21. Application 68.8 27 4 PCT-US95.0 Sequence 22. Application 68.8 28 4 PCT-US95.0 Sequence 23. Application 68.8 28 4 PCT-US95.0 Sequence 25. Application 68.8 32 4 PCT-US95.0 Sequence 25. Application 68.8 32 4 PCT-US95.0 Sequence 25. Application 68.8 32 4 PCT-US95.0 Sequence 26. Application 68.8 32 4 PCT-US95.0 Sequence 27. Application 68.8 32 4 PCT-US95.0 Sequence 28. Application 68.8 32 4 PCT-US95.0 Sequence 28. Application 68.8 32 4 PCT-US95.0 Sequence 28. Application 68.8 32 4 PCT-US95.0 Sequence 29. Application 68.8 32 4 PCT-US95.0 Sequence 29. Application 68.8 33 4 PCT-US95.0 Sequence 29. Application 68.8 30 4 PCT-US95.0 Sequence 29. Application 68.8 30 4 PCT-US95.0 Sequence 29. Application 69.8 30 4 PCT-US95.0	00000000000000000000000000000000000000	Sid Kitting	
4.1. Sequence 27. 5.0 Sequence 27. 5.0 Sequence 27. 5.0 Sequence 27. 5.0 Sequence 28. 5.1 Sequence 28. 5.1 Sequence 28. 5.2 Sequence 28. 5.3 Sequence 28. 5.4 Sequence 28. 5.5 Sequence 28. 5.6 Sequence 28. 5.6 Sequence 28. 5.7 Sequence 28. 5.8 Sequence 28. 5.9 Sequence 28. 5.0 S	ppplication to be possible to be pos	1.00 mm	
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		1-615A-2 ST 2, Application 2, Application 10, 556228 2, INVENTION 2, OF INVENTION 3, OF INVENTION 3, OF SEQUENCES 3, SECONDES	GGTH: 317 AMIN PE: AMINO ACID RANDEDNESS:
25. 25. 25. 25. 25. 25. 25. 25. 25. 25.	400r000040m400r0000400	D x 0	

US-09-142-524A-7.rai

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STANDARD:
                              STANDARD
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Matches 6: Confidence
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                           US-09-065-075-2
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                RESULT
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                                                        Score 50: DB 2: Length 317: Pred. No. 4.45e+01: 2: Mismatches 1: indeis
                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08951889
Patent No. 6008032
CENERL INFORMATION:
APPLICANT Matinut, E., et al.
TILLE OF INVENTION: Carboxymethyl Cellulase from TILLE OF INVENTION: Thermotoga Maritima NUMBER OF SEQUENCES: 4
COMMERS PROBLES: ADDRESS:
ADDRESSED: CAMBILLA, BYRNE, BAIN, GILFILLAN, STREET: 6 RECKER FARM RUAD
CITY: ROSELAND
STREET: MAW JERSEY
COUNTRY, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50: DB 3: Length 317: Pred. No. 4.45e+01: 2: Mismatches :: Indels
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CLASSITICATION, 435
PHOR APPRILORION DAIA.

APPLICATION DAIA.

APPLICATION DAIA.

APPLICATION DAIA.

AITONNEY/ASENT. APPLICATION.

NAME: FERFANC. SHEDONY D.

REFERENCE/DOCKET NUMBER: 331400-20
REFERENCE/DOCKET NUMBER: 331400-20
TELEPHONE: 201-994-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCMPUTER REAGABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
PERATING SYSTEM: MS-10G
SOCTWARE: WORD PREFECT 5.2
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/51.489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPCLOGY: LINEAR
MCLECULE TYPE: PROTEIN
JENCE 317 AA: 37355 MW; 525334 CN;
            MOLECULE TYPE: PROTEIN
SEQUENCE 317 AA: 37355 MW: 525334 CN:
                                                                                                                                                                                                               53.
                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08951889
                                                                                                                                                                                                               STANDARD
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Best Local Similarity 56.7%;
Matches 6: Conservative
                                                        Cuery Match
Best Local Similarity 66.7%;
Matches 6, Conservative
LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                    72 FFKRVDEVI 80
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TOPOLOGY:
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GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L,
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Kaser, Matthew
APPLICANT: Machur, Preete
ITLE OF INVENTION: HUMAN GROWTH-RELATED CDC10 HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.6%; Score 49: DB 1: Length 255: Best Local Similarity 66.7%; Pred. No. 5 76e+61: Matches 6: Conservative 2: Mismatches 1: Indels
                                                         COMPUTER READBLE FORM:
COMPUTER: FISOPD disk
COMPUTER: IBM PC COCPATIBLE
COMPUTER: IBM PC COCPATIBLE
COMPUTER: PSYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
FILING DATE: 02-70: 995
CLASSIFICATION: 435
                                                                                                                                                   ATORNEY/AGENT INFORMATION:
NAME: ROblinson, Joseph R
REGISTRAIION NUMBER: 33 418
REFERENCE/DOCKET NUMBER: 0646/18026-GS3
TELERPONICATION INFORMATION:
TELERPONE: 212-757-77
TELERAX: 23687
INFORMATION FOR SED IN NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDENSS: Single
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Aito
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 AA: 27847 MW; 349504 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08976182 Patent No. 5849556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08978182
 ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus cereus
IMMEDIATE SCURCE:
CLONE: B-LACTAMASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MCLECULE IYPE: peptide
ORIGINAL SOURCE:
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US-08-978-182-1
                                      STATE: N
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Patent No. 5705340
GENERAL INFORMATION:
BAPLICANT: BASMOSSEN, Beth A
APPLICANT: TALLY, Francis P
APPLICANT: TALLY, Francis P
APPLICANT: TALLY, Francis P
APPLICANT: TALLY, PAKOV
IIILE OF INVENTION: OF CLASS B BETA-LACTAMASE ENZYMES FROM BACTEROIDES
TITLE OF INVENTION: PROGILIS
NUMBER OF SECUENCES: 9
CORRESPONDENCE ADDRESS:
APPLICANT: RASMUSSEN, Beth A
APPLICANT: TALLY, Francis P
APPLICANT: GLUZMAN, YAKOV
11TLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCES
TITLE OF INVENTION: OF CLASS B BETA-LACTAMASE ENZYMES FROM BACTEROIDES
TITLE OF INVENTION: FRAGILIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saps
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                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version: #1.30 CURRENT APPLICATION DATA: PLICATION NUMBER: US/08/459,263 FILING DATE: 02-JUN 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: RODISSON, JOSEPH
REGISTRATION NUMBER: 33.448
REFERENCE/COCKET NUMBER: 0646/18026-US2
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus cereus
IMMEDIATE SOURCE:
CLONE: B-LACTAMASE
FENCE 255 AA. 27847 MW: 349604 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08459264
                                                                                                ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                    TELEYAX: 212-753-6237
TELEX: 235667
INFORMATION FOR SO ID NO: 4:
SECUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: BACILLUS CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%:
Matches 6: Conservative
                                                                                                                                                        ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                               35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 FOKRVIDVI 111
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                                                                                                                                              COUNTRY:
                                                                                                                                     STATE:
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PRIOR APPLICATION DATA:
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CHERTAL INSTRUCTION CAPACITYS

APPLICANT HILDMAN JOHNSTON
APPLICANT YES HENRY
APPLICANT RASEL, MATCHER
APPLICANT RASEL, SPORTER
TITLE OF INVENTION: SCHOOL STREET
APPRESSEL: INCYLE PARTHACCLICALS INC.
STREET 3174 FORTER DILVE
CITY: Palo Aito

CHAPLE CA
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Local Similarity 55.6%: Pred. No. 9.57e+01;
tes 5: Conservative 4: Mismitches 0: Indels
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARD: FarisEd for Windows Version 2.C
CURRENT APPLICATION GATA:
APPLICATION NUMBER: US/08/978,182
ILLING LATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTER: DOS SOFTWARE: FASTERQ DOS SOFTWARE: FASTERQ CON WINDOWS VERSION 2.0 AFPILICATION NUMBER: US/09/205.681 FILLING DATE:
                                                                                          NAME: Allings, Lucy J.
REGISTRATION NUMBER: 36.749
REPERNOL/DCCKET NUMBER: PF-6426 US
FELSCOMMUNICATION INFORMATION:
TELEPHONE: 650-855-655
TELEFRAX: 650-845-4166
                                                                                                                                                                                                                              424 AA; 47734 MW: 301865 CN:
                                                                                                                                                                                                                                                                                                                                - [Ad
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1 Application 09/09205681
                                                                                                                                                    INFORMATION FOR SEQ IS NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CPERATING SYSTEM: DUS
                                                                                                                                                                    LENGTH: 424 amino acids
TYPE: arino acid
STRANDEDNESS: simile
TOPOLOGY: linear
                                                                                  ALTORNEY/AGENT INFORMATIONS
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: TLYMNOT06
CLONE: 3003826
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Sequence 80, Application U: 38086428B
Patent No. 551439
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TILE OF INVENTION: NST. ECTIDE AND DEDUCED
TITLE OF INVENTION: OF 51 ISOLATES OF HEPAINTIS C AND THE USE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPAINTIS C AND THE USE
TITLE OF INVENTION: OF FACENTS DERIVED FROM THESE SEDJEMCES INTOMBER OF SEQUENCES: S. ST. NOMBER OF SEQUENCES: 
                                                                                                                                                                                                                          Score 45; DB 2; Length 192;
Pred, No. 1.58e+02;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOUR: FEACHAGE FOREY DISK COMPOURS: FOREY DISK COMPUTER: FOORPY DISK COMPUTER: FOORPY DISK COMPUTER: FOORPY DISK COMPUTER: FOORPY DISK SOFTWARE: FOO SOFTWARE: JOSCHAMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKI:
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INDIVIDUAL ISOLATE: US10
HCE 192 AA: 20855 MW; 200760 CN;
                                                                                                                               ORGANISM: homosapien
individual isolate: 310
CE 192 Aa; 20855 Mw 200750 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 80, Application 13/080864288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
CRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDRESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANUARDS
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Best Local Similarity 44.4%;
Matches 4; Conservative
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US-08-086-4288-80
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                                                                                                                                                                              SECUENCE
                                                                                                                                                                                                                             Query Match
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APPLICANT: PURCELL, R.H.
ITILE OF INVENTION: AND OEDUCED
TITLE OF INVENTION: AND OED SEQUENCES OF THE ENVELOPE I AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES. 283
AND METHODS AND VACCINES
AND METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.3%; Score 45; DB 4; Length 192; Best Local Similarity 44.4%; Pred. No. 1.586-02; Matches 4; Conservative 5; Mismatches 3: Indels
NAME: RICHARD W. BCRK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHIONE: (212) 758-4800
TELEX: 421792
INFORMATION FOR SECILO NO: 90: SEQUENCE CHARACTERISTICS:
EEGNTH: 192 aming acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCMPUTER REACABLE FORM:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PG COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290.665A
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                         CRGANISM: homosapiens
INDIVIDUAL ISOLATE: USIQ
SEQUENCE 192 AA; 20855 MW; 200760 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 80, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80, Application US/08290665A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
RECISTRATION NUMBER: 36.459
REFERENCE/DOCKET NUMBER: 2026-
IELECOMMUNICATION: NORMATION:
TELEFHONE: (212) 759-4800
IELERA: (212) 751-6849
IELERA: 42179
INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORGAN & FIN
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 5: ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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Score 45: DB 1: Length .zz./
Pred. No. 1.58e-02:
Transches 3: Indels
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                                                                                                                                                              192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
RGG:STRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US;
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

ADDION TYPE: FLOHPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTUMARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NOMBER: CS/08/469.570
FILING DATE: 6-111/195
CLASSIFICATION LAIA
RIGH APPLICATION LAIA
CLASSIFICATION NOMBER: 09/106/42#
FILING DATE: 29-10M-1943
CLASSIFICATION LAIA
                                                                                                                                                                                                                                                                                                                          MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: homosepiens
INDIVIDIAL ISOLATE: US10
UENCE 192 AA: 20855 WW: 20076C CN;
                                                                                                                                                              PPT
                                                                                                                                                                                                                                                                              80, Application US/08468570
0, 5871962
                                                                                                                                                                                                                                                 Sequence 80. Application US/08468570
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENJE CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ 10 NO: 80: SEQUENCE CHARACTERISTICS:
                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 amino acids
                                                                                                                                                                                                                                                       Sequence 80, Application 1
Parent No. 5875952
SENERAL INFORMATION
APPLICANT PURCELL R.H
TILLE OF INVENTION: ONU
TILLE OF INVENTION: OF 1
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STRANDEDNESS: unknown
TOPOLOGY: unknown
            Query Match
Best Local Similarity 44.4%;
Matches 4: Conservative
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                                                                    145 YVMRVPEVI 153
                                                                                                  1 FIKEVSNVI 9
                                                                                                                                             JT 11
US-08-468-570-80
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145 YVMRVPEVI 153

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Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Medication:
TITLE OF INVENTION: Of Vesicular Release
NUMBER OF SCHENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger 6 Associates
STREE: 350 Cambridge Avenue. Suite 250
CITY: Palo Alto
STATE: CA
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Pred. No. 1.58e+02:
7: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-INS/MS-UNS
SCTUMARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION LATA:
APPLICATION NUMBER: US/UE/194.995
                                                                    205 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
RESISTATION NUMBER: 39.7.5
REFERENCE/POCKET NUMBER: 86.0.-0152
TELECOMMUNICATION INFORMATION:
                                                                    PRI:
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206 AA: 23:15 MW: 177393 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 76, Application US/08118270 Patent No. 5508184 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/08118270
                                                                                                                                                                 Sequence 18, Application US/08393985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-0986
TELEFAX: (415) 324-0986
INSCRMATION FOR SEL IT N. 18
SECTION FOR SEL IT N. 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20% after at 15
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Best Local Similarity 71.45.
5: Conservative
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3Y: linear
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US-08-393-985-18
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1 FIKRVSNVI 9
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Search completed: Tue Jun 20 13:35:15 2000
                                                 OPERATING SYSTEM:
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| FIKRVSNVI 9
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                                                   AMPLICANT: Schuster, David I.

TILLE OF INVENTION: POLYPEPTIDES CF G-COUPLED PROTEIN
TITLE OF INVENTION: POLYPEPTIDES CF G-COUPLED PROTEIN
HITTLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
STREET: 419 Seventh Street, N.W., Suite 300
STREET: 0.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 76. Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New YOAK University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                   CCMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
COMPUTER: DAY
COMPUTER: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 419 Seventh Street, N.W., Suite 3GC CITY: Mashington SIATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PK1
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298 AA; 33548 WW: 467538 CN;
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COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NC: 76: SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
IYPE: amino acids
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CCMPUTUR READABLE FORM:
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FNCE TAPE: pept
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USA
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PCT-US93-08528-76
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                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: de Kievit, Teresa

IIIE OF INVENTION: No. 5994072el Proteins Involved in the Synthusis and Assem

IIIE OF INVENTION: Of 0-Antiqen in Pseudomonas Aeruginosa

FILE REFERENCE: 6580-089

CURRENI APPLICATION NUMBER: US/38/846.762A

CURRENI FILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 298
            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 4; L
Pred. No. 1.58e+02;
                                                                           FILING DATE: 09-SEP-1943
PRIOR APPLICATION DOTA:
APPLICATION NUMBER: US 67/943.236
FILING DATE: 10-SEP-1992
ATTORNEZ/ASTNI INCORMATION:
NAME: TOWNSEND, KEVIN G.
REGISTRATION NUMBER: 34.033
RESISENCE/COCKE: NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
OUENCE 316 AA; 33805 MW; 521677 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCLEJULE TYPE: peptide
SEQUENCE 298 AA: 33548 MW; :67538 CN:
PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9. Application US/08846762A Patent No. 5994072 GENERAL INFOFMATION. GRAPLICANT: Lam. Joseph S APPLICANT: Rurrows, Lorial APPLICANT: Rurrows, Lorial APPLICANT: Charter, Debotah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08:46762A
                                                                                                                                                                                                                                                                                                                                                                     : 298 amino acids
amino acid
                                                                                                                                                                                                                                                                                  TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR ESQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 296 antito acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
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55.6%;
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Best Local Similarity 33.3%;
Matches 3; Conservative
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Best Local Similarity 55 00.
5; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Cxford Molecular Ltd

MPsrch_pp = protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:24:27 2000: MasPar time 10:17 Seconds 89:137 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-7 (1.9) trom US09142524A.pep 54 1 FIKRVSNVI 9

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

721208 seqs. 100755575 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-pending lipCT 2:05 3:050 4:07 5:080 5:081 7:082 8:083 9:084A lor084B 11:085 12:086 13:057 14:088 15:089 16:090 17:091 18:092 19:093 20:094 21:095 22:NEWP 23:NEWD6 24:NEWU8 25:NEWU9

Mean 18.575; Variance 43.933; scale 0.423 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+C0	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e-00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	
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201	36.	35,	36,	35,	35,	35,	9	4	5,	62,	ď	62,	62,	62,	62	52,	Ļ	'n	ě	15,	
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sednesce	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sednesce	Sequence	Sequence	Sequence	Se juence	Sequence	
a i	US-08-468-	US-08-467	US-07-938-	US-08-226-	CS-08-467-	CS-08-35C-	US-08-467-	US-09-142-	US-09-142-	US-07-938-	US-08-468-	US-08-226-	CS-08-467-	US-08-467-	- 38 - 3		US-39-142-	US-09-142-	US-09-142-	US-08-526-	
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Length	20	2 C	20	2 C	20	3C	20	37	31	ე9	09	99	96	9	9	9	80	105	134	353	
Suery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
Score	64	54	64	54	64	99	54	9	\$ 9	₹	54	54	\$	\$ G	54	94	54	54	64	54	
Result	7	7	3	4	S	Q.	7	80	σn	10	11	12	13	14	15	16	17	81	6.1	20	

S. 08-467 - Sequence 2, Applicatio 2,93e-00 S. 07-729 - Sequence 2, Applicatio 2,93e-00 S. 07-938 - Sequence 2, Applicatio 2,93e-00 S. 07-938 - Sequence 2, Applicatio 2,93e-00 S. 07-938 - Sequence 2, Applicatio 2,93e-00 S. 07-730 - Sequence 3380, Applicatio 2,93e-00 S. 08-134 - Sequence 5908, Applicatio 2,93e-00 S. 09-134 - Sequence 5908, Applicatio 2,93e-02 S. 09-134 - Sequence 4208, Applicatio 2,93e-02 S. 09-135 - Sequence 4208, Applicatio 2,93e-02 S. 09-136 - Sequence 4208, Applicatio 2,93e-02 S. 09-328 - Sequence 591, Applicatio 2,93e-02 S. 09-328 - Sequence 591, Applicatio 2,93e-02 S. 09-468 - Sequence 95, Applicatio 2,92e-02 S. 09-467 - Sequence 97, Applicatio 2,92e-02 S. 09-467 - Sequence 97, Applicatio 2,92e-02 S. 09-467 - Sequence 1, Applicatio 2,92e-02 S. 09-467 - Sequence 1, Applicatio 2,92e-02 S. 09-467 - Sequence 1, Applicatio 2,92e-02 S. 09-467 - Sequence 97, Applicatio 2,92e-02 S. 09-467 - Sequence 1, Applicatio 2,	ALIGNMENTS DARD: PHI: 20 AA. US/NE 68940 Es 168940 Es 168940 Es 168940 Es 168940 Es 168940 Es 100 AB
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Query Match
Best Local Similarity 190.0%;
Matches 9: Conservative
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ID US-07-938-990A-36
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GENERAL INFORMATION:
APPLICANT Griffeth, Irwin J.;
APPLICANT Griffeth, Johnson
APPLICANT BOND, JALLAN F.;
APPLICANT Garman, Richard D.;
APPLICANT Yeury, Modern B.;
APPLICANT Yeury, Modern B.;
APPLICANT Fraucr, Modern B.;
CORRESPONDER FORFERS 26,
ADDRESSINGER ADDRESS 26,
ADDRESSINGER ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. STREET 510 Lincoin St CITY: Waltham
                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                             vuery Match 100.0%: Score 64: DB 10: Length 26:
Sest Local Similarity 100.0%: Pred. No. 2.93e+00:
Matches 9: Conservative 0: Mismatches 0: Indels
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1993
ATDORNEY/AGENT INCRMATION:
NAME: CATALIGN NUMBER: 35,729
REFERENCE/OCKET NUMBER: 025,6 US (IMI-0280F2)
FELECOWALNICATION INFORMATION:
TELEPHONE: (617) 466-6000
INFORMATION FOR SEQ. 10 NO: 36: SRUGENCE CHARACIERISTICS:
LENGTH: 20 minito acid
TYPE: aminto acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/467,006
FILING DAIE: June 6, 1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATJORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/08457005
                                                                                                                                                                                                                                                TOPOLOGY: Ilrear
MOLECULE TYPE: peptide
FRAGMENT TYPE: interval
HENCE 20 AA: 2080 MW: 2304 CN:
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                                                           Gaps
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TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Apparese Cedar Pollen NUMBER OF SEQUENCES: 201
                                                           ö
                                                                                                                                                                                                                                                                                                                                  SSEE: Immulogic Pharmaceutic : Corporation, Inc
F: 610 Lincoln St
Waitham
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER VAISA

COMPUTER VAISA

MEDIUM TYPE: Filepy disk
COMPUTER: HW PC compatible
COMPUTER: HW PC compatible
COMPUTER: Patentin PC-DS/MS-DNS

SOFTWARE: Patentin Release #1.0. Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25,248A

FILING DATE: April 8, 1994

CLASSIFICATION 1424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,990

FILING DATE: September 1, 1992

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: January 15, 1993

ATIONNEY/AGENT INFORMATION:
                                                           0; Indels
                                        Score 54: DB 4: Length 20:
Pred. No. 2.93e+00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Darlene A. Vansiche
REJISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-5000
                                                                                                                               20 AA
                                                           0; Mismatches
                                                                                                                               P.8.7
                                                                                                                                                                                                  Sequence 36. Application US/08226248A GENERAL INDEXMATION: APPLICANT: GTIEfeth, JUNIO 3.; APPLICANT: POLIOCK, Joanne:
                                                                                                                                                                                   Sequence 36. Application US/08225248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA: 2080 MM: 2364 CN:
TOPOLDGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 25 AA: 2090 XW: 2304 CN:
                                                                                                                                                                                                                                    Bond, Julian F.;
Garman, Richard D;
                                                                                                                                                                                                                                                    Kuo, Mei-Chang:
Yeung, Siu-mei H.;
                                                                                                                                                                                                                                                                        Brauer, Andrew:
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 466 6340
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 amino acids
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                                        Query Match
Rest Local Similarity 100.0%;
Matches 9; Conservative
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3Y: linear
                                                                                                                                                                                                                                                                                                                                                                       USA
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STAIE: MA
COUNTRY: USA
TE: 02154
                                                                            9 FIKRVSNVI 17
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STREET: 61
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APPLICANT:
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APPLICANI:
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APPLICANT:
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TILLE OF INVENTION: Allergenic Proteins And Peptides First TILLE OF INVENTION: Japanese Gedar Polien
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
STREET: 610 Lincoln St
CITY: Walthar
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MEDIUM TYPE: Floppy disk
COMPUTER: INM PO COMPUTER:
DPERMINS INM PO COMPATIBLE
DPERMINS SYSIES:
SCHWARE: Patchin Polease Flor. Version #1 25
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION HOMBER: 693550.225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jahe E. Remillard
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 025.6 USC2 (IMI-028CPS2)
TELECOMMUCATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-7401
INFORMATION FOR SEC ID NO: 35:
SEQUENCE CHRRACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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      Length 20,
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Pred. No. 2.93e+00;
0; Mismatches 0;
Store 64: DB 7: L
Fred. No. 2.93e+00:
0: Mismatches 0
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AL INFORMATION:
ICANT: Stiffeth, Irwin J.;
ICANT: POllock, Joanne:
ICANT: Bond, Julian F.:
ICANT: Garman, Richard D;
ICANT: Kuo, Mel-Chang:
                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application Us/08467023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA; 2080 MW; 2304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew:
APPLICANT: Exley, Mark A.;
                                                                                                                                                                                                           STANDARD;
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Best Local Similarity 100.0%;
Matches 9; Conservative
    Ouery Match 150.0%;
Best Local Similarity 150.0%;
Matches 9; Conservative
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GY: linear
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COUNTRY: US
ZIP: 02154
                                                                                    9 FIKRVSNVI 17
                                                                                                         JS-08-467-023-36
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APPLICANT:
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Query Match.
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GENERAL INFORMATION:
APPLICANT Griffeth, Irwin J.;
APPLICANT POllock, Joanne;
APPLICANT BOND, Julian F.;
APPLICANT BOND, Weichard D;
APPLICANT Garman, Richard D;
APPLICANT Garman, Richard D;
APPLICANT Braner, Andrew;
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CLASSIFICATION 424
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/226,24#
FILING DATE: April 8, 1994
APPLICATION NUMBER: 07/938,99;
FILING DATE: September: 1, 1993
APPLICATION NUMBER: 07/938,99;
FILING DATE: Can.ary 15, 1993
APPLICATION NUMBER: FOLYCS93/0:139
FILING DATE: Can.ary 15, 1993
APPLICATION NUMBER: FOLYCS93/0:139
FILING DATE: Can.ary 15, 1993
APPLICATION NUMBER: 35,79
REFRENCE/COCKET NUMBER: 35,79
REFRENCE/COCKET NUMBER: 35,79
FILEPHONE: (517) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Immulogic Pharmaceutical Corporation, 610 Lincels St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDZIM TYPE: Florey disk
COMPUTER: Elorey disk
COMPUTER: IBM PC Compatible
DPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Re-ease #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION WHERE: US/09/350,225
FILING DATE: December 6, 1994
CLASSIFICATION: 424
                                                                                                     AA
                                                                                                     PRI
                                                                                                                                                                                                                         Sequence 36, Application US/08350255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA; 2080 MW; 2304 CN;
                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 20 amino acids
amino acid
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Local Similarity 100.0%;
les 9: Conservative
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MEDIUM IYPE: Floppy
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FIRRVSNVI 9
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                                                                                                                                                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT CHIFFETH, ITWIN 5.:

APPLICANT BOILOCK JUGENE,

APPLICANT GATTAN, Richard D.

APPLICANT GATTAN, Richard D.

APPLICANT YEAR, SIU-mel H.:

APPLICANT YEAR, SIU-mel H.:

APPLICANT YEAR, Mark A.:

APPLICANT EXLEY, Mark A.:

APPLICANT EXLEY, Mark A.:

APPLICANT EXTERY, Mark A.:

APPLICANT BOWERS, Steven P.

ITILE OF INVENTION: Allergenic Profession

NUMBER OF ESCHENCES: 261

CORRESPONDENCE ADDRESS:

ADDRESSES Immunogic Pharmaceutical Corporation, Inc.

STREET 610 Lincoln St.

CITYE WA! LAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-D: /MS-DCS
SOFTWARE: Patentin Reichse #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05/467.697
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 594
ATONEY/AGENT INPORMATION:
NAME: December 6, 594
NAME: BEERINGE/YOCKET NUMBER: 18:P12
RESISTRATION NUMBER: 18:P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match.
100.0%: S ore 64; DB 10; Length 20;
Best Local Similarity 100.0%: F ed. No. 2.93e+00;
Matches 9; Conservative v: Mismatches 0; Indels
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     20 AA
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                                                                                                                                                Sequence 36, Application US/38467697
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FRAGMENT TYPE: internal
SEQUENCE 20 AA: 2080 MW: 2364 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEC 15 No. 361
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (1sk
     STANDARD.
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US-08-467-697-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-142-524-4
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Sequence 62, Application US/07938990A
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: POlicek, Joanne
APPLICANT: Bolicek, Joanne
APPLICANT: Bood Julian
IIILE OF INVENTION: Allergenic Proteins And Peptides Firm
TITLE OF INVENTION: Apparese Cedar Pollen
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSE: Lahive 6 Cockiteld
SIRET: Sixty State Street
CITY: Boston
                                                      <u>:</u>:
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COMPUTER READBLE FORF

MEDIUM TYPE: F.OPP

COMPUTER: IBM PC C. 1th:
COMPUTER: Datentin Release #1.5. Version #1.25

SOFTWARE: Patentin Release #1.5. Version #1.25

CURSIFICATION NUMBER: US/V.938,990A

FILING DATE: 199209C1

CLASSIFICATION NUMBER: US/V.438,990A

APPLICATION NUMBER: US/V.434

FILING DATE: July 15, 194;
FILING DATE: July 15, 194;
FILING DATE: July 16, 194;
FILING DATE: July 16, 194;
FILING DATE: MANDRAGOURAS

REGISTRATION NUMBER: 16C-025CC (IM:-028)

TELECOMMUNICATION INMBER: 16C-025CC (IM:-028)

TELECOMMUNICATION INMBER: 16C-025CC (IM:-028)
                                                      0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
103.0%; Score 64; DB 4; Length 60;
Best Local Similarity 106.0%; Pred. No. 2.93e+00;
Matches 9; Conservative 6; Mismatches 0; Indels
                          Score 54; DB 17; Length 31;
Pred. No. 2.93e+60;
0; Mismatches 0: Indels
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                                                                                                                                                                                                                                                      Sequence 62, Application US/07938990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 60. AA; 6644 MW: 19464 CN;
31 AA; 3585 MW; 4902 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7460
IELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 amino acids
                          Owery Match 100.6%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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US-07-938-99CA-62
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                                                                                  23 FIKRVSNVI 31
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| FIAKVSKVI 9
                                                                                                  TOPOLOGY:
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SEQUENCE
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                                                                                                                                                                                              Sequence 5, Application 15/59142524
GENERAL INFORMATION:
APPLICANT: Soncy Toskio
APPLICANT: Kare, Akinori
APPLICANT: Kare, Kohsuke
TILLE OF INVENTION: Peptide-based Immunotherapeutic Agent For Treating
TITLE OF INVENTION: Allergic Diseases
TITLE OF INVENTION: Allergic Diseases
FILE REFERENCE: Docket NO. SPO-10.3
CURRENT APPLICATION NUMBER: US/09/142,524
CURRENT FILING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: B/86/702
EARLIER FILING DATE: 1996-03-10
EARLIER FILING DATE: 1996-03-10
EARLIER FILING DATE: 1997-03-10
NUMBER OF SEO ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                               Sequence 4, Application US/03142524

GENERAL INFORMATION:
APPLICANT: Sone, Toshio
APPLICANT: Kariki, Kazuo
APPLICANT: Kume, Akinon
APPLICANT: Kume, Akinon
APPLICANT: Kume, Akinon
APPLICANT: Kume, Akinon
APPLICANT: Kume, Kohsike
APPLICANT: Kino, Kohsike
APPLICANT: Kino, Kohsike
ITILE OF INVENTION: Allergio Diseases
FILE OF INVENTION: Allergio Diseases
FILE OF INVENTION: Allergio Diseases
FILE REFERENCE: Docket NO. SPO-103
CURRENT PRILING DATE: 1996-01-04
EARLIER APPLICATION NUMBER: 8/80/702
EARLIER FILING DATE: 1996-03-10
EARLIER FILING DATE: 1996-03-10
NUMBER: OF SCO ID NOS: 5
SEO ID NO 4
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Unknown Organism:peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64, DB 17; Length 31; Pred, No. 2.93e+00; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFI
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                                          Sequence 4, Application US/09142524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    obery Match
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5
LENGTH: 31
IYFE: PRT
ORGANISM: UDKNOWD
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 FIKRVSNVI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FIKRVSNVI 9
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                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                             APPLICANT Griffeth, Irwin J.;
APPLICANT Griffeth, Irwin J.;
APPLICANT Bond, Julian F.;
APPLICANT Bond, Julian F.;
APPLICANT Garman, Recland S.
APPLICANT Yeung, Siu-mei H.;
APPLICANT Yeung, Siu-mei H.;
APPLICANT Exley, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT FOWER, Steven P.
IIILE OF INVENTION A.lergenic Proteins And Peptides From IIILE OF INVENTION. Japanese Gedar Pollen.
NUMBER OF SEQUENCES: 251
CORRESPONDENCE. ADDRESS:
ADDRESSED A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \ddot{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 10; Length 50; Pred. No. 2.93e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0: Indels
                                                                                                                                                                                                                                                                                                    E: ImmuLogic Pharmaceutical Corporation,
610 tincoin St
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
UPERATINS SYSTEM: PC-DCS/MS-DCS
SOFTMARE: Patentin PC-BCS/MS-UCS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/28/468.946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Darlene A Vassione
PEGISTRATION NUMBER: 35,729
RELECOMMUNICATION INFORMATION:
TELEBHONE: (617) 466-6000
INFORMATION FOR SEQ 10 NO: 55,000
INFORMATION FOR SEQ 10 NO: 62: SEQUENCE CHARACTERISTICS:
            60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 424
PRIOR DATE: DECEMBER: 6,1994
FILING DATE: DECEMBER: 6,1994
FILING DATE: DECEMBER: 6,1994
APPLICATION NUMBER: 08/226,248
FILING DATE: APRIL 8, 1994
APPLICATION NUMBER: 07/38,993
FILING DATE: September: 1,3992
APPLICATION NUMBER: $47/VS93/28139
FILING DATE: 2dmary 15: 1993
AICHNEY/AGENT INFORMATION:
             PRT;
                                                                                                           Sequence 52, Application US/08468940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MCLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 60 AA: 6644 WW: 19464 CN:
                                                                                     Sequence 52, Application US/08458940
             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 60 amino acids
amino acid
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Fest Local Similarity 106.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 62154
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                             CITY: Waltham
STATE: MA
                                                                                                                                                                                                                                                                                                                                                        SA
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 T 11
US-08-468-940-62
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APPLICANT: Collon F.

APPLICANT: Garman, Richard U.

APPLICANT: Kuo, Mel-Chang.

APPLICANT: Young, Siu-mei ii.

APPLICANT: Exiey, Mark A.

APPLICANT: Exiey, Mark A.

APPLICANT: Exiey, Mark A.

APPLICANT: Powers, Steven.

ITLE OF INVENTION: Ailery iic Proteins And Peptides From VITLE OF INVENTION: Jafanese Codar Polien

NUMBER OF SEQUENCES: 201
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SOFTWARE: Patentin Release 41.0, Version 41.25
CURRENT APPLICATION DATA.

APPLICATION NUMBER: 05/08/226,248A
FILING DATE: 424
PRIOR APPLICATION DATA: 424
PRIOR APPLICATION DATE: 424
PRIOR APPLICATION NUMBER: 67/958,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 67/9591/61149
FILING DATE: January 15, 1947
ATTORNEY/AGENT INFORMATION: NUMBER: 05/124
REFERENCE/DOCKET NUMBER: 65/124
REFERENCE/DOCKET NUMBER: 65/124
REFERENCE/DOCKET NUMBER: 65/124
REFERENCE/DOCKET NUMBER: 65/124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: ImmuLogic Pharmaceutical Corporation, 610 Lincoln St.
                                      60 AA
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                                      53.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IM PC compatible
OPERATING SYSTEM: PC-DG/S/MS-DOS
                                                                                                                                                                                                                                               Sequence 62, Application PG/08226248A
GENERAL INFORMATION:
APPLICANT: Griffeth, in U.:
                                                                                                                                                                                                   Sequence 62, Application US/38226248A
                                                                                                                                                                                                                                                                                                          Griffeth, in C.:
Poliock, Jeanne:
Bond, Julian F.:
Garman, Richard D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WI TYPE: internal
60 AA: 5644 MW; 19464 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 466-5040 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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STREET: 610 Lir
CITY: Waltham
STATE: MA
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CC APPLICANT: POLICA

CC APPLICANT: FOR APPLICANT: EXAME

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CC CONTINY: Walthan

CC CONTINY: W
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ID US-08-457-697-62
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SEQUENCE
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                                                                                                                                                                                                               APPLICANT GILIECTH, Irwin J.;
APPLICANT Bollock, Joanne;
APPLICANT Bollock, Joanne;
APPLICANT Garman, Richard J.;
APPLICANT Kuch McFard J.;
APPLICANT Kuch McFard J.;
APPLICANT Yeurgh, Sturmel H.;
APPLICANT Fardy, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT Bracer, Steven P.;
IILE OF INVENTION: Allergenic Proteins and Peptides From IILE OF INVENTION: Japanese Cedar Pollon NUMBER SECUROES: 261
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Immulgal Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDIOM TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, V rsion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.697
FILING DATE: June 6. 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jane E. Remiliard
REGISTRATION NUMBER: 38.32
REGISTRATION NUMBER: 025.6 USD4 (INT-028CPD4)
TELEPHONE: (517) 227-7400
TELEPHONE: (517) 227-7400
INFORMATION FOR SEQ 10 NO: 62.
SEQUENCE CHARACTERRSITOS.
LENGTH: 60 Amilio acid
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                                                                                                                                                                     Sequence 62, Application US/08467697
GENERAL INFORMATION:
APPLICANI: Griffeth, Irwin J.:
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FRAGMENT TYPE: internal
JENCE 60 AA: 6644 MW; 19464 CN:
                                                                                                                          Sequence 62, Application US/08467697
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Matches 9; Conservative
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APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer. Andre.,
APPLICANT: Brauer. Andre.,
APPLICANT: Powers, Steven.,
TITLE OF INVENTION: Aller wic Proteins And Peptidus Frum
TITLE OF INVENTION: Japa ve Cedar Poblen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                        maceutical Corporation, Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC cor-atible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.023
FILING DATE: Jane 6, 1995
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 025.6 USD2 (IMI-028CPD2)
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
  Application US/ 467023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/08:50225
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60 AA: 6644 MW: 19464 DK.
                                         Griffeth, Irwin J.;
Pollock, Jeanne;
Bond, Julian F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,672
REFERENCE/DOCKET NUMBER: 025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7-19
TELEFAX: (617) 227-594.
INFORMATION FOR SEQ ID NO: 5-2:
SEQUENCE CHARACTERISTICS
LENGTH: 60 amino acids
                                                                                                             Garman, Richard D:
                                                                                                                                                                                                                                                                                                                 STREE: ImmuLogic F
STREET: 610 Lincoin S'
CITY: Maltham
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Sequence 62, Application GENERAL INFORMATION:
APPLICANT: Griffet) APPLICANT: POLIOCK
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ZIP: 02154
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APPLICANT:
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APPLICAN: Gurran. Richard D. APPLICAN: Kao. Mei-Chang.
APPLICANT: Kao. Mei-Chang.
APPLICANT: Young. Siu-mei H.:
APPLICANT: Brauer. Andrew:
APPLICANT: Brauer. Andrew:
APPLICANT: Brauer. Andrew:
APPLICANT: Brauer. Altergenic Proteins And Peptides From TITLE OF INVENTION: Altergenic Proteins And Peptides From TITLE OF INVENTION: Jupanese Cedar Pollen
NIMBER OF SEQUENCES. 251
OCHRESPED: ImmuLodic Pharmaceutical Corporation. Inc. STREET: 610 Lincoln St.
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STATE: MATCHALL
STATE: MATCHAL
SPENDIN TYPE: Flopy disk
COMPATING THE FLOPY DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACCHIE Release #1.0, Version #1.25
CHENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACCHIE Release #1.0, Version #1.25
FILING DATE: December 6, 1994
STATING DATE: December 6, 1994
STATING DATE: APPLICATION NUMBER: 98/256,248
FILING DATE: APPLICATION NUMBER: 97/38,99
FILING DATE: SEPTEMBER: 97/29
FILING DATE: SEPTEMBER: 97/29
FILING DATE: MATCHANION:
NAME: DATON NUMBER: 97/29
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Matches 9: Conservative 0: Mismatches 0: indeis
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49 FIKRVSNVI 57

1 FIKRVSNVI 9

Search completed: Mon Jun 19 16:25:06 2000 Job time : 39 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Jun 19 15:05:27 2000; MasPar thre 5.08 Seconds 83.618 Million cell updates/sec MPsrch_pp Res on:

Tabular output not generated.

>US-09-142-524A-7 (1-9) from USC9142524A.pep 64 Title: Description: Perfect Score: Sequence:

] FIKRVSNVI 9

142080 seqs. 47172406 residues PAM 150 Cap 15 Searched:

Scoring table:

Minimum Match 0% Listing first 45 summaries Prist-processing:

pir62 1:pirl 2:pir2 3:pir3 4:pir4

Database:

Mean 23,798: Variance 28,919: scale 0,823 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Fred. No.	or allergen Cry	or allergen Crv 1 8.0	ase lyase - Asper 3 16e-	othetical protein 5.98	se (EC 3, 9.56e+	erm 9.50	protein 9.	protein 9.5	n requiat 1.52	a-lactamase (EC 3. 1.	(EC 3. 1.52e-	20 1.	membrane pro 1.	membrane pro 1.	cal protein 1.52e+	NA ligase 1.	phosphates 2.3	rd 2.3	avy chain, c 2.39e-	tical protein 3.75	ycerate ki 3.75	375
see d: 8	JC212	302123	551539	\$50920	32017	B72216	B70541	F70965	B72330	1 PNBS2S bet	PNBSU2	S56193	S46187	563322	64403	D71368	A64472	G70983	A44357	112519	E7508C	T04814
ry ch Tength D	.0 374	.0 37	.1 32	. 7 . 7.2		.: 31	.1 47	.1 47	.6 19	.6 25	.6 25	.و	.6 37	.6 38	.6 43	.6 52	7 0.	9 0.	.0 47	.4 234	7	5
Clery Score Match	54 100	100	۲-		50 78	0	8.0	0	9 76	9 76	ار. ئ	σ		9 16	6	9 75		75	8 75	7.3		47 73
Result No. S		5	m	7.7	2	9	7	80	6	10	H	12	13	14	15	16	17	18	19	20	21	22

JC2123 *type complete major allergen Cry ; I precursor (clone pCCI-2-2) . Japanese cedar cedar allergen Cry to a japonica *common_name Japa:ese cedar *formal_name Cryptomeria japonica *common_name Japa:ese cedar 14-Jul-1994 *sequence_revision 14-Jul-1994 *text_change

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RESULT ENTRY TITLE

ORGANISM DATE

Db 130 FIKRVSNVI 138

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**residues
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                                                                                   *Submission
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REFERENCE
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*product mujor allerden Cry j I (clone pCCI-2-2) *status
predicted *label MAI\
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Fauthors Bit M.C.: White-end, M.F.: Cleveland, 1 E.: Death F.A.
Fauthors Cont. Jenet, (1995) 27:142-149
Fille Cont. Jenet analysis of the Aspertitus middlens pertains to pelA agne and evidence for binding or promoter regions to pelA a requision of carbon catabolite repression.
FCDOS: references RUID: 95308536
FACCOSSIDE SEASON SSISSON SSISSON SSISSON SSISSON SSISSON.
                                           #duthors Sure. T.: Komiyama, N.: Shimizu, K.: Kusakabe, T.: Morikubo K.: Kimo, K.: Kimo, K.: Blophys. Res. Commun. (1994) 199:619-625
#ititle Cloning and sequencing of CDNA coding for CTy 1.: a major altergen of Capanese cedar polien.
                                                                                                                                                   -*residues 1-374 ##label SON
##cross-refurences GB:D26544; NID:q493631; PID:d1006086; PID:q493632
##experimental_source pullen
"cession PC2065
##molecur.
                                                                                                                                                                                                                                                                                                                                                                                                                         4 *binding_site carbohydrate (Asn) (covalent) *status
predicted
*!ength 374 *molecular weight 40645 *checksum 2920
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Flormal_name Aspergillus sp.
15.Ju.1995 *sequence_revision 19.Apr-1996 *text_change
851509
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hypothetical protein YMR192W - yeast (Saccharomyces
cerevisiae)
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Pred. No. 3.16e-01;
2: Mismatches C: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              udery Match
Best Local Similarity 100.0%; Pred. No. 8.03e-03:
Matches 9; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                         #Superfamily pectate lyase LAT59 alycoprotein; police
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -326 ##label HOM
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26-Aug-1999
JC2123; PC2065
JC2123
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                       ##molecule_type mRNA
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OBGANISM
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B72216
A7200
Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McConald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Gotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.G.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *authors Lim, B.M.: Pene, J.C.: Shaw, R.W.
*journal J. Bacteriol. (1988) 170;2873-2878
*title Channey, nucleotide sequence, and expression of the Harilius cereus 5/8/6 beta-lactamase il structural qene.
*crees MJID:88227879
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##cross-reterences GB:M19530: 41D:9143127; P1DN:AAA22562.1: F11:4143528
FICATION #superfamily beta-inclamase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #domain Signal Sequence #status predicted #jate) $50% #predict Actaria turnse II #status predicted #jutel MAI #jecqti v5% #mouse militaria will #jak #mojecks.m 7%.
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*formal_name Thermotoga maritima
11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change
11-Jun-1999
*sequence_revision 12-May-1995 *text_Channe
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                                                                                                      Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, January 1995
850920
                                                                                                                                                                                                                                                                                             *map_position 13R
SUMMARY Flength 720 #Folecular-Weight 82131 #checksum
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Best Local Similarity (6.7%) Find: No. 9-564-50;
Matches 5: Conservative 2: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                          Score 51: DB 2. Length 72G:
Pred No. 5.98e-00:
4. Mismatches 0: Indels
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                                                                                                                                                                                                             1-720 ##label PEA
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Best Local Similarity 55.6%;
Matches 5; Conservative
                            21-Nov-1997
  10-Feb-1995
                                                                                                                                                                                   **molecule_type DNA **residues :-72
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#authors Goto, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, Colo, S.T.; Brosch, S.V.; Eiglmeler, R.; Gas. S.; Barry III. C.E.; Tekalar, S.V.; Eiglmeler, R.; Basham, D.; Brown, D.; Chillinqworth, T.; Connor, R.; Davies, R.; Perluell, T.; Gentles, S.; Hamilu, N.; Holroyd, S.; Hurchsy, C.; Gentles, S.; Hamilu, N.; Holroyd, S.; Hurchsy, C.; Oliver, S.; Caborne, J.; Quall, M.A.; Skeiton, S.; Squares, S.; Squares, R.; Steper, K.; Skeiton, S.; Squares, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Ison, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Barrell, B.G.; Parlor, R.; Whitehead, S.; Barrell, B.G.; Parlor, C.; Parlor, C
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**cross-references GB:295586; GB:ALL23456: NID:93261785; PID:e317181;
PID:92117261
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17-Jul-1998 *sequence_revision 17-Jul-1998 *text_change
Atitie Evidence for lateral gene transfer between Archaea and
Bacteria from genome sequence of Thermotoga maritima.
*cross-references MUID:99287316
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translation not shown
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                                                                                                                                           preliminary
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Best Local Similarity 66,7%;
Matches 6: Conservative
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DATE
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Cole S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeicr, K.; Gas, S.; Barry, III. C.E.; Fekaia, F.; Badocock, R.; Bashar, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Deville, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Horrby, T.; Jagels, K.; Kroph, A.; McLeen, J.; Xwille, S.; Horrby, T.; Jagels, K.; Krope, A.; McLeen, J.; Seeger, R.; Salandream, M.A.; Rogers, S.; Gabres, T.; Guail, M.A.; Rogers, S.; Sarres, R.; Suston, J.E.; Selton, S.; Guares, S.; Sarres, R.; Suston, J.E.; Taylor, K.; Itehead, S.; Barrell, B.G.; Suston, J.E.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
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FRUCE A7220

FRUTHOUS NUISON K.E. Clayton B A. Dill S R. GWIBL M E. Dodson. R. W.C. Ketchum K.A. McDonald, L. Utterback, T. N. Malek, W.C. Ketchum K.A. McDonald, L. Utterback, T. N. Malek, J.A. Dinher, K.D. Garrett, M.W. Stewart, A.M. Gotton. M.D. Bratt, M.S. Phillips, C.A. Richardson D. Heidelberg, J.: Sutton, G.G. Fleischmann, R.D. White, O.: Salzberg, S.L. Saxth, H.O. Venter, J.C. Fraser, C.M. Stibeng, B. Sutton, G.G. Fleischmann, R.D. White, O.: Fraser, C.M. Satisfies Evidence for lateral gene transfer between Archaea and Actions-references MUID: 99287316
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**molecule_type DNA
**residues 1-190 **label ARN
**residues 1-190 **Label ARN
**ross-references GB:AEC01749; GB:AEC00512; NID:g4981346; P.E.:q4981354;
**TIGR::M0823
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es GB:280225; GB:AL:23456; NID:93242265; PID:0-266521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Thermotoga maritima
11-Jun-1999 #seq.conce_revision 11-Jun-1999 #text_chanac
20-Aug-1999
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Pred. No. 1.52e+01;
2: Mismatches 1: Indels
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Best Local Similarity 66.7%;
Matches 6; Conservative
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17-Jul-1998
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                                                                               *authors
                         ACCESSIONS
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*product beta-lactamase II *status predicted *label BL2\
*active_Site Giu *status predicted\
*binding_site zinc, high affinity (His, His, Cys, His)
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##Cross-references GB.M15380; NID:q142601; PIDN:AAA22275.1; PID:q142602
##exporimental_source strain 170
reession #24393
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FEBS Lett. (1985) 189:207-211
The amino acid Sequence of thy zinc requiring beta-lactamase
If from the bacterium Facillus cereus 569.
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tecta-uscumase (FC 15.5.2) procisso - Pacillus dereus
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                                                                                                                    beta-lactamuse (EC 3.5.2.6) II precursor - Bacillus sp. penicillinase II
*formal_name Bacillus sp. 3: Oce-1988 *text_change 3: Oce-1988 *text_change 18-Jun-1999
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Hassald, M.: Carlino, A.: Madonna, M.J.: Lampen, J.O.
J. Bacteriol, (1985) 164:223-229
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                                                                                                                                                                                                                                     #authors Kato, C.; Kudo, T.; Watanabe, K.; Horikoshi, K.; #journal, J. Gen. Microbiol. (1985) 131:3317-3324
#title Nocleotide sequence of the beta-lactanase gene a lkalophilic Bacillus sp. strain 173;
#cross-references MUD:86:70399
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Murakami, Y.: Nat. | M.: Haqiwara, H.: Shihata, T.: Gawa. Murakami, Y.: Sanda, B.: Sadbuma, M.: Tsuchiya, Y.: Sanda, E.: Yokoyama, K.: Lamazaki, M.: Tashiro, H.: Eki, T.: Sabmitted to the PMS: (ata library, Nay 1995 Adalysis of the mellectide sequence of chromos me. V. Iram Saccatosiynes represent chromos me. V. Iram Saccatosiynes represent
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##cross-references EMBL:D44603; NID:9871957; PIDN:BAA080577.3
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Submitted to the EMBL Data Library, December 1994
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75.6%; Score 49;

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Potier, S.: Souciet, J.S.
Fjournal veast (1995) 11:667-672
Fille sequence of a 9.8 kb seqment of yeast chromosome II including fille three ganes of the MAL3 locus and three unidentified open reading frames.

Across::eferences MJD:9669:909
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hypothetical procein YBR212: hypothetical protein YM4987.03:
hypothetical protein YM132:
#tornal_name Saccharomyces cerevisiae
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probable membrane protein YKL219W homolog YBR302c - yeast
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submitted to the Protein Sequence Database, August 1994
846187
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#submission submitted to the Protein Sequence Database, August 1994
Paccession 546185
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###Csidues 1-47 ##!abel FEL
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ENTRY
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#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fletschmann, R.D.; Sutton, G.G.; Blake, J.A.; FlttGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.E.; Adman, M.D.; Retch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.E.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kehley, J.M.; Peterson, J.D.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Hurst, M.A.; Kanlee, B.P.; Borodovsky, M.; Klenk, H.D.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Conton Methanococcus sequence of the methanogenic archaeon, Methanococcus jannaschil.
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hypothetical protein MJ6831 - Methanococcus jannaschii
*formal_name Methanococcus jannaschii
13-Sep-1996 *sequence_revision 13-Sep-1996 *text_change
10-0ct-1997
                                                                                                                                        Sape
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*formal_name Succharonyces cerevisiae
27-Apr-1996 *seq: nce_revision 03-May-1996 *t+xt_change
24-Sep-1999
Obermaler, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, April 1996
863322
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                                                         Score 49: DB 2; Length: 3/9/:
Fled No. 1.52e-01;
Controles 0; Indexs
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxiord Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:05:39 2000; MasPar time 3.40 Seconds 80.554 Million cell updates/sec R ::: on:

Tabular cutput not generated.

PUS-09-142-524A-7 (1-9) from USC9142524A.pep 64 Title: Description: Perfect Score: Sequence:

: FIKRVSNVI 9

PAR 150 3ap 15 Scoring table:

83857 seqs, 30454973 residues Searched:

Fost-processing:

Minimum Match 0% Listing first 45 summaries

Statistics:

swiss-prot38 1:swissprot Urrabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 24.343; Variance 25.165; scale 1.967

SUMMARIES

Pred No.	6.81e-04	4.67e-02	1.366-00	. 32	2.32e+03	3.94e+00	3.94e-00	3.94e+00	3.94e+00	3.94e+00	3.94e-00	3.94e-00		6.52e+00	6.62e+00	1.10e+01	1.10e+01	1.10e-01	1.82e-01	.82	1.82e+01	1.82e+01	1.82e+01
Description	SUGI BASIC PROTEIN PRE	PECTAIE LYASE PRECURSO	HYPOTHETICAL 82.1 KD P	CYSTATIN PRECURSOR (OV	, TYI	BETA-LACTAMASE, TYPE I	BETA-LACTAMASE, TYPE I	.3 KD	7	HYPOTHETICAL 45.3 KD P	HYPOTHETICAL PROTEIN M	CYSTEINYL-IRNA SYNTHET	HYPOTHETICAL 68.8 KD P	4 - HYDROXYBENZOATE OCTA	DYNEIN HEAVY CHAIN, CY	PYRUVATE KINASE (EC 2.	LARVAL SERUM PROTEIN 1	HYPOTHETICAL 103.6 KD	ADENOSYLMETHIONINE-8-A	HYPOTHETICAL PROTEIN H	JDP-GLUCURONOSYLTRANSF	JDP-GLUCURONOSYLTRANSF	UDP-GIUCURONOSYLIRANSF
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QC432;
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bloinformatics Institute. There are no restrictions on its mess by anon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license isb-sib.ch).
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Ho M.C., Whitehead M.P., Cleveland T.E., Dear R.A.:

Ego W.C. analysis of the Aspergillus middians pectate lyase pela

gene and evidence for binding of promoter regions to GREA, a

regulator of carbon catabolite repression.;

curr, Genet. 27:42-149(1895).

-! CATALYIC 27:42-149(1895).

CIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-MANN-4-ENURONOSYL GROUPS

AT THIS NOW REDUCING ENDS.

THIS NOW REDUCING SECRETED (POTENTIAL).

-! SIMILARITY: BELONGS IC THE POLYSACCHARIDE LYASE FAMILY 1.
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Eukaryota, Findi: Ascomynota: Piectomyretes: Euroflaies:
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74AB25950248F56F CR754;
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B + -> 7 (IN CRY J 1-8
C -> 5 (IN CRY J 1-8
C -> 5 (IN CRY J 1-8
C -> 6 (IN CRY J 1-8
C -> 0 (IN CRY J 1-8
C -> 0 (IN CRY J 1-8
POTENTIAL.
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PRINTS: PRC0807: AMBALLERGEN.
Allergen; Glycoprotein: Multigene family; Signal.
SIGNAL 22 374 SUGI BASIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64: DB 1: D6
Pred: No. 6:81e-64;
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15-DEC-1998 (Rel. 37, Last Sequence update)
PECIATE LYASE PRECURSOR (ET 4.2.2.2)
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EMBL: D26545: BAA05543.1:
EMBL: D34639: BAA07020.1:
PIR: A44773: A44773.
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Best Local Similarity 100.0%:
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Trichocomaceae, Emericella.
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Q00645;
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This SMISS-PROT entry is crivight. It is produced through a collaboration between the SMISS institution of Bicinformatics and the EMBL offstation the European Bloinformatics. Stitute. There are no restrictions on its use by non-profit institutions as iong as its content is him to way modified and this statement is not removed. Usage by and ion connected entities requires a license agreement (See http://www.isbis.ch.cancounce.or send an email to license@isbis.b.ch.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Actinopteryaii;
Neopterygii: Teleostei: Euteleostei: Ostarlophysi: Cypriniformes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycetes: Saccharomyceta.es
Saccharomycetaceae: Saccharomyces.
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MEDLINE: 96208938.
TSai Y. -1., Chang G.-D., Huang C.-J., Chang Y.-S., Huang F.-L.;
*Purific Fion and molecular cining of carp ovarian cystatin.".
Comp. Biochem. Physiol. 113B:573-580(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
WPYOTHETICAL 82.1 KD PROTEIN IN SGSI-MRPU24 INTERGENIC REGION
WRI32W OR YM9646.04.
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STRAIN-S288C / AB972:
Peatson D. Bowman S. Barrell B.G., Rajandream M.A.:
Peatson C. Bowman S. Barrell B.G., Rajandream M.A.:
Submitted (JAN-1995) to the EMBL/GenBank/DGB databases.
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Lanity 55.8%: Pred. No. 1 More C.
Conservative 4: Rismatches C. Issels
                                                                                                                                                                                   Score 57, DB 1; Length 325;
Pred, No. 4.67e-02;
Transfehes 0; Indels
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77.38;
EMBL: U05592; AAA80568.1;
PFAM: PF00544; pec_lyase;
Lyase: Signal.
SIGNAL 15
CHAIN 16 326
                                                                                                                                                                                                                                                                        7; Conservative
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SEQUENCE 720 AA: 8
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FIKRVSNVI 9
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                                                                                                                                This SWISS-PRUT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or sond an email to license@isb-sib.ch).
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Lim H.M., Iyer R.K., Pene J.J.;

Lim H.M., Iyer R.K., Pene J.J.;

"Site-directed mutagenesss of dicarboxylic acids near the active site of Bacillus cereus 5/B/6 beta-lactamase II.";

of Bacillus cereus 5/B/6 beta-lactamase II.";

elsocken, J. 275:40:-404(1991).

-!- FUNCTION: CAN HYDROLYZE CARBAPENEM COMPOUNDS.

-!- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)C * A SUBSTITUTED BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUIANEWBASSS.
MEDINE: 89308559.
Lim H.M., Pene J.J.:
"Mutations affecting the catalytic activity of Bacillus cereus 5/B/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim H.M., Pene J.J., Shaw R.W., "The Bacillus cereus "Cloning, nucleotide sequence, and expression of the Bacillus cereus 5/2/6 beta-lactamase II structural gene."; "Sacteriol, 170:2873-2878(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
-!- FUNCTION: CYSTEINE PROTEINASE INHIBITOR.
-!- TISSUE SPECIFICITY: DETECTED IN OVARY BUT NOT IN ALL THE OTHER EXAMINED TISSUES.
-!- PIN: THIS PROTEIN IS FURTHER PROCESSED BY AN INTRAMOLECULAR CLEAVAGE TO PRODUCE TWO CHAINS LINKED BY A DISULFIDE BRIDGE.
-!- SIMILARITY: BELONGS IC THE TYPE 2 CYSTAIIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61-JAN-1990 (Rel. 13, Created)
61-JAN-1990 (Rel. 13, Last sequence update)
15-UUL-1999 (Rel. 39, Last annotation update)
BETA-LACTAMSE, TYPE II FRECURSOR (EL 3.5.2.6) (RENICILLINASE)
(CEPHALOSPORINASE).
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REACTIVE SITE (BY SIMILARITY).
SECONDARY AREA OF CONTACT.
BY SIMILARITY.
CLEAVAGE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 2.32e+00;
4; Mismatches 0;
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Bacillus/Staphylococcus aroup: Bacillus.
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Matches 5: Conservative
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MEDLINE; 88227879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 FVRKVSKVI 62
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P14498;
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MEDLINE: 86065446.
Ambler R.P., Daniel M., Fleming J., Hermoso J.M., Pang C., Waley S.G.,
The amino acid sequence of the zinc-requiring beta-lactamase ll from
the bacterium Bacilius cereus 569.";
FEBS Lett. 189:207-211(1985).
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MEDLINE; 86008C56.
Hussain M., Carlino A., Madonna M.J., Lampen J.C.;
"Cloning and sequencing of the retallathioprotein beta-lactamas" if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sapo
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20-WAR-1967 (Bel. 04, Last Shiphoner spoutd)
15-FEB-2000 (Bel. 39, Last aboutdite spoutd)
BETA-LACIAMASE, TYPE II (1977) F (E. 4, 7, 7, 4, 7) (FENCOLLINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·_;
-:- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
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D->N,E: INACTIVATES THE ENZYME.
G->E: INACTIVATES THE ENZYME.
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MEDLINE: 98133841.
Sutton B.J., Artymlsk P.J., Cordero-Borboa A.E., Little C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig. 50, DB 1; Length 256; 1ed, No. 2,32e+60; Msmatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA-LACTAWASE, TYPE 11.
21NC 1 (BY SIMILARITY).
21NC 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670F62378C355C2D CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria: Firmicutes: Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                      HSSP: PG4190; IBMC.
PROSITE; PS00743; BETA_LAC:AMASE_B_1: i.
PROSITE; PS00744; BETA_LACTAMASE_B_2: i.
PFAW: PFC0753; lactamase_B: i.
Hydrolase: Zinc: Antibiotic resistance. Signal.
SIGNAL
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PIR; A32017; A32017.
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Indels

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Mismatches

6; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                MEDZINE; 98400945.
Rablanc S.M., Sohi M.K., Wan I., Payne D.J., Bateson J.H.,
Mitchell I., Sutton B.J.;
"Crystal structure of the zinc-dependent beta-lactamase from Bacillus cereus at 1.9-A resolution: binuclear active site with features of a Biochemistry 37:12404-12411(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fablanc S.M., Schi M.K., Sutton B.C.; Submitted (SEP-1997) to the PDB data bank.
-!- FUNCTION: CAN HYDROLYZE CARBAPENEM COMPOUNDS.
-!- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O + A SUBSITIUTED BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips D.C., Waley S.G.:
"An X-ray-crystallographic study of beta-lactamase :I from Bacillus cereus at 0.35-nm resolution.";
                                                                                                                                  "The 3.D structure of a zinc metallo-beta-lactamase from Bacillis cereus reveals a new type of protein fold.";
EMBO J. 14:4914-4921(1995).
                                                                                                                                                                                                                     ories, A., Duce E., Gallen: M., Frere J.-M., Dideberg O.:
"1.85-A resolution structure of the zinc (II) beta-lactamase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc: Antibiotic resistance: Signal; 3D-structure.
                                                                               MEDLINE, 96067120.
Carri A., Pares S., Duec E., Galleni M., Duez C., Frere J.-M. Dideberg G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 257;
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ZINC 1, HIGH-AFFINITY.
ZINC 1, HIGH-AFFINITY.
ZINC 2, LOW-AFFINITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 1; L. Pred. No. 3.94e+00;
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PROSITE: PS00744: BETA_LACTAMASE_B_2: i.
PFAM: PF00753: lactamase_B: 1.
Hydrolase: Zing: Antibiotic resistance: 8
                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE: 98437525.
                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                                                                                                                                                                                         Bacilius cereus.":
Acta Crystallogr. D 54:313-323(1998).
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                                                 Bicchem. J. 248:181-188(1987).
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PIR: A01006: PNBSU2.
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PDB: 1BME: 07-JUL-97.
PDB: 1BVT: 24-SEP-98.
PDB: 1BC2: 14-OCT-98.
PDB: 28C2: 20-APR-99.
PDB: 38C2: 20-APR-99.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kato C., Kudo T., Matanabe K., Horikoshi K.:
*Nucleotide sequence of the beta-lactamuse gene of alkaluphility
Bacilius sp. strain 170. *;
J. Gen. Microbiol. 13.317 3324(1985)
-:- FUNCTION: CAN HYDROLYZE GARBABENEM COMPOUNDS.
-:- CATALYTIC ACTIVITY: A BETA-LACTAM - H(2)O - A SUBSTITUTED BETA-
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'atton update)
's (EC 8.5.2.6) (PENICILLINASE)
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Bacillus sp. (strain 170).
Bacteria: Firmicutes: Bacillo, Tostridium group:
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PROSITE: PS00743: BETA_LACIAWA'E_B_1: .
PROSITE: PS00744: BETA_LACIA: %E_B_2: .
Hydrolase: Zinc: Actibiotic Fissance: Sidna.
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01-NOV-1995 (Rel. 32, Last sequence update)
NOV-1997 (Rel. 35, Last annotation update)
HYPOTHEFICAL 45.3 KD PROTEIN IN THIS S'REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2: Mismatches
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Pred. No. 3.94
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 31-48 MEDLINE; 86170399.
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01-MAR-1989 (Rel. 10, Last se
15-JUL-1999 (Rel. 38, Last a
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Best Local Similarity
Matches 6: Conser
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105 FOKRVIDVI 113
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                               | FIKRVSNVI 9
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P43542;
                                                                                                                                                                 B1A2_BACSP
P10425;
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01-0GT-1994 (Rel. 30, List sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
14-YPOTHETICAL 45.2 KD PROTEIN IN MALJS 3'REGION AND IN COXI4 5'REGION.
(YBR302C OR YBR2121) AND (YML132W OR YM4987.03).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowman S., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V., Submitted (JUL-1995) to the EMBL/GenBank/DOBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS IC THE DUP FAMILY.
   Eukaryota; Fungi: Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                              STRAIN-S288C / AB972;
MEDLINE: 95400292
MEDLINE: 95400292
Mandakami Y., Najibou M., Haqixara H., Shibbata T., Ozawa M.,
Sasanima S.-Ii., Sasanima M., Tsuchiya Y., Soeda E., Yokoyama K.,
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycetes: Saccharomycetales:
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Fewermann M., Potier S., Souciet J.-L.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
Submitted (AUG-1994) to the EMBL/GenBank/DDB3 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
6822561BC9890275 CRC64:
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Pred. No. 3.94e+00:
4; Mismatches 0;
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TRANSMEM 43 63 POTENTIAL
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                                      Saccharomycetadeae: Saccharomyces
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233 253 PO
255 275 PO
379 AA: 45312 MW:
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STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: D50617: SAA09179.1; -. EMBL: D44603: SAA08057.1; -. PFAM: PF00674: DUP: 2.
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t Local Similarity 55.6%;
ches 5; Conservative
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                                                                                                         SECUENCE FROM N.A.
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P38363:
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SEQUENCE
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This SWISS FPOT energy is capprobled. It is produced through a constation between the Swiss lostifier of Energies and the EXECUTION the European Stockholms of Execution that was by non-profit institutions as long as its customers in no way modified and this statement is not removed. Usage by and for connection entities requires a license agreement (See http://www.isbrsib.ch/announce/or send an email to license@isb-sib.ch).
the European Bioinformatics istitute. There are no restrictors on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for connectial entitles requires a license afreement (See http://www.isbisit.ch/announce/or send an email to license: 5-515.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota: Saccharomycetes: Saccharomycetases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obermaler B., Piravandi E., Rinke M.;
Submitted (MAY-1996) to The EMPLGenBank/DDBJ databases.
-!- SUBCEELUBER LOCATION: INTEGRAL MEMBRANE PROTEIN (PCTENIIAL)
-!- SIMILARITY: BELCNGS TC THE DUP FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 76.6%: Score 49: UB 1: Legath, 379: Best Local Similarity 55.6%: Pred, No. 3.94e+UC; Matches 5: Conservative 4: Mismatches 0: Indels Matches
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Pred. No. 3.94e+00;
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                                                                                                                                                                                                                                                                                                                              2AAB51B60103AF61 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NO-1997 (Rel. 35, Last annotation update)
YML336W OR N0275.
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01-NOV-1997 (Rel. 35, Last st uence update)
                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL
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                                                                                                                                                                                                                                                      Transmembrane
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                                                                                                                                              EMBL: 236171: CAA65267.1: ..
EMBL: 250178 CAA60551.1: ..
PIR: S46187: S46187.
PFAM: PF00674: DUP: 2.
Hypothetical protein: Transmer TRANSMEM 255 275 E
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275
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275
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381 AA;
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Matches 5; Conserv
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| FIKRVSNVI 9
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| FIKRVSNVI 9
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MEDLINE: 98332770.
MEDLINE: 98332770.
Freer C.M., Norris S.J., Weinstock G.M., White D., Sutton G.G.,
Dodson R., Grinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaran M., Jiterback I.,
McDonald L., Artiach P., Borman C., Cotton M.D., Fujii C., Gariand S.,
Hazch E., Horst K., Roberts K., Sandusky M., Weldman J., Shith H.C.,
                                                                                                 DEQUENTE FROM N.H.

STRAIN JAL 1 / DSR 2661 / AICC 43067;

WEDLINE: 9637999.

WEDLINE: 9637999.

Built Ci., White D., Oisen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Flitzgerald L.M., Clayton K.A., Godayne J.D.,

Kerlavage A.P., Doughery B.A., Tomb J.-F. Adams M.D., Reich C.I.,

CVerbork R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodck A.,

Scott J.L., Jecuhagen N.S.M., Weidman J.F., Fuhrmann J.L., Mayen D.,

Ctterbock T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Ctterbock T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Kienk M.-P., Fraser C.M., Smith H.D., Wosse C.R., Venter J.C.;

"Complete victure sequence of the methanogenic archaeon, Methanocoocus

Science 273:1058+107(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of ireponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 281:375-388(1998).
-!- GAJALYIIC ACTIVITY: ATP + L-CYSTEINE + TRNA(CYS) + AMP PYROPHOSPHATE + L-CYSTEINYL-TRNA(CYS).
                                      Methanococcus jannaschii.
Archaea: Euryarchaecta: Methanococcales: Methanococcaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49: DB 1: Length 432;
Pred. No. 3.94e+C0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          48835 MW; OEB95018802B41E3 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum.
Bacteria: Spirochaetales: Spirochaetaceae: Treponema.
 C1-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN MJ0831.
                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO M. JANNASCHII MJ6977.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: 067526: AAB98830.1: -.
IIGR: MJ0831: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coery Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM: PF01368: DHH: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 432 AA: 4:
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                                                                                          SEQUENCE FROM N.A.
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                                                                   Methanococcus
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                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMEL of station the Buropean Boinformatics institute. There are no restrictions in its use by non-profit institutions as 10009 as its content is in twenty modified and this statement is not removed. Usage by and for numerical entities requires a license agreement (See http://www.isb.sil.ch/announce/or send an email to license isb.sil.ch).
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SUBCNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
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SKAIN-972;
Skeiten J., Chircher T. M., Labtell F. Furdomesm H.A., Wh.d.V.
Skeiten J., Chircher T. M., Labtell F. G., Furdomesm H.A., Wh.d.V.
Supmitted (ADG-1997) to the EMBL/Jonehus./FilM. databases
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66.7%; Pred. No. 3.94e-00;
vative 2: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49: DB 1: Length 520:
Pred: No. 3:94e+00;
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Eukaryota: Fungi: Asconycota: Schirosaccharomycetales
Schizosaccharomycetaceae. Schizosaccharomyces.
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Hypothetical protein.
DOMAIN 70 73
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nes 6; Conservative
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Best Local Similarity 44.4%:
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STRAIN-AX3:

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PFAM: PF01040; CUX10_cta9_cycE: 1.
Ubiquinone bicsynthesis: Transferase: Transmembrane; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARIIY).
--- PATHWAY: SECOND SIEP IN UBIQUINONE BIOSYNIHESIS.
--- SCHOELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (BY SIMILARIIY).
                                                                                                                                                                                              UBIA OR AARE.
Providencia stuartii.
Bacteria: Proteobacteria: qamma subdivision: Enterobacteriaceae;
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                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-) (4-HB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 1; Length 298; Pred. No. 6.62e+00;
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Paradise M.R., Gook G.M., Poole R.K., Rather P.N.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-F58-1994 (Rel. 28, Created)
01-F58-1994 (Rel. 28, Last sequence update)
15-F58-2000 (Rel. 39, Last annotation update)
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                          288 AA
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Eukaryota: Dictyosteliida: Dictyostelium.
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55.6%;
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                          STANDARD:
                                                                                                                                                                    POLYPRENYLIRANSFERASE).
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RESULT 14
1D UBIA_PROST
AC 052356:
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J. ELABORITHM.

1. ELABORITHM.

1. FUNCTION: DYNEIN HAS AFRASE ACTIVITY. CYTOPLASMIC CYNEIN ACTS AS MOTOR FOR THE INTRACELLULAR METRICHADE MYTLLITY DE VESTULES AND ROGARELLES ALONG MICROTOBULES.

1. SUBJUIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.

1. SUBGELLULAR LOCATIONS: CYTOPLASMIC.

1. SUBGELLULAR LOCATIONS: CYTOPLASMIC.

1. SIMILARITY: BELONGS TO THE LYNEIN HEAVY CHAIN FAMILY.
            MEDZINE; 93107159.

KRONCE M.P., Grissom P.M., McIntosh J.R.;
Dynein From Discussioning primary structure comparisons between cytoplasmic motor enzyme and flagellar dynein.";
J. Cell Biol. 119:1597-1664(1992).
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MITYGOURULE-BINDING (PCTENTAL)
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ATP (POTENTIAL)
WW: 9A0419915D579D3A CRC64:
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                                                                                                                                Koonde M.P., Grissom P.M., Lyon M., Pope T., McIntosh, "Molecular characterization of a hytoplasmic dynein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48: DB 1: I
Pred. No. 6.52e+00:
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                                                                                                                 MEDLINE, 95170719.
Koonce M.P., Grissom P.M., Lyon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein: Microtubules;
1 854 897
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Best Local Similarity 55.6%;
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PIR; A44357; A44357.
DICIYDB; DDC1045; DHCA.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyriai: (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:06:00 2000; MasPar time 8.22 Seconds 75.905 Million cell updates/sec Run on:

not denerated. Tubular output

>US-39-142-524A-7 (1-9) from US09142524A.pep 64 Title: Description: Perfect Score:

L FIKRVSNVI 9 Sequence: PAM 150 Gap 15 Sporing table:

225878 seqs, 69334122 residu s Sourched:

Minimum Match 0% Listing first 45 summaries st-processing:

sptremb112 Dutabase

isp_arches_2:sp_bacteria -:sp_frug; 4:sp_human 5:sp_invertubrate 6:sp_manual_7:sp_mtc 8:sp_organelle 9:sp_phag 10:sp_plant 11:sp_rodeut 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is detired by analysis of the total score distribution. Mean 23.348: Variance 25.366; scale 6.920 S. atistics

SUMMARIES

BETA-N-ACETYLGLCOSAMI 9.55e-02
HYPOTHETICAL 41.5 KD P 1.70e-01
ENDOGLOGANASE. 9.03e-01
HYPOTHETICAL 51.5 KD P 4.50e-00
HYPOTHETICAL 51.1 KD P 4.50e-00
HYPOTHETICAL 51.1 KD P 4.50e-00
TRANSCR.PTIONAL REGULA 7.58e-00
HOSB21.2 PROTEIN. 7.58e-00
PARA PROTEIN. 7.58e-00
PRENOMOR RECEPTOR. 7.58e-00
HYPOTHETICAL 68.6 KD P 1.27e-01
HYPOTHETICAL 68.6 KD P 1.27e-01
HYPOTHETICAL 51.5 KD P 2.10e-01
HYPOTHETICAL 51.5 KD P 2.10e-01
HYPOTHETICAL 51.5 KD P 2.10e-01 Pred. No Description 0.922 H39 0.992 Query Match Length DB 483 350 311 321 322 451 451 475 Score Result

SEQUENCE FROM N.A.

STRAIN-L171;

2.1.8+01 2.100+01 3.450+01	300	1,450-01	7,456-01	÷ .	3.45.6±01	ġ.		456	- 05 F. s	-	4.456.5	7	·	3.45e+01	4	8,45e+01	3.450+31	4 4 Sec. 02	3,450+01
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ALIGNMENTS

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Bacteria: Protecbacteria: gamma subdivision: Alteromonadaceue.
Pseudoaiteromonas.
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Best Local Similarity 77.8%: Pred. No. 9.65e-02;
Matches 7: Conservative :: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10 · eated)
01-MAY-1999 (TrEMBLrel. 10, last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HPPCTHETICAL 41.5 KD PROTEIN.
Leptospika borgpetersenii.
Bacteria: Spirochaetales: Leptospiraceae: Leptospira.
LT 1

O92H39

O92H39

O1-MAY-1999 (IrEMBLIE) 10, Created)

O1-MAY-1999 (IrEMBLIE) 10, Last sequence update)

O1-NOV-1999 (IrEMBLIE) 10, Last sequence update)

BITA-N-ACETYLGLUCOSAMINIDASE.

CHIO.
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EMBL, AF072214, AAC80237.1; -.
EMBL, SECOST, 108C.
SECOSTCE 783 AA. 88856 MW. FF87EDF8 CR032.
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092GL9;
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KALAMBAHETI T., BULACH D.M., RACAKUMAR K., ADLER B.:
"Genetic Organization of the Lipopolysaccharide O-antigen Biosynthetic
Locus of Loptospira borgpetersenii Serovar Hardjobovis.";
Submitted (UIL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF078-355, ADD12950.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENTE FROM N.A.
MEDININE, 99287316.
MEDININE, 99287316.
MART D.B., GLATION R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HATT D.B., HICKEY E.K., PETERSON J.D., NEJSON W.C., KETCHUM K.A.,
MODONALD L., OTTERBACK T.R., MALEK J.A., LIMBER K.D., GARRETH M.N.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERS S.L.,
SWITH BLO, VENTER J.C., FRASER C.M.,
"Exidence for lateral grow transfer between Archaea and bacteria from
qenome sequence of Thermotoga maritima.";
                                                                                                                                                                                      Caps
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MEDLINE: 9307214.
MEDLINE: 9307214.
MEDLINE: 930721 A.,
ONDERDOK LE. CONNE M.J., TZIANABOS A.C., PANTOSTI A.,
ONDERDOK A.B., KASPER D.L.;
"Analysis of a capsular polysaccharide biosynthesis locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53: 08-2: Locato 511;
Prod. No. 9:03e-01;
2: Miscatches 1: Indels
                                                                                                                                               Cuery Match 87.5%: Score 56: DB 2: Leagth 360: Best Local Similarity 77.8%: Pred. No. 1.70e-01: Autobes 7: Conservative 1: Mismatches 1: Indels Matches
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                                                                                                                                                                                                                                                                                                                                                          Cl-N/V-1999 (TrEMBLrel, 12, Created)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-NOV-1999 (TrEMBLrel, 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Cytophagales, Bacteroidaceae, Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteroides fragaliss":
Intert Immon, 67:3525-3512(1999).
Intert AFO461749: ADA90712.1; -
SEQUENCE 511 An. 58642 MW. D419628B CR312:
                                                                                                i protein.
360 AA: 41546 MW: 822Clee3 CRC32:
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Bacteria, Thermotogales: Thermotoga
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Pest Local Symilarity 66,7%:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                            PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteroides tracilis.
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TM1751.
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Q9XDK3:
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Actinomycetales, Corynebacterineae, Mycobacteridoeae, Mycobacterium
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HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KEICHUM K.A., MODOMALD L., UTFERBACK T.R., MALEK D.A., LINHER K.D., GARKELL M. STEMART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., BICHARPES N.D. BEIDELBERG J., SUTTON G.G., E.ESCHWANN R.D., WHITE G., SALIZHENG SMITH H.G., VENTER J.C., FRANCE, C.M., C.M., SALIZHENG SMITH H.G., VENTER J.C., FRANCE, C.M., SALIZHENG SMITH H.G., VENTER J.C., FRANCE, C.M., SERBL, A.M., SEBLL B.B., SALIZHENG SMITH A.G., VENTER J.C., RADISBELL B.C., SALIZHENG G.M., SERBL, A.M., SEFALICE G.M., SALIZHENG ST.A., ST.863 MK., SEFALICE GROZZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN*H37RV;
BEDILORD 96181548;
MELLIPE WOOL, POLEST S. FIRMOTER K. PASTUPELLA L.:
BALANUSRAMANIAN V., HOWER B. PERMERS Y KL. M. B.K. JATAR W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 473:
                                                                                                                                          Query Match 78.1%; Score 50, 19.2; Lonath 317. Best Local Similarity 56.7%; Pred. No. 4 50er00; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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01-JAN-1998 (TEMBLEC1. 05, Created)
01-JAN-1998 (TEMBLEC1. 05, Last sequence update)
01-JAN-1998 (TEMBLEC1. 05, Last annotation update)
HYPOTHETICAL 51.1 KD PROTEIN CY441.19.
MYCOSACTERIUM tuberculosis.
Bacteria, Firmicutes; Actinobacteria, Actinobacteridae:
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Submitted (MAY-1997) to the EMBL/34mBunk/2005J databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BARRELL B.G., RAJANDREAM M.A., FARKHILL J.,
Submitted (MAY-1997) to the EMBL/Combank/JJDAJ databusers
                                                                                                                                                                                                                                                                                                      C26614 PRELIMINARY; PRT: 473 AA.
006614; 006614; 007120L-1997 (TEMBLED). 04. Usasted)
01-JUL-1997 (TEMBLED). 04. Usast sequence update)
01-JUNOV-1996 (TEMBLED). 08. Last senioration ipdate)
HYPOTHERICAL 50.5 KD PROTEIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 93:3122-31;7(1996)
EMBL: 295886: CABO9051.1: -.
PLOCINCIDED PROTEIN: 50474 MM: 1081A279 CR032;
SECURING 473 AA: 50474 MM: 1081A279 CR032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50: 08 2: L4
Pred. No. 4.50e-00:
2: Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEÇUENCE FROM N.A.
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BARRELL B.G.,
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MURPHY L., HA
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda:
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081969
061969:
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NELSON K.E., CLAYTON R.A., GILL S.R., GWINN W.L., DODSON R.J.,
NELSON K.E., CLAYTON R.A., GILL S.R., GWINN W.C., KETCHUM K.A.,
MCDONALD L., GITERBACK T.R., MALEK J.A., LINHER K.D., GARREIT M.M.,
STEWARI A.M., COTTON M.D., PRAIT W.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.,
"Evidence for lateral gene transfer between Archaea and bacteria from
genore sequence of Themploaa maritima.")
Nature 399:324-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUNDE FROM N.A. STELL S.R. GWINN M.L., DUDGSON R.J., BEGGON K.J., PURCON W.C., DUDGSON R.J., HAFT D.H., GLKEY E.K., PUTERSON J.D., NELSON W.C., KETCHIJK K.A., MODONID, L., UITHERACK E.K., DARREIT M.H. GLENONID, L., UITHERACK E.K., DANTE D.H. STERMART A.M. CITHON M.G. FLEISCHMANN R.D. WHITE O., SALZRERG S.L. STITON G.G., FLEISCHMANN R.D. WHITE O., SALZRERG S.L. SALDHIJH H.C., VENIER J.C., FRASER C.M., SALDHIJH H.C., VENIER J.C., SALDHIJH H.C., SAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Actinomycetales: Corynebacterineae: Mycos acteriaceae: Mycobacterium
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                                                                                         SKECTON J., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.)
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: STRONG, TO M. TUBERCULOSIS MTCY336.28.
EMBL: $280225; CAB02329.1; -.
HYDOLDELICAL Protein.
SEQUENCE 479 AA: 51099 MW: 6DA262E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2; Length 190;
Pred, No. 7.58e+00;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                        Length 479;
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01-NCV-1996 (TREMBLrel. 01, Last sequence update)
01-NCV-1999 (TREMBLrel. 12, Last annotation update)
CYTCCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9WZTC PRELIMINARY: PRI: 190 AA. 09WZTG: 09WZTG: 180 AA. 09WZTG: 01WOV-1999 (TEMBLEEL 12, Last sequence update) 01-NOV-1999 (TEMBLEEL 12, Last sequence update) 17ANSCRIPTIONAL REGULATOR, TETR FAMILY.
                                                                                                                                                                                                                                              Score 50: DB 2; Li
Pred. No. 4. 9e+C0:
2; Mismatc: s 1
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Local Similarity 66.7%:
es 6: Conservative
                                                                                                                                                                                                                                                   query Match
Best Local Similarity 55.7%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                               154 FVKRVSNPV 162
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                                                SEQUENCE FROM N.A.
STRAIN-H37RV:
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Q37300
Q37300:
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FERRICAL CATALYTIC ALLIVAL...

FERRICAL COPER A AND HEME SHOUP.

C. 1. COFACTOR: COPER A AND HEME SHOUP.

C. 1. STALLENIN. (MITSCH. NUFIAL).

C. 1. STALLENIN. CONTRET.

DR REAL: X9554. CAA64821.

DR PRAM: PROSITE: PSG0078: COX2; 1.

PROSITE: PSG0078: COX2; 1.

FT METAL 163 163 167 COPER A (PROBABLE).

FT METAL 167 COPER A (PROBABLE).

FT METAL 200 200 COPPER A (PROBABLE).

FT METAL 200 200 COPPER A (PROBABLE).

FT METAL 201 204 COPPER A (PROBABLE).

FT METAL 202 205 COPPER A (PROBABLE).

FT METAL 204 204 COPPER A (PROBABLE).

FT METAL 204 204 COPPER A (PROBABLE).

FT METAL 207 205 COPPER A (PROBABLE).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE PROBLE N. 2:

MELSON R. AINSCOUGH R., ANDERSON K. BAYNES C., BERKS M., COULS:N A., BONFIELD J., BORTON J., CONNELL M., COPERT J., COOPER J., COULS:N A., CRAXTON M., DEAR S., DU Z., TREIN R., FAVELLO A., FULTON L., AGANDNER A., GREEN P., HAMMIN T., HILLIER L., JIER M., JOHNSIN L., LICHTON J., LAGHTING J., LLOPD C., MCWJRRAF A., MORTHMORE B., O'CALLAGHAN M., ARRIGON J., PERCY C., RIFKEN L., ROOPER A., SULNDER B., SHOWNKEEN R., SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THOMAS K., VAUDIN M., WOGHAN N., WALLSON P., MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., RATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., WILLISTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., T., WILLISTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., T., WILLISTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., T., WILLISTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., T., T., WILLISTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., T., T., WILLISTON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., T., T., T., T., WILLISTON A., WEINSTON A., WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Rhabditida.
Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhakditis
                                                                                                                                                                                                      STRAIN-ESC;

BEDLINE, 96244738.

SZYMCKA J. M., LUNT D.H., HEWITI G.M.:

"The sequence and structure of the meadow grasshopper (Clorthiggus arrallelus) mitochondrial srRNA. NO2. COI. COII ATPASSE and 9 tenna genes. "Insect Mol. Biol. 5:127-135(1996).
Pterygota: Neoptera: Orthopteroidea: Orthoptera: Caelifera:
Acridomorpha: Acridoidea: Acrididae: Gomphocerinae: Charthippus
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Fed. No. 7 58e-00;
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C1-A0G-1998 (TEMBLE), C2, Last sequence space)
C1-NOV-1999 (TEMBLE), Last accidation opdate;
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Best Local Similarity
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DOETSCH N.A., THOMPSON M.D., HALLICK R.B.:
"A mailtrase-encodating group III twintron is conserved in deeply rooted
"Barilization of the edge";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
"EMAL: 799834: CAR16950.1:
"EMAL: 799834: CAR16950.1:
"EMAL: 799834: CAR16950.1:
"EMAL: 799834: CAR16950.1:
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Plasmid Incli Collb-P9.
Bacteria: Promeobacteria: gamma subdivision: Enterobacteriaceae:
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SAMPEL G., MIZOBUCHI K.,
SAMPEL G., MIZOBUCHI K.,
"Organization and diversification of plasmid genomes: complete
nuclotule sequence of the Coilb-P9 genome.";
Submitted (DEC.1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB021078: RAA75111.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lepocinclis buetschlit.
Eukaryota: Euglenozoa: Euglenida; Euglenales; Lepocinclis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.6%: Score 49: DB 2: Lenath 326: Sest Local Similarity 66.7%; Pred: No. 7.586-00: Matches 6: Conservative 3: Mismatches U: Indels
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Rest Local Similality 77.8%: Pred. No. 7.58e+00:
Matches 7: Tonsorvative 1: Mismatches 1: Indels
                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2:
WATERSTON R.;
Submitted (MAY-1598) to the EMBL/GenBank/DDBJ databases.
EMBL: AF066347: AAC.7764.1: -.
PFAM: PF01604: 7tm_5: 1.
SEQUENCE 325 AA: 37398 MW; AAF37C26 CRC32:
MILLER N.:
Submitted (JUN-1998) to the EMBL/SenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
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Last annotation update)
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01-MAY-1999 (TrEMBLIEL 10,
01-MAY-1999 (TREMBLIEL 10,
PARA PROTEIN,
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C9260
O92690:
01-NVV-1998 (TrEMBLrel: 08
01-NVV-1998 (TrEMBLrel: 08
MAII:
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0924E5
0924E5:
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                                                                                                                                                                          Fugu rubripes (Japanese putferfish) (Takifuja rubripes).
Bukaryotai Metaboai Chordatai Graniatai Vertebiatai Actinojtorjain.
Nepteryoji, Taleosteii Euteleisteli Aconthopleryoji: Perometifua
Tetraodoniformes, Tetraodonifoldai: Tetraodonifoae: Figu
                                                                                                                                                                                                                                                                        . YAMAMOTO .. NUZAKI Y., TOMURA K., HAZAMA
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Actinomycetales: Corynebacterineae; Nocardiaceae: Rhodonocous
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 868:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49: UB 13: Length 868
Pred, No. 7.58e-00:
2: Mismatches U: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.0%; Score 48; DB 2; Length 251; Best Local Similarity 55.6%; Pred. No. 1.27e+01; Matches 5: Conservative 3; Mismatches 1; Indels
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Last annotation quante)
                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                              Rhodococcus strain 124.";
Appl. Microbiol. Biotechnol. 0:0-C(1999).
EMBL: AF121905; AAD2539B.1; -22E5ACD5 CRC32;
SEQUENCE. 251 AA; 27374 MM; 22E5ACD5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                             868 AA; 95531 MW; DA037862 CRC32
                                                                              858 AA
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01-NOV-1999 (THEMSCREEL LL.
01-NOV-1999 (THEMSCREEL LZ.
NIDD ALDCLASE.
                                                                                                        01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-NOV-1999 (TrEMBLrel. 12, PHEROMONE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                       75.6%:
75.0%:
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE 98226788.
NAITO I., SAITO Y., YAMAMO
NAKANISHI S., BRENNER S.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00248; GPCRMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY:
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Best Local S milarity
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325 FLRRVKNII 333
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1 FIKRVSNVI 9
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               1 FIKRVSNVI
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SEQUENCE
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09X596
09X596:
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073636;
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STEINER P. FUSSINGGER M., BAILEY J.E., SAUER U.:
"Cloning and expression of the Zymomonas mobilis pyruvate kinase gene
"In Escherichia Colis.";
Submitted (JIL-1998) to the EMBL/GenBank/DDBJ databases.
"I-CARALYTIC ACTIVITY: ATP + PYRUVATE - ADP + PHOSPHOENOLPYRUVATE.
EMBL, PRO79586; AAC20164.1: -.
PRIN: PRO79586; ARC20164.1: -.
PRIN: PRO79586; ARC20164.1: -.
PRIN: PRO79586; ARC20164.1: -.
PRIN: PRO79586; ARC20164.1: -.
PRIN: SP079586; ARC20164.1: -.
PRIN: ACC20164.1: -.
BPURVATE: TIANSFERSE.
SEQUENCE 475 AR. 51445 AR.; 28F3CA3B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of mountain cedar (Juniperus ashei) pollen major allergen, Jun all."
Submitted (NOV-1969) to the EMBL/GenBank/DDBJ databases.
EMBL: AFI05662: AAD03609.1: .
EMBL: AFI05662: AAD03608.1: .
EMBL: AFI05662: AAD03608.1: .
EMBL: AFI05662: AAD03608.1: .
EMBL: AFI05662: AAD03608.35644.
ENDIEL: 3544: Junas: 1086: 35644.
ENDIEL: 35545: Junas: 1086: 35644.
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                                            01-MAY-1999 (TEMBLEEL 1C, Created)
01-MAY-1999 (TEMBLEEL 1C, Last sequence update)
01-MAY-1999 (TEMBLEEL 12, Last annotation update)
01-NOV-1999 (TEMBLEEL 12, Last annotation update)
POLLEN MAJOR ALLERGEN 1-2.
Eukaryotus ashei (Dzark White cedar).
Eukaryotus Viridiplantse: Streptophyta: Embryophyta: Tracheophyta: euphyllophytus: Spermatophytus: Coniferopsida: Coniferales:
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10 086020
A 086020
A 086020
D 0.009-1998 (TERMBLrel. 08, Careated)
D 0.1-NOV-1998 (TERMBLrel. 08, Last Sequence update)
D 0.1-NOV-1998 (TERMBLrel. 12, Last annoctation update)
D 10-NOV-1998 (TERMBLrel. 12, Last annoctation update)
D 10-NOV-1998 (TERMBLrel. 13, Lest annoctation update)
D 10-NOV-1998 (TERMBLrel. 12, Lest annoctation update)
D 10-NOV-1998 (TERMBLrel. 12, Lest annoctation update)
D 10-NOV-1998 (TERMBLrel. 12, Last annoctation up
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Bacteria: Protrotanteria: alpha subdivision: Zymominas group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 75.0%; Score 48; DB 10; Length 367; Local Similarity 55.6%; Pred. No. 1.27e+01; es 5; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MIDGRO-HORIU:: T.M., GCLDRLUM R.M., KUROSKY A., WOOD T.G.,
BROOKS E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48: DB 2: Length 475: Pred. No. 1.27e+01; 2: Mismatches 2: Indels
                             367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Mon Jun 19 16:06:09 2000 Job time : 9 secs.
                             PRT;
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Rest Local Similarity 55.6%;
Matches 5; Conservative
                             PRELIMINARY
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RESULT 14
10 Q92NU7
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edicburgh, U.K. Distribution rights by Oxford Molecular Ltd

profein - protein database search, using Smith-Materman algorithm Mon Jun 19 16:08:27 2000: MasPar time 3.97 Seconds 101.521 Million cell updates/sec Tabular output not generated. MPsrch_pp R .:: On:

>US-09-142-524A-8 (1-17) from USU9142524A.pep 11.4 1 EEYLILSARDVLAVVSK 17 Description: Perfect Score: Sequence:

PAM 150 Gap 15 soring table:

Minimum Match 0% Listing first 45 summaries Pust-processing:

188963 segs, 23686106 residues

Starched:

Variance 70.029: scale 0.285 Mean 20,062: a-deneseq35 l:geneseqp Statistics:

Pred. No. is the number of results predimed by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sesult		Suery					
NO.	Score	Xa: Cr	Length	ä	ñ	Description	Prod. No.
		1.		: .			
-	7	20.00	74	-1	K5/380	M. eprae Stobs.lke p	∠.83e-04
2	103	9C.4	102	٠.	Ç,	structural prot	4.15e-03
m	r. 0,	6.69	66	~	RC5700	7 protein.	1.20e+00
-5	10	÷#.	\$6	-	m	GroES-like protein.	9.21e+00
'n	6.5	57.0	94	~	33	C. perfincens GroES-li	2.77e-0.
ഹ	A:	۲.	ري		R67390	E. coli GroES-like pro	2.776-01
7	6.5	۲.	136	. •	28	ri GHPC 1543	7
æ	61	,	118	٠,	R67373	k protein H	6.57e+01
σ	61	ď	118	~	m	r pylori	
7.0	61	۳.	118	٠.	W06731	H. pylori heat shock p	•
11	99	52.6	1006		W72256	eptor type t	8.13e+C1
12	9	į,	1006	٦	W70525	recepto	.13
13	9C	ď.	1521	۲,	W70526		8.13e+01
14	62	Ξ.	74	۲,	W74801	Human secreted protein	i.01e-02
15	58	Ö	102	~	R13334	HypA protein.	1.24e+02
16	58		753	~	W93495	N. menicaltidis strain	1.24e+02
1.7	57	0	861	1	W69977	Staphylococcus aureus	1.53e+02
æ,	1.0	Ö	1096	-	W01596	Inositol-1.4,5-triphos	1.53e+02
19	63	c.	1612	. 4	90	zekii	1.53e+02
20	0 0 0 0		609	-	W55485	S	1.89e+02
21	35		101	~	29	nia intracellul	2.32e+02
22	55	*	315	7	68	G-protein coupled huma	7
23	S	48.2	312	- 4	R48713		ď

	4,29e+02 4,29e+02 4,29e+02
related in transport of the control	Lung cancer associated Renal cancer associate IBDV GLS structural pr
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ALIGNMENTS

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RESULT 1

ROTATE AND SESTIONAL STATEMENTS AND RESULT 1

ROTATE AND SESTIONAL SET OF SE
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R22364 standard; Protein: 102 AA. R2364: 29-JUL-1992 (first entry) GroES structura; protein: Heat shock protein; groEs gene. Streptomyces albus. W9920482-A. 19-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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AC R29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-1988: 205444.
18-AUG-1988: 205444.
18-AUG-1988: 19-265444.
AJIN) Ajinomoro KK.
MPI: 90-103125/14.
No bacteria-derived MPH-57 protein -
used esp. in diagnosis of tuberculosis.
Claim 7: Fig. 2: 10pp. agamese.
Large quantities of MF-57 protein can be derived from a cultured transformant and used in diagnosis of tuberculosis by ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orease: immunogen: vaccino: diagnostic: heat shock protein: HSP:
GroES:like prototo: Helicobacter felis.
Thermopoliic bacterium.
WC9426901-A.
                                                                     (INSP.) INST PASTEUR.

Mazodier P. Guglielmi G:
Mazodier Pasteur Control inducible promoter and heterologous
gene - also vertors. transformed cells and new heat shock
proteins of Streptococcus albus
Disclosure: Fig 5: 50pp. French
The sequence is that of the Groes protein which is encoded by the
structural gene groes. See also 92477-922486.
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19-MAY-1994.

19-MAY-1993. ED-101369.

19-MAY-1993. WO-E013259.

(INR) INST NAT SANTE & RECH MEDICALE.

(INR) INST PARTEUR.

POLITOR: Jabigne A. Scerbaum S. Thiberge J.:

NOTE: S. Jabigne J. Japigne J. J
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Pred. No. 1.20e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-1990 (ILLEE entry)
MPB-57 protein.
BCG; Luberculosis: MPB-57; ELISA:
MCDacteriur bowis BCG.
22-FEB-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R05700 standard) protein: 99
R05700:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Rest Local Similarity 75.5%;
Matches 13: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 EEYLVLSARDVLAIIEK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲.
        03-SEP-1991; F00701.
10-SEP-1990: FR-011186.
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Rest Local Similarity (
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Disclosure: Fig. 78(i-ii); 168pp; English.

The sequence of the Heilcobacter pylori heat shock protein H (given in R6733) was compared to that of other GroES-like proteins from Legionella pneumophila (R67387), Escherichia coli (R67386), Clostridium perfringens (R67389), Mycobacterium leptangensian thempophilic bacterium (R67388), and regions of homology were identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leftar
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22-UN-1995 (first entry)
E coll Gross-like protein.
Urease immunogen: vaccine; diagnostic; heat shock profein; HSP:
Gross-like protein; Helicobacter fells.
Escherichia coll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA from Relicobacter pylori and Helicobacter feits rused to develop prods. for detection, treatment and prevention of Helicobacter infection
Disclosure: Fig. 78(1-14): 18H;. English.
The sequence of the Helicobacte, pylori heat snock protein he gaiven. (186733) was compared to that of others cribes inke proteins from Legionella pneurophila (1867387), Escherichia of 1867380). Clostridium perfringuas (1867389). Mycobacterium lupiar (1867386) and thermophilic bacterium (1867389), and regions sequence 94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1995 (first entry)
C. perfingens GroES-like protein.
Grees immunogen; vaccine; diagnostic; heat shock protein: HSi
GroES-like protein: Helicobacter fells.
Clostridium perfringens.
                                                                                                                                                                                                                                                                Score 70: DB 1: Length 94: Pred. No. 9.21e-00: 3: Mismatches 3: Indels
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(INSP.) INST PASTEUR.
FETTETO R. Labigne A. Sterbaum S. Thiberge J:
WPI: 95-036797/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrero R. Labigne A. Suerbaum S. Thibetge J. WPI: 95-006797/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1993, EP-401329.
19-NOV-1993, WO-E03259.
(INSW ) INST WAT SANTE 6 RECH MEDICALE.
(INSP ) INST PASTEUR.
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867389 standard; Protein: 94 AA.
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                                                                                                                                                                                                                                                             Match 61.4%;
Local Similarity 57.1%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 REYTLIRODDILATV 93
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19-MAY-1994; EC1625,
19-MAY-1993; EP-401309,
19-NOV-1993; WO-EO3259,
                                                                                                                                                                                                                                                                                                                                                                             80 EYMILRESDILAVI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EYLILSARDVLAVV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-NOV-1994.
19-MAY-1994; E01625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09426901-A
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R67389:
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N-PSDB: 090181
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                                                                                                                                                                                                                            Sednence
                                                                                                                                                                                                                                                                          Matches
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   ű.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Now isolated Helicobacter polynacleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and pastrointestinal diseases.

Claim 8: Page 349-349-2054pp. English.

This sequence represents a Helicobacter pylori GHPD protein of the movention. The polypeptides can be used for preventing or treating Helicobacter infections, and usertangular diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases. e.g. dastric and duodenal licers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                               31.MAR.1999 (first entry)
H. Cylori GHPO 1543 protein.
GENO protein: Helicobacter infection: gastroducdenal disease; gastritis; peptic ulcer disease.
Helicobacter pyicri.
ROBG4378-Al.
01-APR-1998: U06371.
29-JUT-1997: US-833457.
24-JUN-1997: US-881227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saps
                                                                                                                                                                            Gaps
DNA from Helicobacter pylori and Helicobacter fells - used to develop prods, for detection, treatment and prevention of Helicobacter infection.

Disclosure, Fig. 74(-ii.) 168pp; English.

The sequence of the Helicobacter pylori heat snock protein B (qiven in R67387) was compared to that of other Griss-like proteins from Legionella pneumophila (R67387), Escretchia coli (R67387), clostridium perfringens (R67389), Mycobacterium leprae (R67385) and thermophilic bacterium (R67388), and regions of homology were identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42-JUN-1995 (first entry)
Heat shock protein HSPB.
Urease: ureA gene: ureB gene: immunogen; vaccine: diagnostic:
Helicobacter pylori: heat shock protein: HSP: chaperonin:
pILL205.
Helicobacter felis ATCC 49179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65: DB 1; Length 136; Pred. No. 2.77e+01; 5; Mismatches 3: Indels
                                                                                                                                                                           3; Indels
                                                                                                                                                   Lenath 97
                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA.) HUMAN GENOME SCI INC.
(INMR.) MERIEUX CRAVAX FASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;
                                                                                                                                                   Score 65: DB 1: Lo
Pred. No. 2.77e+01;
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                          W98289 standard; Protein: 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                                                                   Query Match
Rest Local Similarity 60.0%:
Matches 9: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EFYLILSARDVLAVVS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 EDYLMLMSREVSAFVG 23
                                                                                                                                                                                                    81 EEVLIMSESDILAIV 95
                                                                                                                                                                                                                           1 EEYLILSARDVIAVV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 98-542293/45
N-PSDB; X14008.
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                                                                                                                                                                                                                                                                                                                  Disclosure, Fig. 6: 168pp. English.

Vaccine compositions include the A and B subunits (given in Rt7-1;)

Of H. Felis urease encoded by the ureA/ureB gene (U75319) region

of the uruse gene cluster of pillics (CNCM i-1355), as well as the

mast shock proteins HSPA (R6534), and HSPB (R67313) encoded by the

urease-associated HSP gene cluster rejonn (Q7531) of pillics9 (CNCM

i-1356). Recombinant products are expressed in Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic composition against Heirottarter interlib. Biso quee fragment(s) and protein(s) from Heirottarter interlib. Biso cluster and heat shock proteins(s). From Heirottarter and heat shock proteins. Biso component of a novel immunogenic composition capable of inducing protective antibodies against Helicobacter Infection. The composition may include the HspB protein (R74339), a urease UreA or UreB protein (R74336, R74337) or the Urei protein (R7436). The composition is used to prepare a vaccine for humans or animals, especially against H. Felis. Antibodies against the proteins may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating Helicobacter infection, and primers/probes to the DNA sequence may be used for detec ion of Helicobacter infection. Sequence 118 AA:
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                                                                                                                                  Ferrero R. Labigne A. Suerbaum S. Thiberge J.;
WPI: 95-006797/01.
N-PSDB: 075321.
DNA from Helicobacter pylori and Helicobacter felis - usuadevelop prods. for detection, treatment and prevention of Helicobacter infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HspA.
: GreA: UreB: Urel;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61: DB 1: Length 118. Pred. No. 6.57e+01; 6: Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rred vaccine component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori heat shock protein H
Heat shock protein: HspA: HspB: urease:
Vaccine; Helicobacter infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1995. EC3259.
19-NOV-1993. EC3259.
19-NOV-1993. WO-E03259.
(INRM ) INST NAT SANTE & RECH MELLICALE.
(INSP ) INST PASTEUR.
FEITEUR R. Labigne A. Suellerim S. WPI: 95-20383/26.
19-MAY-1994; EC1625.
19-MAY-1993; EP-401309.
19-MOV-1993; WO-E03259.
(INEW ) INST NAT SANIE 6 RECH MEDICALE.
(INSP ) INST PASTECR.
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R74338 standard; Protein; 118 AA
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/note= "p:
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Similarity 40.0%;
6; Conservative
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Best Local Similarity 40.0%;
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Best Local Similarity
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1006 AA;

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- for PGX probes in Studying HEP receptors

This sequence represents a novel human Eph family-like receptor type tyrosine kinase-like protein. The encoding DNA may be used as PGX probes in studying HEP receptors. The proteins show dominant negative (vaxiant being dominant) or signal modification and/or amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines to protect humans or other animals (esp. dats and dogs) against Helloobacter infection, or for treatment of such infections. The Coterminal tragment (see also W06728) of HspA is a preferred
                                                                                                                                                                                                                                                                                                                                              Helicobacter for treatment and prevention of esp. H pylori infection, also new antibodies specific for these antigens. Example 3. Page 110, 184pp. English of the specific for these antigens. Heat shock proteins HapA (W06731) and HapB (W06732) are products of a Helicobacter pylori gene cluster (see also t45681) in plasmid pille89 (CMCM 1-1356). Recombinant HapA and HapB can be produced in transformed host cells for use (esp. HapA) with Helicobacter urease subscribe (see also W06739-30) in novel immunogenic compans. These compans, can provoke a mucosal response and are useful as
                                                                          vaccine: immunoqen: antiqen; antibody; chronic qustritis; ulcer;
                                   07 MAR-1997 (Lirst entry)
H. pylori heat shock protein HspA.
Heat shock protein: HspA: HspB: chaperonin: urease: UreA: UreB:
                                                                                                                               92. 118
/note= "this region of HspA resembles a metal binding domain and is a preferred fragment for use in compses. of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1998 (tirst entry)
Human receptor type tyrosine kinase-like protein.
Tyrosine kinase: receptor: Eph ramily: human: HEP receptor:
modification; amplification.
Homo sapiens.
W09746586-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61: 58 1: Length 118;
Pred. No. 6.57e-01;
6: Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                  contq. UreB and HspA antidens of
                                                                                                                                                                                                                                                                                   ro RL, Labiqne A, Suerbann S, Thiberge J;
94-505400/50.
                                                                                                                                                                                                                                                               (INRM.) INST NAT SANTE & RECH MEDICALE. (INSP.) INST PASTEOR.
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT ::
W72256 standard: Protein. 1,06 AA.
W72256;
T 10
W06731 standard: Protein: 118 AA
                                                                                          pILL689.
Helicobacter pylori strain 85P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-1997.
04-JUN-1997. J01887.
04-JUN-1996: JP-141849.
04-JUN-1996: JP-141849.
MATS:1 7.
WPI: 98-04212:/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caery Match
Best Local Similarity 40.0%;
Matches 6: Conservative
                                                                                                                                                                                    (Claim 3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             component of such compsns
Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                     New immunogenic compsn.
Helicobacter - for trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z EYLILSARUVLAVVS 16
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02-MAY-1996, E01834,
19-MAY-1995, US-447177,
19-MAY-1995, US-432697,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB: V62177
                                                                                                                                                                                                                                                                                                                     N-PSDB; 145681
                                                                                                                                                                                                 W09634624-A3
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New isolated thymus receptor tyrosine kinase - is used to develup roducts for the diagnosis and profileration diseases involving aberrant cell profileration cancers and other diseases involving aberrant cell profileration.

This is the amino acid sequence of 1 of 2 (see also W76526) putative novel human thymus receptor tyrosine kinases (TSTKs) as deduced from the nucleotide sequence of a CDNA clone (see V3667) obtained from a human foetal cell coll collaboration for the novel laws a deduced moi will not a 139.3 kMa. The novel laws share sequence howing with collaboration and a financial for the fight family of kTKs and collaborations are thus rembers if the Eph family of kTKs and collaboration such as endered the financially involved to diseases resulting in alterations in corration of involved in haematopoietic development. The involved to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRIK polymericates and polypeptides (including the mature protein, soluble polypeptides, the extracellular, transmembrane and intracellular domains, and epitope-bearing portions of such polypeptides), vectors, host cells and recombinant methods of producing these. Also provided are diagnostic methods for defecting disease states associated with the aberrant expression of TRIK and therapeutic methods for treating such disease states, especially cancer. IRIK is believed to be involved in a number of disease
                                                                                                       Sars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 states such as cancers, e.g. testicular carcinoma, pancreatic carcinoma, colon carcinoma, lung adenocarcinoma, mammary carcinoma
                                                                                                                                                                                                                                                                                                                                                                                            Human thymus receptor tyros—kinase (TRTK).
Thymus receptor tyrosine kinase: TRTK human; colon carcinoma.
Lesticolar carcinoma; pancreatic carcinoma; lunu adenocarcinoma:
breast carcinoma; heptacellular carcinoma; cancer:
cell proliferation; diagnosis; therapy; prognosis.
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                    Score 60: DB 1: Lenath :000.
Pred. No. 8.13e-01:
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Pred. No. 8.13e+01;
3; Mismatches 2;
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W70525 standard; Protein; 1996 AA.
W70525;
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Ruben SM, Soppet DR;
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Sequence 1005 AA:
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/label- Tra-
508
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Local Similarity 61.5%;
es 8: Conservative
                                           52.6%;
51.5%;
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/label= 577
579
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                                                                                                    Conservative
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28-MAR-1997; US-042856.
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                                                                                                                                                                                                            3 YLILSARDVLAVV 15
                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                        02-FEB-1999
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Best Local S
Seguence
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diagnosis; neurodegenerative disease.
             Homo sapiens.
M. Postatification of the control of
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                                               Admin 1999 (first entry)

Humen thymus receptor tytosine kinase (IRTK).

Thymus receptor tytosine kinase: TRTK, human; colon carcinoma;

testicular carcinoma: percreatic carcinoma: lung adenocarcinoma:

testicular carcinoma: percreatic carcinoma: cancer;

cell proliferation; diagnosis: therapy; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W7480; standard; Protein: 74 AA. W7480; 25-70A-1999 (first entry) 49man secreted protein encoded by gene 72 clone HBIA195. Human: secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer: central nervous system; seizure;
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Pred. No. 8.13e+01;
3; Mismatches 2.
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/label= Extracellular
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623. :102:
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|abel= Mat_protein
                                                                                                                                                                     Socation/Qualifiers
                                                                                                                                                                                                   label - Sic_peptide
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W76526 standard: Protein: 1021 AA.
W76526;
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ches 8; Conservative
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Location/Qual : rers
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US-040334-
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11-APR-1997;
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US-09-142-524A-8.rag

y. 100

Indels

pred. No. 1.0le+02; 3; Mismatches 3;

Best Local Similarity 53.8%; Matches 7; Conservative

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New isolated luram genes and the secreted polyperlude(s) they encode useful for diagnosis and treatment of e.g. canners, neurological disolates. Inflammation or blood disorders and secrete beliable to the page 582-583; 721pp; English.

This sequence represents a socreted human protein encoded by the nucleic sequence represents a socreted human protein encoded by the nucleic molecule designated done 72 from the human convoluting to the gene of miman immunoglobulin For portion (e.g. v59602) for increasing the stability of the fused protein as compared to the human protein only. The lavention relates to 186 novel genes and their fragments (nucleic actual for preventing, treating or ameliotating medical conditions of the useful for preventing, treating or mambloogical conditions can be diagnosed by determining the amount of the new polypoptides in a sample of the uses are described for each of the 188 polynucleotides. Based on which tissues they are most highly expressed in (see V5511 for described)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bednarik DP, Brower LA, Carter KC, Duan R, Ebner R, Endress GA, Feng P, Forric AM, Fischer CL, Fiorence KA, Greene JM, Hu JS, Kyaw H, Laffent DM, Li Y, Moore FA, Ni J, Olson HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zenu Z, WPI; 98-506354/41
                                                                                                                                                                                                                                                                                                                                                                                                                                               22-A3G 1997; US-065903.
22-A3G 1997; US-055908.
22-A4G 1997; US-055909.
22-A4G 1997; US-055910.
22-A4G 1997; US-055911.
05-SEP-1997; US-057650.
05-SEP-1997; US-05766.
12-SEP-1997; US-05786.
                                   US-049610.
US-051926.
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08-056630
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N. PEDBS. (0313) 3.

Disclosure; Fig 5: 51pp: Engli. b.

S. Disclosure; Fig 5: 51pp: Engli. b.

The sequence was deduced from the first of two CKFs tound in cloud pGPS7, prepd. from C. psitta : genomic ENA and contg. the Hyp GPS7, prepd. from C. psitta : genomic ENA and contg. the Hyp openion. It is the hypA prover, or expross. 12 KD; analogous to the GroEs heat shock provein o. E. coil. The recombinant protein can be used to to raise antiho. es and in the preparation of vacchnes for the treatment o: ...umydial infertions.

See also R1335-R1337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypa protein.
Antibodies: heat shock: hypersens: Live: allergen: MSPKU: Grobs.
Chlamydia psittaci GPIC.
US753:317-A
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Pr d. No. 1.246+02;
5 Mismatches 3: Indels
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                                                                                                                                                                                                                           RESULT 15

ID RESULT 15

ID REJASA standard; Protein: 102 A. RIJASA; PETOLE; P
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Best Local Similarity 46.7%;
Matches 7; Conservative
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52 EEYLILMNKALLT 64
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Job time : 8 secs.

51.8%; Score 59;

Query Match

DB 1: Length 74:

Release 3.1A John F. Collins. Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein protein database search using Smith-Waterman algorithm

Tue Jun 20 13:38:33 2000; MasPar time 2.33 Seconds 105:377 Million cell updates/sec

Tabular output not generated.

>US-C9-142-524A-8 (1-17) from USC9142524A.pep 114 : EEYLILSARDVLAVVSK 17 Title: Description: Perfect Score: Sequence:

PAM 150 Cap 15 Smoring table:

145341 seqs, 14437480 residues Scarched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database

a-issued l:5A_COMB_2:5B_COMB_3:6_COMB_4:PCT_COMB_5:backfiles1 Mean 18.743: Variance 56.315; scale U.283 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1.47e+02 1.47e+02 80e-02 47e+02 Sequence 16. Applications Sequence 36. Applications Sequence 29. Applications Sequence 29. Applications Sequence 34. Applications Sequence 34. Applications Sequence 34. Applications Sequence 35. Applications Sequence 36. Applications Sequence 36. Applications Sequence 36. Applications Sequence 4. Applications Sequence 4. Applications Sequence 4. Applications Sequence 5. Applications 5 mergatiose. CS-06-467-CS-06-467-US-08-467-US-08-467-US-08-1100-US-08-110 SUMMARIES Query Match Length \(\)
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2 EYLILSARDVLAVV 15
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-467-822-39
                                                                                                                                                                                                                                                                                                                     SEQUENCE
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         Sequence 38. Application US/08467922
Patch No. 5843460
GENERAL INFORMATION:
APPLICANT Labique, Addes
APPLICANT Saverbaum. Sebasiten
APPLICANT: Exerrbaum. Sebasiten
APPLICANT: Forrero, Richard L.
APPLICANT: Thiberae, Jean-Michel
TITLE OF INVENTION: IMMINOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
ADMHER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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STREET: 1500 I Street, N.W.
CITY, Washington
STATE: 0.0.
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NAME: Megers, Kenneth J.
REGISTATION NUMBER: 25.146
REFERENCEZOCKET NUMBER: 03495 0137-02000
JELECCHMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIF/CATION: 435
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRI
                                                                                                                                                                                                                                                                                                                                       MRUECULE TYPE: protein
JENGE 93 AA: 10002 MW: 48030 GN:
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD
                                                                                                                                                                                                                                   LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               Waery March
Hest Local Similarity 100.0%:
Matches 17: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 BEYLILSARDVLAVVSK 93
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AX XXXXX

DIX SEQUENCE 38, APPLICAN

CONTRACT INVENT

CONTRACT

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APPLICANT: Labine, Agres
APPLICANT: Saverbarn, Sebastion
APPLICANT: Saverbarn, Sebastion
APPLICANT: Saverbarn, Sebastion
APPLICANT: Fire and Archer, Laborate, James Allows
TITLE OF INVENTION: IMMUNICANTER INFECTION POLYPERTIDES F. R. USE IN THE
TITLE OF INVENTION: COMPOSITIONS AND NUCLEIC ACID SEQUENCES ENCOING SAID
TITLE OF INVENTION: POLYPERTIDES
TITLE OF INVENTION: POLYPERTIDES
CHRESPONDENCES 44
CURRESPONDENCE ADDRESS:
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STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSED During STREET. N.W. STREET. N.W. STREET. 1300 I SELECT OCCUR. N.W. STREET. 1300 I SELECT OCCUR. STATE 120 CONT. PT. 1304 CONT. PT. 1304 CONT. PT. 1306 COMPUTER. I BM FG COMPUTER. POSPY, CISA DEFAULT SYSTEM. PO-DCS/MS-LUSS SOFTWARE: Patentin Release *1.0, Version *1.30 COMPUTER. Dob.JUN-1995 CLASSIFICATION MAMBER: US 08/447.177 FILING DATE: 19-MAY 1995 CLASSIFICATION NUMBER: US 08/432.697 FILING DATE: 29-MAY 1995 CLASSIFICATION: 435 PRICASSIFICATION: 435 PRICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 70: (AB.2) Length 94:
57.1%; Pred No. 4:52e+00;
dative 3: Mismatches 3: Indels
     03495.0137-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 94 AA: 10343 MW: 45288 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/08467622
REFERENCE/DOCKET NUMBER: 0349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acids
STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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Sequence 29, Application US/08467822

Patent No. 584360

GENERAL INFORMATION:
APPLICANT: Labique, Aqui, Sciestien
APPLICANT: Labique, Aqui, Sciestien
APPLICANT: Thiberge, Jean-Michel
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPETIDES F.M. USE IN THE
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPETIDES F.M. USE IN THE
TITLE OF INVENTION: CORPOSITIONS, AND NUCLEIC ACID SEQUENCES, 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: Dunner CORRESSEE: Dunner CORRESPEE: DUNER CORRESPEE: DUNNER CORRESPEE:
                                                                                                                                                                                                                              Score 65: DB 2: Length 97;
Pred. No. 1.38e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IRM PT COMPATIBLE
COMPATING SYSTEM: PCT-DT-S/MS-DL-S
SOFTMAKE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGERENCE/DOCKET NUMBER: 03495,0137-02000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/C8/467,822
CLASSIFICATION 435
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DAIE: 02-MAY-1995
CLASSIFICATION 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 97 AA; 10387 MW; 48352 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/08:67822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (222) 409-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 29:
SEGUENCE CHARACTERISICS:
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INFORMATION FOR SEQ ID ' : SEQUENCE CHARACTERIST : LENGIH: 97 amino acids
                                                                                                                                                                                                                              57.08;
60.08;
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COMPUTER READABLE FURM:
MEDIUM IYPE: Floppy o
                                                                                                     single
                                                                                                                                                                                                                                                                                     9; Conservative
                                                                          TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                   81 EEVLIMSESDILAIV 95
                                                                                                                                                                                                                                                                                                                                                                 1 EEYLLESARDVLAVV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-467-822-29
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                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                                                                                                  Matches
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  888888888
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APPLICANT: Saverbaum, Sebastien
APPLICANT: Saverbaum, Sebastien
APPLICANT: Saverbaum, Sebastien
APPLICANT: Terrero, Richard L.
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SALD
NUMBER OF SEQUENCES: 44
CORRESPONDENT ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
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SUBJECT OF STATE: 1.05A

ZIP: 2005-3315

COMPUTER NEADABLE FORM: SAME MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COTPATIBLE
OPPRATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PATENTIN PC DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
FILING DATE: 19+MAY-1995
CLASSIFICATION: 435
FILING DATE: 19+MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                   4: Indels
                                                                                                                                                                                                                                                                               Score 65, DB 2, Length 94, Pred. No. 1.38e+01, 2, Mismatches 4: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 22.MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/28467822 Patent No. 5843460 GENERAL INFORMATION:
                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 94 AA; 10308 MW; 46635 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application US/08467822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET. N.W. STREET, N.W. CITY: Washington STATE: D.C.
  (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 408-4000
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                     TELEFAX: (202) 408 4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                      single
                                                                                                                                                                                                                                                                                  S7.0%;
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEYLILSARDVLAVV 15
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EXXXXX

EXXXXX

EXXXXX

Sequence 40, Applicated to the control of th
        TELEPHONE:
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APPLICANT: Ching, Wei Mei
APPLICANT: Dasch, Gregory A
TITLE OF INVENTION: Gene and Protein Applicable to the
TITLE OF INVENTION: Preparation of Vaccines for Rickettsia provatekt) and
TITLE OF INVENTION: Rickettsia typh, and the Detection of 9.1h
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34. Application US/UBILETO

Patent No. 5508364
GENERAL INFORMATION:
APPLICANT: Murphy. Recept 18.
APPLICANT: SCHOOLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHOLS HEREP
TOMESPONDENCES: 348
CORRESPONDENCE ADDRESS
ADDRESSEE: BROWEN AND NEIMARK
STREET: 419 SOVERTH Street, N.W., Suite 300
CITY: Washington
STATE: 0.C.
COUTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   v 57. CB 1: Length 1612:
No. 7 Perch:
Miscalones 4: Indels
                                                              ADDRESSEE: ________Navil Medical N & D Command STREET: Bldq. 1, T-12, P-11 Wisconsin Ave. CITY: Bethesda
                                                                                                                                                         COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISW PC compatible
OPERATING SYSTEM: PC-JOSZ/MS-U-S
SOFTWARE: Patentin Release #1.0. Version #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/UH/1/1/9 y27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spevack, A. Davii
REG.STRATION NUMBER: 24,743
REFERENCE/OOCKET NUMBER: 75,976
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1612 amino arids
                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION UNTA:
APPLICATION NUMBER: U.s. 1/742.12E
FILING DAIE: 68/09/91
ATTOHNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/08114270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGLECULE IYPE: protein
JENCE 1512 AA: 166924 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
Local Similarity 37.5%;
es 6; Conservative
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                                                                                                                                        COUNTRY: USA
ZIP: 20889-5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                Gaps
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Patent No. 6013479
GENERAL INFORMATION:
APPLICANT: X: Hond
APPLICANT: Stuart, Susan G
TILLE OF INVENTION: HOMAN EMRI-LIKE G PROTEIN COUPLED
TILLE OF INVENTION: HOMAN EMRI-LIKE G PROTEIN COUPLED
TILLE OF INVENTION: HOMAN EMRI-LIKE G PROTEIN COUPLED
CURRENT APPLICATION NUMBER: US/COURRENT FILLING DATE: 1999-07-02
NUMBER CF ECC ID NOS: 4
SCHIMMER FILLING AMER: 499-07-02
SEC ID NO 4
SCHIMMER BASISEY for Windows Version 3:0
SEC ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coery March (0), x South (2), the relationship 411.
Pest Local Similaring (2), by Prod. No. (1960-0).
Matches 8: Conservative 5: Miscarches 0, Indexs.
                                                                                                                                     Score 61: DB 2: Length 118: Pred. No. 3.30e-01: 6; Mismatches 3: Indels
                                                                            NAME/KEY: Protein
LOCATION: L.I.E.
(THESE INFORMATION: /Product* "H. pylor: - Hsp A.
NCE II8 AA: 12999 MM: 68071 CN:
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                                                                                                                                                                                                                                                                 PKT.
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Patoni No. 5783441
GENERAL INFORMATION:
APPLICANT: Car', Mitchell
APPLICANT: Dobson, Michael E.
                                                                                                                                                                                                                                                                                                                                        Segmence 4, Application US/09110116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2. Application US/08169927
LENGTH: 118 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
                                                                                                                                                                                                                                                                 STANDARD
                                 CPOLOGY: linear M. (ECULE TYPE: profesion PEATORE)
                                                                                                                                     Cuery Match
Fest Local Similarity 46.0%:
Matches 6: Conservative
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 YUBURARN-UTVVN 186
                                                                                                                                                                                         76 BYMVLEUEDILGIVG 90
                                                                                                                                                                                                              Z SYLILSARDVLAVVS 16
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                                                                                                                SECUENCE
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6: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-673-789-11
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TILLE OF INVENTION: HOLYPERTIDES OF G-COUPLED PROTEIN
TILLE OF INVENTION: HOLYPERTIDES OF G-COUPLED PROTEIN
TILLE OF INVENTION: HOLYPERTIDES OF G-COMPOSTIINS AND METH-US THEREDE
UNRBER OF SEQUENCES.
ADDRESSE: 349
COMPRESSORE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
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COMPUTER TEADABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC1/US93/06528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: CS C7/943,236
FILING DATE: 10-SEP-1993
ATIORNEY/AGENT INCRMATION:
ANALY TORNEY/AGENT INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
Tac
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
JENCE 315 AA: 34874 MW: 534513 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Appincation PC/TUS9308528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                               amino acids
                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 YLVFAVRFVLGVLGN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YLILSAROVLAVVSK 17
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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CO SEGUENCE 34, Apriloc

CO SEGUENCE 34, Apriloc

CO SEGUENCE 34, Apriloc

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CO COMPUTER 
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Patent No. 5814479
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: 21-00, RENPIN SCHULZ, NICHOLAS,
APPLICANT: 1-1 KROMER, AWRENCE, F.: VANDE WOUDE,
APPLICANT: 1-1 KROMER, AWRENCE, F.: VANDE WOUDE,
APPLICANT: 1-1 KROMER, AWRENCE, F.: VANDE WOUDE,
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIF
TITLE OF INVENTION: METHADS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                            Score 55, DB 4, Length 315,
Fred. No. 1.19c-02,
7: Mismatches 2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612 AA
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2026-4105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATINLE OPERATING SYSTEM: PC-6/5/NS-50/S SOFTWARE: WORDFERECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/673,789
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 315 AA; 34874 MM: 534514 CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application USZC-673789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CAROL M. GRUPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUN.CATION INFORMATION:
TELEFAN: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: 421792
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEGILLY CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENTE
                                                                   TELEFAX: 202-737-3528
TELEFAX: 208-737-3528
TELEX: 248633
INFORMATION FOR SED 1D NO: 34:
SEQUENCE CHARACTERISTICS.
LENGTH: 315 amino ac; s
IYPE: amino aci s
TYPE: amino aci s
STRANDEDNESS: single
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                            Query Match 48.2%;
Best Local Similarity 40.0%;
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Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajadi, Fereydoun G.
TITLE CF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SQUIENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                             Length 612;
                                                                                    3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.C. V :sion #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSED: CAMPBELL AND FLORES
STREET: 4370 La Jolla Villade Drive, Suite 700
                                                                                                                                                                                          973 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 1; Le
Pred. No. 1.19e+02;
                                                            Score 55; DB 2; Lo
Pred. No. 1.19e+02;
7; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Carpbell Arthron A.
REGISTATION NUMBER: 31.815
REFRENCE/COCKT NUMBER: P-13 9503
TELECCMMUNICATION INFORMATION:
FELEPHONE: (619) 535-9031
TELEPHONE: (619) 535-9031
(NPCRMATION FOR SEQIED NO: 8:
SEGIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECCLE TYPE: protein
JENCE 973 AA: 108597 MM: 4992047 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La Jolla Village Di.,
CITY: San Diego
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIPICATION: 5:4
ATTORNEY/AGENT INFORMATION:
TYPE: AMING ACID
STRANDEDNESS: UNKNOWN
STROCCT: UNKNOWN
SECUENCE 612 AA: 68803 MW; 1972484 CN;
                                                                                                                                                                                          D 2.1
                                                                                                                                                                                                                                                                    Sequence 8, Application US/U8162809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 973 amino acids amino acids
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                query Match
Post Local Similarity 33.3%;
Matches 5; Conservative
                                                             Query Match

Best Local Similarity 33.3%:
Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 FLVIAAIAILAIIFK 557
                                                                                                              182 FLVIAAIAILAIIFK 196
                                                                                                                                       3 YLILSARDVLAVVSK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YULLSARDVLAVVSK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
IC PCT-US95-10194-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92122
                                                                                                                                                                            RESULT 11
ID US-08-162-809-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY
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327 AA

P.K.T.

STANDARD;

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Sequence 35, Application PC/10S5519194
GENERAL INFORMATION:
APPLICANT: THE TRUSTEES: Colombia Chiversity in the City of New York APPLICANT: City
ITLE OF INVENTION: UNIQUE ASS/CHATED KAPOSI'S SARGUMA VIPOS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SECUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application US/084202353
Patest No. 5801642
GENERAL INFORMATION:
APPLICANT: Chads, Yean
APPLICANT: Chads, Yean
APPLICANT: Moore, Patrick S.
ITTLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
ITTLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 45185-C-PGT/JPW/MSC
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 278-3400
IELEPRONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk CCMPUTER: IBM PC COMPALID: PC POEMALID: PC POEMAS-CANS SOFTWARE: PATENTIN PC-FOSMS-CANS CURRENT APPLICATION DATA: PCT/US95/10194 FLLING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Areticas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
SEQUENCE 327 AA; 36122 MW, 554271 CN;
                                                                                                                                Sequence 35, Application PC/7039510194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/08420235B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28.678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 327 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match Local Similarity 31.3%. Per 6. Consentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * CANDARD BENDARY OF STREET
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1185 ... CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EYLILSARDVLAVVSK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LI 13
US-08-420-235B-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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GENERAL INFORMATION:

APPLICANT: ERIESVAG HELDA
APPLICANT: VALLA, SVEIN
APPLICANT: VALLA, SVEIN
APPLICANT: LARSEN, BJOH*
TITLE OF INVENTION: ENGINE MANNURGNAN C-5-EPIMERANE
NUMBER OF INVENTION: ENGINE MANNURGNAN C-5-EPIMERANE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               Score 54: 18 2: Length 572: Pred. No. 1.47e-02: 5: Misratches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FEAGULE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 25/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSES: BIRCH. STEWART, KOLASCH & BIRCH, LLE
STREET: P.C.BOX 747
CLIY: PALLS CHORCH
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997 AA
NAME: Billings, Lucy 7.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0151 US
TELECOMMUNICATION INFERMATION:
TELEPHONE: (415) 845-0555
TELEPKONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURHY 3R, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8050
                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
:MMEGIATE SOURCE:
LIBRARY: CLORE: CLORE: CLORE: CONSUMER STARY CONSUMERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/083879420
Patent No. 5939289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4. Application US/083879420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-205-0000
INFORMATION FOR SEG ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 997 amino acids
TYPE: amino acid
                                                                                                                                      LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARE
                                                                                                                                                                                                                                                                                                                 47.48;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.7%,
Matches 5, Conservative
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US-08-387-942C-4
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                                                                                                                                                                                                                                                                              SEQUENCE
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Pred. No. 1.47e-02;
9; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 586146
GENERAL INFORMATION:
APPLICANI: HILMAN, DELOIFER I.
APPLICANI: HAWKINS, Philip P.
IITLE OF INVENTION: HURAN SQUALENE EPOXIDASE
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
                                                                            COMPUTER PEADBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: PROPERTIES
OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: PARENTER RELEASE #1.25
CURRENT AFPLICATION DATA:
APPLICATION DATA:
APPLICATION TAY:
APPLICATION TAY:
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
RECISTRANDORET INFORMATION:
FLECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF ACCOUNTY OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPENATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,934
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
     1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCLECULE TYPE: protein
SEQUENCE 327 AA; 36122 MW: 556271 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.8.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08745934
Patent No. 5861496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08745934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuery Match 47,4%; Best Local Similarity 31,3%; Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 DYLIIPSYDIPALITM 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EYLILSARDVLAVVSK 17
                                         New York
                                                                        10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 14
US-08-745 934-1
                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xxxxxx
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CC NOIECUE TYPE: protein screeness protein screeness pg7 As; 103083 MM; 4504141 CN; CC NOIECUE TYPE: protein 4504141 CN; Cuery Match 47.4%; Score 54: DB 2: Cenoth 997; East Local Similarity 80.0%; Pred: No. 1.476+02; Matches 8: Conservative 9: Mismatches 2: indels 0: Caps 0: CC NOIECUARITY 81 CONSERVATIVE 827 C
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Search completed: Tue Jun 20 13:35:38 20:0 Job time : 5 secs US-09-142-524A-8.rap

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyriant (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

Misschipp protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 15:25:24 2000; MasPar time 15:36 Seconds 11:509 Million cell updates/sec Run on:

Tunular output not generated.

>US-09-142-524A-8 (1-17) from USC9142524A.pep 114 I EEYLILSARDVLAVVSK 17 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Souring table:

721208 segs, 100765575 residues Sourched:

Minimum Match 0% Listing first 45 summaries Pust-processing:

3-pending 1:p0T 2:06 3:060 4:07 5:080 6:081 7:082 8:083 9:084A 10:08418:10:08 12:086 13:087 14:086 15:089 16:090 17:091 18:092 19:093 20:094 2::055 22:NEWP 23:NEWD60 24:NEWU8 25:NEWU9 Darabase.

Mean 22,684: Variance 64,308: scale 0.353 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		se			SUMMARIES			
Frish t	Score	C.ery Match	Leadt.	Ξ	C!	Description		Pred No.
-1	7::	100.0			CS-08-466-	Sequence if. Applicat	cat:	1.00e-04
17	1.4				US-08-432-	Sequence 36, Applicati	cati	1.00e-04
.**\	7.2				.28-09-107-	Sequence 5969	lica	1.23e-01
₹	9.5	61.4			US-08-432-	Sequence	cati	2.07e+01
S	26				CS-08-456-	Sequence 38, Ap	cati	2.07e+01
9	3.0				US-09-134-	Sequence 4557,	Applica	2.07e+01
۲	55	67.6	111		08-09-450-	Sequence 6163,	Applica	5.73e-01
œ	65	L)			US-08-466-	39, Ap	cati	7.37e+01
5	55	(A)	6	ďν	US-58-432-	39,	cati	7.37e+01
10	un G	57.0			JS-08-432-		cati	7.37e+01
1.	65 5	57.0			DS-69-472-	4.	atio	7.37e+01
12	65	57.0			CS-08-466-		cati	7.37e+01
13	55	57.0	129		US-09-252-	7178,	Applica	7.37e+01
1.0	65	57.0			PCT-US98-0	178,	Applicat	7.37e+01
15	ស្ត	57.0			US-08-833-	178,	Applicat	7.37e+01
1.6	63	55.3			US-09-252-	ć	cati	1.21e-02
17	61	53.5			US-08-432-	Sequence 29, Applicati	cati	1.99e-02
18	4	53.5			US-08-466-	29,	cati	1.99e+02
19	¥.	53.5	154	13	CS-C9-107-	Sequence 6000, App	Applica	1.99e+02
20	61	53.5			-861-09-SA	Sequence 1255, App.	ica	1.99e-02

APPLICATION NUMBER: US 08/432,697 FILING DATE: 02-MAY-1995

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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/ 4/107,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: ATLITELLO, PRINCIA DURANT RECISERATION NUMBER: 40.489
REFERENCE/POCKET NUMBER: GTC-612
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                 Sequence 6969, Application US/093, 7532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA; 12807 MW; 74418 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus sectum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION CATA:
APPLICATION NUMBER: ("#559E
FILING FATE: May 14. "
PRIOR APPLICATION NUMBER: ("#559E
PRIOR APPLICATION NUMBER: ("#559E
FILING DATE: CUIN 2. 1497
ATTORNEY/AGENT INFORMATION.
                                               .NO 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (781)893-6277
INFORMATION FOR SEQ ID NO: 0969:
SECUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBABLE FORM:
MEDIUM TYPE: CD/ROM ISC9560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_featu:e
                                  MOLECULE TYPE: protein
SEQUENCE 93 AA: 10002 MW: 3
                                                                                                                                                                                            STANDA
         iss: single
licear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                     Query Match
Best Local Similarity 100.08:
Matches 17, Conservative
                                                                                                                   77 EEYLILSARDVLAVVSK 93
                                                                                                                                  : EEYLILSARDVLAVSK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: licear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
STATE: Massach
                                                                                                                                                                                                                                                                                                                                                                                                                                      CCUNTRY: USA
ZIP: 02354
                                                                                                                                                                              RESULT 3
ID US-09-107-532-6969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                     XXXXXX
                                                                                                                                                                                            22 22 28
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Labione, Agnes
APPLICANT: Suerbaum. Sebastien
APPLICANT: Suerbaum. Sebastien
APPLICANT: Suerbaum. Sebastien
APPLICANT: Thistory. Jean-Michel
TILLE OF INVENTION: IMMUNOCENIC OM SITIONS AGAINS:
TILLE OF INVENTION: EMBLICORACIER IN ECTION, POLYPEPPLIDES FOR USE IN THE
TILLE OF INVENTION: COMPOSITIONS, AN: NOTLEIC ACID SEQUENCES ENCODING SAID
TILLE OF INVENTION: POLYPEPTIDES
TILLE OF INVENTION: POLYPEPTIDES
TILLE OF INVENTION: POLYPEPTIDES
TOWNSER OF SECUENCES: 44
COMPRESSIONDENCE ADDRESS:
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                                                                                                                                                                                                        Score 114: DB 10: Length 93: Pred, No. 1 00e-04: C: Mismatches 0: indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
PURESSEE: 1800 1 Street, N.W.
CITY, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z.D. 2005-3315
Z.D. 20005-3315
C.M.POTER READALE FORM:
WEDICH TYPE: Floppy disk
COMPUTER: 18M PC Compatible
C.PERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PATENTIE Re-base #1.0. Version #1.30
CURRENT APPLICATION NUMBER: US/C8/432,697
FILING CALE: 02-MMY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MAYOR MANGER 15.146

PEGISTRATION NUMBER: 25.146

REFERENCE/COCKET NUMBER: C3495.C137-00000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 406-400

INFORMATION FOR SEQ ID NO. 36:
SECUENCE CHARACTER SETIES:
LENGTH: 93 amino acids
                                   RESISTRATION NUMBER: 25.146
RESISTRATION NUMBER: 25.146
REFERENCE/COCKET NUMBER: 03495.0137-02000
TELECOMMULTATION INFORMATION:
FELEPHONE: (202) 408-400
INFORMATION FOR SECIED NU-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            93 AA.
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
                                                                                                                                                           TOPOLOGY: Threat
MCLECUSE TYPE: protes:
JENSE 91 AA: 10002 MW: 48030 CN.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36. Application US/08432697
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            STANDARD
                          Meyers, Kenneth J
                                                                                                                       LENGTH: $3 amino acids IYPE: amino acid stranceDNESS: single
                                                                                                                                                                                                        cuery Match
Rest Local Similarity 100.0%:
Matches 17; Conservative
                                                                                                                                                                                                                                                       77 EEYLILSARDVLAVVSK 93
                                                                                                                                                                                                                                                                        1 BEYLILSARDVLAVSK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z3.0
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US-06-432-692-36
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                                                                                                                                                                                   SEQUENCE
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Sequence 6969. Application USCUPINEST
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE 
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Sc. P 114: DB 9: Length 9: 
Flod: No. 1:00e-04:
F. Mismatches - C: Ind-is
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Sequence 38, Application US/08465248

C GENERAL INFORMATION:
APPLICANT: Lab grace, Agg. s
APPLICANT: Sauerbaur, S.tastien
APPLICANT: Erreto, Richard L.
APPLICANT: Ferreto, RICHARD L.
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Januer
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Pred. No. 2.07e+01: 
3: Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 200C5-3315
COMPUTER READABLE FORM:
MEDUNI TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DSS/MS-DCS
SOFTWARE: PATENTIA RElease #1.0, Version #1.30
CURRENT APPLICATION DATA
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers. Kenneth C. REGISTRATION NUMER: 25.146
RESIESTRENCE/POCKET NUMBER: 25.146
RESIESTRENCE/POCKET NUMBER: 0.445.6127.02000
TELEPRONCHOATION INFORMATION
TELEBRANCE (20.2) 418.4 % 0.7
TELEBRANCE (20.2) 418.4 %
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
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APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: C2-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI
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SEQUENCE 94 AA: 10343 MW: 45288 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1%:
tes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 94 amino
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EYLILSARDVLAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000-4557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                        XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Labique, Agnes
APPLICANT: Sauerbaum. Sebastien
APPLICANT: Sauerbaum. Sebastien
APPLICANT: Triberge, Jean-Michei
Title OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBRACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
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0
                       Length 119
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SOTTWARE PARENTIN Release #1.6. FIRST CHREET APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE: C2-MAY 1995
CLASSIFICATION: 424
ATTONNEY/AGNT: INCOMMATION:

NAME: Weyers: Kenneth J. REGARATION:

REGISTRATION NUMBER: 25,146
REFRENCE/POCKET NUMBER: 25,146
RECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 100 4000
INFORMATION FOR SEC 100 4.00
INFORMATION FOR SEC 100 4.00
INFORMATION FOR SEC 100 4.00

LEGISTRATION FOR SEC 100 4.00

LEGIS
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Pred. No. 2.07e+01:
3: Mismatches 3: Indels
                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 AA.
                                                                                                                                                                                                                                                                                                                                94 AA.
                    Score 72: DB 17;
Pred. No. 1.23e+01;
                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT.
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/08432697 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 94 AA: 10343 MM: 45288 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/08432697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREE: 1300 I Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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ilarity 57.1%:
Conservative
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                       63.2%;
50.0%;
Overy Match
Best Local Similarity 50.00,
7: Conservative
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                                                                                                                                            105 EYLIVAGKDIMAIV 118
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                                                                                                                                                                                                           2 EYLILSARDVLAVV 15
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AXXXXX

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SEQUENCE 38, Appliance

CENERAL INFORMATION

CONTRIBUTION

CONTRIBUTI
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ID US-08-466-248-38
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APPLICANT: FETERO, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMONOSENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACITE INFECTION, PCLYPEFILIES FOR USE IN THE
TITLE OF INVENTION: CCMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENTION GAID
TITLE OF INVENTION: POLYFETIDES
NUMBER OF SEQUENCES: 4
ADDRESSEE: Finnegan, Henderson, Farabow, Gairet, s
ADDRESSEE: Dunner
STREET: 1300 i Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
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                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

LIP: 2005-3315
COMPUTER: EDOPO disk
MEDIUM TYPE: Floppy disk
COMPUTER: EDM FO compatible
COMPUTER: EDM FO compatible
COMPUTER: EDM FO COMPATIBLE
COMPUTER: PREDITE PORTION SYSTEM: PC-705/MS:US
SOFTWARE: Patentin Release #1.0, Version #1.3,
CURRENT APPLICATION NO DAIR:
ETLING DAIE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Section 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kennentium:
NAME: Meyers, Kennentium:
REGISTRATION NUMBER: 25.14
REFERENCE/DOCKET NUMBER: 0345.0137-0200C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 406-4400
TELEFAX: (202) 406-4400
INFORMATION FOR SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
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PRIOR APPLICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19 MAY-1595
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ADDIT
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APPLICATION NUMBER: US 08/432.697
FILING DATE: 02-MAX-1995
CLASS:PECATION: 435
ALTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauchaum, Sebastien
APPLICANT: Ferrero, Richard U.
APPLICANT: Thiberge, Jean-Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
TENCE 94 AA; 10308 MW: 46636 CN:
Sauerbaum, Sebastien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/U:432697
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linear
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                                                                              Sequence 4557, Application US/09134006A

SENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TILE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO ENTEROCOCCU
TITLE OF INVENTION: PECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 3TC-065
CURRENT APPLICATION NUMBER: US/09/134.00CA
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 4557
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6163, Application US/09453969
GENERAL INFORMATION:
APPLICANT: Lynon Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOC
TITLE OF INVENTION: UPDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/450,969
CURRENT FILING DATE: 1999-11-29
SEC ID NOS: 7544
SEC ID NO 6163
LENGTH: 11:
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Pred. No. 5.73e+61:
4: Mismatches 2: Indels
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                                                       Sequence 4557. Application US/09134000A
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Enterococcus faeralis
QUENCE 104 AA: 11303 MW; 63709 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6163, Application US/09450959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRI
ORGANISM: S.ep.Germidis
QUENCE ::: AA. 12(46 KW: 61750 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cuery Match
Bost Local Similarity 53.8+)
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.4%;
Similarity 64.3%;
9; Conservative
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Rest Local Similarity
Matches 9: Conser
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: SOGG, RAZANO
APPLICANT: YORG, TAKASHI
TITLE OF INVENTION: TRIGGER FAT: FENT FESSION FLANHIS
FILE REFERENCE: 1422-459P
CURRENT FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: JP10-372965
NUMBER FILING DATE: 1999-12-28
EARLIER FILING DATE: 1999-12-28
SARIER FILING DATE: 1999-12-28
SOFTAME OF SOG ID NOS: 7
SOFTAME.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUW TYPE: Ficppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DDS/MS-DDS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412.697
FILING DATE: U2-MAY-1595
CLASSIFICATION NUMBER: US/08/412.697
AITORNEY/AGENT INFORMATION:
NAME: MAYERS KENNELCE:
REGISTRATION NUMBER: 25.146
REFERENCE/DOCKET NUMBER: U3455.0137-0000
TELE OMMUNICATION NUMBER: U3455.0137-0000
TELEPAX: (202) 408-4400
INFORMATION FOR SEG ID NO: 40:
SEGUENCE CHARACTERISTICS:
FURTHER: 47 Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 20; Length 97; Pred. No. 7.37e+01; 3: Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Query Match

57.0%; Score 65: 58 9: Length 97:
Best Local Similarity 60.0%; Pred: No. 7.37e-31;
Matches 9: Conservative 3: Endels
Matches 3: Endels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
36.
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ORGANISM: Escherichia coli
QUENCE 97 AA: 10387 MW: 4:352 CN:
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 97 AA: 10387 MW: 48352 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4. Application US/39472971
                                                                                                                                                                                                                                                                                      LENGTH: 97 amino deids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD
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Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          81 EEVLIMSESDILAIV 95
                                                                                                                                                                                                                                                                                                                                linear
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US-09-472-971-4
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LENGTH: 97
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GENERAL INFORMATION:
APPLICANT: Labigne. Agnes
APPLICANT: Seture and Sequence and Septicant: Seture and Septicant: Applicant: Seture and Septicant: This of Seture and Septicant: This of Sequence and Septicant: This of Sequence and Septicant: Title of Invention: Impurion: Title of Invention: Polypeptice and Sequences Encoding Sald Title of Invention: Polypeptibes
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
          IMMUNOGENIC COMPOSITIONS AGAINST
HELICOSACTER INFECTION, POLYPEPTIDES FOR USE IN THE
POLYPEPTIDES.
POLYPEPTIDES
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       TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS AGAINST CITLE OF INVENTION: HELICOGRACIER INFECTION, POLYPEPPITIE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SETTILE OF INVENTION: POLYPEPTIDES NUMBER OF SIQUENCES: 44
CURRESPROPENTE ADDRESS: ADDRESS: Fincegan, Henderson, Faradow, Gairett & ADDRESSEE: Fincegan, Henderson, Faradow, Gairett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                           CZIP: 20005-3315

CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CPERATING SYSTEM PC-DOS/MS-FD/S
SOFTAMED: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION NOTA:
NAME: MAYERS. Renneth J.
REGISTRATION: NOTA:
NAME: MAYERS. 120,146
AT:CARRITON TORNEY MORES: 25,146
REPERENCY/POCKET NUMBER: 03495.0137-00000
TELEPHORE: (202) 468-4400
INTERPREDICATION SECOND NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Firnegan, Henderson, Farabow, Garrett & ADDRESSE: Dunner 3300 I Street, N.W. STREET: 4300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65: 38 9: Length 94;
Pred. No. 7.37e+31;
2; Mismatches 4: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MCLECULE TYPE: protein JENCE 94 AA: 10308 MW; 46636 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40, Application US/08432697
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Washington
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                                                                                                                                               STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
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Sequence 178, Application FC/TUS9868371
GENERAL INFORMATION
APPLICANT RELIGIOUS GRAVAX SUCIELE EN NOM COLLECTIF GASIEUR
APPLICANT: MERIEUX SERUKS ET VACCINS S.A. HUMAN GRAVME
TITLE OF INVENTION: Identitication of Polynochectides
TITLE OF INVENTION: Genome
NUMBER OF SEQUENCES: 1376
CORRESPONDENCE ADDRESS:
                                                                                         APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NOTHEL ACTO AND AMINO ACTO SECUENCES FELATIN: TO ENTEROB
TITLE OF INVENTION: CLOACEE FOR DIAGNOSTICS AND THERAPEUTICS.
TITLE OF INVENTION: CLOACEE FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/US/252.691H
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 7178
LENGTH: 129
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Pred. No. 7.37e-02:
Timmfohes 3: Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPETWARING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/06371
FILING DATE: 01-APR-98
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         FRT:
                                                                   Sequence 7178, Application US/73252691B
GENERAL INFORMATION:
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                                             Sequence 7178, Application 35/092526918
                                                                                                                                                                                                               ORGANISM: Enterobacter clodcae
UENCE 129 AA: 13636 MW: 85820 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: C8/881,227
FILING DATE: 24-JUN-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/902,515
FILING DATE: 25-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833.457
FILING DATE: 01.APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/881,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark & E.L. : 111
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Local Similarity 60.08:
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STREET 1...
TAY: HOSTON
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PCT-US98-06371-178
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Sequence 40. Application US/08465248

GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Labigne, Agnes
APPLICANT: Sauchabam, Sebastien
APPLICANT: Successor, Jean-Michel
ITILE OF INVENTION: LAMBORIED INFECTION, POLYPEPTIDES FOR USE IN THE
ITILE OF INVENTION: CAMPOSITIONS AND NUCLEIC ACID SEQUENCES ENCODING SAID
ITILE OF INVENTION: POLYPEPTIDES
NUMBER OF SOUTHORS: 44
CORRESPONDENCE ADORESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunney
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NAME: Meyers, Kennelh J.
REGISTRATION NUMBER: 25,146
FERRENCE/SOCKET NUMBER: 03445.0137-02060
TELEFORMINICATION INFORMATION:
TELEPHINE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; 28 10; 3
Pred. No. 7,37e+01;
3; Mismatches 3.
           97 AA.
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PRIOR APPLICATION NUMBER: US 68/447,177
FILING DATE: 19-78Y-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432.697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
            PRI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MCLECULE TYPE: protein
JENCE 97 AA: 10387 MW: 48352 CN:
                                                                                 Sequence 40, Application US/C8466248
                                                                                                                                                                                                                                                                            STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 408-4000 TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO. 401 SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
            STANDARD;
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Best Local Similarity 60.0%:
Matches 9; Conservative
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US-09-252-691-7178
 RESULT 12
15 US-08-466-248-40
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ore 65; OB 14; Length 196; d. No. 7.37e+61; Mismatches 3: Indels
 MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE 136 AA: 15614 MW: :30717 CN;
                                                                                                                                                                        Search completed: Mon Jun 19 14:21 45 2000
                                                      Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                        8 EDYLMIMSREVSAFVG 23
                                                                                                                         Job time : 21 secs.
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GENERAL INFORMATION:
Tarold Kleanthous et al.
TILE OF INVENTION: Jeanthlication of Polynucleotides
TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobact
TITLE OF INVENTION: Genome
NUMBER OF SEQUENCES: 370
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                Ċ
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Pred. No. 7.37e+01:
5: Mismatches 3: Indels
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C.MOUTER READABLE FORM:

MEDIUM IYPE: Diskette

COMPUTER: LBM Compatible

SPERATING SYSTEM: JOS

SCFTWARE: RASESC FOR Windows Version 2.0

SCFTWARE: PASTSC FOR Windows Version 2.0

CLASSIFICATION NOMBER: US/08/0833,457

FLING DATE: 01-APR-97

CLASSIFICATION: 435

ALTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

RELEPHONE: 617-428-7045

TELEPHONE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                    PRT: 136 AA
         NAME: Clark, Paul I.
REGISTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 06132/041WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFACNE: 617-428-7045
                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: Protein FRASHENT TYPE: internal SEQUENCE 136 AA: 15614 MW: 100717 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 178. Application US/35833457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                   INFORMATION FOR SEQ 10 NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 anino acids
TYPE: anino acid
STRANDEGNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 178:
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 AITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   Query Match
Rest Local Similarity 50.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                        8 EDYLMLMSREVSAFVG 23
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US-08-833-457-178
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Rulease 3.1A John F. Collins, Biocomputing Research Joit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Misrch_pp protein - protein database search using Smith-Waterman algorithm

Mon Jin 19 16:08:02 2000: MasPar time 5.39 Seconds 148.858 Million cell updates/sec R ::: on:

Tabular output not generated.

>US-09-142-524A-8 (1-17) from USO9142524A.pep 114 1 EEYLLISAROVLAVVSK 17 Title: Description: Perfect Score: Sequence:

142080 segs, 47172406 residues PAM 15C Gap 15 Smoring table:

Sourched

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 29.138; Variance 41.987; scale 0.694 Statistics: Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score	7:7	114	114	114	105	103	90	90	5.6	78	9.	7.5	7.5	74	73	5 ب	7.7	7.	7.0	70	69	58	29
Result	7	7	8	7	'n	w	L-	00	6	10		12	13	7.7	51	15	17	18	61	20	21	22	23

24 67 588 25 27 28 65 57 28 28 65 57 28 28 65 57 38 38 38 38 38 38 38 38 38 38 38 38 38	122 2 B70489 GroEs - Aquifex aeoli 7.24e-01 2 2 22343 chaperonin groEs - Cl 1.65e-00 102 2 5.92343 chaperonin groEs - Cl 1.65e-00 102 2 5.9232 chaperonin groEs - Ch 1.65e-00 103 2 2.9232 chaperonin groEs - Ch 1.65e-00 154 2 H6562 chaperonin 10 - Spina - Eco-00 103 2 2 A46176 chaperonin 10 - Spina - Eco-00 103 2 2 A46176 chaperonin 10 - Spina - Cl 1.66e-00 10 - A46176 chaperonin groEs - Ha 3.10e-00 10 - A46176 chaperonin groEs - Ha 4.10e-00 10 - A46176	ALIGNMENTS S25180 *type complete heat Shock protein groES * Mycobacterium leprae 10x chaperon: **formal name Mycobacterium leprae 03**eb=1994 **sequence_revision 03**Feb-1994 *text_change 25**auq-1999 \$25180 ** \$25180 ** \$72597 \$25180 ** P.K.M. van Soolingen, D.; Orijihout, J.; Schoeningn, R.; Mycobacteria con iin two groEL genes: the second Mycobacterium leprae groEL genes: the second T. 100 **label DSM **The DNA **The DNA **The authors translated the initiation coden GT for Tesique 1 us val ST.554 **Shell, D k.; E.b.; Sur **The authors translated the initiation coden GT for Tesique 1 us val ST.554 **Presidue 1 us val ST.557 **Presidue 1 us	PID:g457129 roES: chpA superfamily chaperonin groES eat shock: stress induced protein length 100 %rc ecular weight 10803 arity 100:0%; Score 114; DB 2; I conservative 0; Mismatches 0; RDVLAVVSK 100 RBVLAVVSK 17
	4 3 4 2 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3	ESULT 1 ITLE LITTER LITTER LITTER LITTER LITTER LITTER LITTER ATE CCESSIONS EFFERNCE ##OUTDA1	ENETICS # gene # start_codon LASSIFICATION EYWORDS UMMARY OUGLY MATCh BEST Local Simi Matches 17 84 EEVILLS 11111111111111111111111111111111111

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*start_codon
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CLASSIFICATION
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                                                                                                                                                                                                                          *journal
*title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE *authors
                                                                                                                                                    *authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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2-100
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Fauthors Shinnick, T.M.: Plikaytis B.B.; Hyche, A.D.; van Landingham, M.M.: Walker, L.M.: Plikaytis B.B.; Hyche, A.D.; van Landingham, a pournal Nucleic Acids Res. (1989) 17:1254
ftitle The Mycobacterium tuberculosis BCG-a protein has homology with the Escherichia coli GroES protein.
                                                                                                                                                                                                                                                                                   #Bauthors Wehra. V.; Bloom, B.R.; Bajardi, A.C.; Grisso, C.L.; Sieling, P.A.; Alland, D.; Convit, J.; Fan. X.; Hunter, S.W.; P.A.; Alland, D.; Convit, J.; Fan. X.; Hunter, S.W.; Brennan, P.J.; Rea, T.B.; Modlin, R.L. Brennan, P.J.; P.S.; 275-284
#journal A. major T. cell antiqee of Mycobacterium leprae is a 10-kD Reat-shock cognate protein.
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#journal J. Gen. Microbiol. (1989) 135:931-939
#title Cloning and sequence analysis of the 10 kba antigen gene of Mycobacterium tuberculosis.
#across-references MJID:90095443
#accession A37166
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JH5556 *type complete
10K T-cell antigen - Mycobacterium leprae
*formal_name Mycobacterium leprae
30.4m-1992 *sequence_revision 30.4mr1992 *text_change
12.5ep-1997
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#journal Nacleic Acids Res. (1988) 16:9047
#fitle A major antigen from Mycobacterium tuberculosis which homelite and the home product of coxicila furnet.
#cross-references Mycobacterium tuberculosis which homelite home product of coxicila furnet.
#accession S01381
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100.0%; Score 114; DB 2; Length 100
Pest Local Similarity 100.0%; Pred. No. 1.07e-10;
Matches 17; Conservative 0; Mismatches 0; Indels
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**cross-reforences EMBL:X12598: NID:g44351: PID:G581358
NGE A37166
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##residues 'V',2-130 ##label BA2
##cross-references GB:MZ5258: GB:Xl2598
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REFERENCE A70500

Ruthors Cole, S.T., Brosch, R.: Parkhill, J.: Garnier, I.: Clurcher, C.: Harris, D.: Gordon, S.V.: Englmeter, R.: Gas. S.: Barry III, C.E.: Tekala, F.: Hadcock, R.: Bashen, D.: Brown, D.: Chillingworth, T.: Connor, R.: Gavies, R.: Davien, D.: Chillingworth, T.: Connor, R.: Gavies, R.: Davien, D.: Feltwell, T.: Gentles, S.: Hamin, N.: Holioyd, S.: Hornsby, T.: Jagels, K.: Kicch, A.: McLeon, J.: Moule, S.: Murphy, L.: Oliver, S.: Schorne, J.: Quall, R.A.: Rajandream, M.: Rowers, J.: Rutter, S.: Schorn, R.: Skeiger, K.: Skeiger, K.: Skeiger, K.: Skeiger, K.: Skeiger, K.: Skeiger, K.: Skeiger, R.: Shorne, J.: Rutter, S.: Schorne, J.: Rutter, S.: Schorne, J.: Rutter, S.: Schorne, J.: Barrell, B.G.: Taylor, K.: Whitehead, S.: Barrell, B.G.: Schorne, J.: Moule, J.E.: Taylor, K.: Whitehead, S.: Barrell, B.G.: Litter, J.E.: The Complete encome Sequence.
#Accession S02727
##molecule_type DNA
##molecule_type DNA
##residues
1-100 ##label SH1
##cross-references EMBL:X13739; NID:q44571; PIDN:CAA32883.1 #10:q893369
REFERENCE A47292
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Shinnick, T.M.
Proc. and Acad. Sci. J.S.A. (1993) 90:2508-2512
Mycobacterium tuborculosis expresses two chapteronic-60
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P.J.; Voedtline, M.S.; Minden, P.; Hosaliten, K.A.;
B.R.; Modlin, E.
J. Impunol. (1992-148:1835-1840
Immunoreactivity of a 10-Kba antigen of Mycobacterium
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                                                                          Leat shock protein chpA - Mycobacterium leprae chaperonin, 10K; protein B1620_C3_27
#formal_name Mycobacterium leprae
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PID:q809756
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##Cross-references EMBL:U03015; NID:q466931; PIDN:AAC43227.1;
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Smith, D.R.: Robison, K.
submitted to the EMBL Data Library, November 1993
Mycobacterium leprae cosmid B1620.
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*superfamily chaperonin groES
heat shock; molecular chaperone; stress-induced
*length 102 *molecular-weight 10946 *checksum
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##residues 1.103 ##label WEB ##residues ceferences GB.MS977: NID:g154519: PIDN:AAA27313 1: PID:g154520 CLASSIFICATION #superfamily chiquitonin groß SCKMARY #length. 103 #poskednat weight 10742 #chocksur 6552
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J. Mol. Biol. (1987) 194:359-383
The organization and sequence of the genes for ATP synthase
subunits in the cyanobacterium Synechococcus 6301. Support
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J. Bacteriol. (1991) 173-7382-7386
Characterization of the grobb-like genes in Streptomyces
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groES protein - . nechococcus sp. (strain PCC 7942)
*formal_name Sync.thococcus sp.
12-Apr-1991 *sequence_revision 12-Apr-1991 *text_change
26-Aug-1999
heat shock protein 18 · Streptomyces albus
heat shock p: ein groES homolog
*formal_name : reptomyces albus
17-Jul-1992 *sequence_revision 17-Jul-1992 *text_cthange
12-Sep-1997
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Pred. No. 3.24e+08;
3; Mismatches 1
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Best Local Similarity 76.5%;
Matches 13; Conservative
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S07286
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Fiths, T.: Costoposius, G., Radford, A.J.: Bacio, A.: Wood,
Fith.
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#fille Firitoation and characterization of major antioens tree
Mycobacterium Boots culture fillinger
#cross-references MJD54147217
#ancession 780278
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heat shock: molecular chaperone; stress-induced protein
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Pred. No. 2.39e-03;
7; Mismatches 1: Indels
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Pred. No. 3.79e-63;
2: Mismatches 0: Indels
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##residues 2-15,187,17-20 ##label FIF
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S01784
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hest Local Similarity 84.68:
Matches 11; Conservative
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Sest Local Similarity 50.0%;
Matches 8: Conservative
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**cross-references GB:Ll: 82; NID:q293069; PIDN:AAA71991.1; PIU:q29x070
**experimental_source sv. copenhageni
                                                                                                                                                                                                                                                                                                                                  *authors Stirewalt, V.L., Michalowski, C.B.; Luffelhardt, W.; Bolmer
H.J.; Bryant, D.A.
*submission submitted for the EMSI Data Library, July 1995
*description Nucleotide sequence of the cyanelle genome from Sydiathala
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chaperonin stype complete chaperadoxa cyanelle chaperonin großs - Cyanophora paradoxa stormal_name cyanelle Cyanophora paradoxa 30-Apr-1999 stext_chana. 26-Apr-1999
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#length 163 #mclecular-weight 11240 #chenksum 657;
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Best Local Similarity $0.0%; Find, No. 5.976-00;
Matches 8: Conservative Essmatches 1: Indels
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#title Cloning, sequencing, mapping, and transcriptional analysis of the groes. open from Bacillus subtills.
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**experimental_source 168, trpC2
##note this sequence is inconsistent with the nucleotide
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**cross-references GELL0132; NID:a289299; PIDN:AAA22751.1; PID:q289299
*#rote sequence extracted from NCBI backbone (NCBIN:129322,
NCBIP:129323;
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                                                                                                                                                                                                                                                                                                                                                      *authors Schon, U.; Schumann, W. **
#journal J. Bacteriol (1992) 175:2465-2469
*title Molecular clonkny, sequencing, and transcriptional analysis of the große. perco from Bacillus stearchbermophilus.
#cross_references_MuID:93224474
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.cal. shock protein Grofs - Bacillus stearothermophilus
.cal. shock protein Grofs - Bacillus stearothermophilus
?? Apri-1994 *sequence_revision 18-Nov-1994 *text_change
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Schmidt, A.; Schiesswohl, M.; Volker, U.: Hecker, M.;
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*length 94 *molecular-weight 10209 *checksum 8757
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Pred. No. 2.30e-02;
3: Mismatches 3: Indels
                                                      4: Indels
                   Length 96:
                   Score 75; DB 2; Le
Pred. No. 1.47e-02;
2; Mismat hes 4
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Matches 9: Conservative
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Austral A. Doas.wara. N. Muszer, I.; Albertini. A. M. Alloni. G.; A. evedo. V.; Bertelo. M.G.; Bessleres. F. Bolostini. G.; A. evedo. V.; Bertelo. M.G.; Bessleres. E.; Bolostini. A.; Borchert. S.; Boroniler. S.; Boroniler. S.; Boroniler. S.; Boroniler. S.; Brushi. C.V.; Talderli. B.; Capuano. V.; Carter. N. M.; Chois. S.K.; C.; Ini. Tal. Commerton. I.F.; Curmings. N. J.; Britali. R. M.; Chois. S.K.; C.; Ini. Tal. Commerton. I.F.; Curmings. N. J.; Enfich. S.L.; Ermerson. P.T.; Entlan. K. Do.; Errinico. J.; Pabret. C.; Fe raif. E.; Foulger. D.; Fritz. C.; Full. Tal. S. Y.; Glaser. D.; Golfeau, A.; Gallzzi, A.; Galleron. N.; Ghia, S.Y.; Glaser. D.; Golfeau, A.; Haiber. M.; Haibert. M.; Haibert. M.; Haibert. M.; Haibert. M.; Ladydus. C.; Rosono. S.; Haiber. M.; Ladydus. C.; Rosono. S.; Kashara. A.; Haibert. M.; Haibert. M.; Maylan. S.; Haibert. M.; Maylan. S.; Haibert. M.; Meetle. C.; Redigue. C.; Mediau. M.; Klehn. C.; Redigue. C.; Mediau. M.; Klehn. C.; Redigue. C.; Mediau. M.; Meetle. D.; Porvolik. S.; Rumano. M.; Meestl. D.; Meetle. D.; Porvolik. S.; Redigue. C.; Mediau. B.; Schroum. E.; Portor. M.; Reynolis. S.; Schroum. E.; Portor. M.; Reynolis. S.; Schroum. E.; Medler. A.; Yananoto, M.; Wananoto, 
                                                         ##residues 1-94 ##label SCH
##cross-references GB:M84955; NID:q143051; PICN:AAA22530 1: PIU:q143052
##experimental_source MB11
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**cross-references GB:010972; GB:001157; NID:9443377; PIUN:BAA225:8.1;
PID:41023:BS: PIU:94433780
                                                                                                                                                                                                                                                                                                                                Fauthors Tozawa, Y.; Yos.ikawa, H.; Kawamura, F.; Itaya, M.; Takahashi, H. Takahashi, H. Biocci. Biotechiol. Biochem. (1992) 56:1995-24042 Filte Tolation and characterization of the groES and groEL avnes forossine MUD:91119 Subhills Mathurg.
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The complete genome sequence of the Gramipositive bicterium
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                                                                                                                                                                                                                                        sequence extracted from NCBI backbone (NCBIN: 1954-12,
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##residues
##cross-references GB:299107; GB:AL009126; NID:q2632865;
##cross-references FIDN:CAB12421.1; PID:e1182581; PID:q2632915
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Search completed: Mon Jun 19 16:08:09 2000
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                                                        mediates protein folding and rematuration
*superfamily chaperonis quoes
ATP: heat shock: molecular chaperone: Stress-induced protein
*length 94 *molecular-weight 10175 #checksum 7456
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JC5130
Xu, X.: Kobayashi, T.: Kudo, T.
Blosci, Bictechnol. Bicchem. (1996) 60:1633-1636
Molecular cloning and nuclectide sequence of the grott gene from the alkaliphilic Bacilius sp. strain C-i25 and
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Yanaqi, M.; Hiraiwa, H.; Hiraiwa, H.; Kagawa, Y.;
*journal Blochem: Blochys. Res. Commun. (1991) 179:665-572
#fitle Gene structure of heat shock proteins 61kba and 12kba
(Thermophilic of heat shock proteins 61kba and 12kba
#Cross-references MUID:91354309
functional chaperonin includes 14 chains of groEL and 7 of
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Neat Shock process thermophilic bacterium PS-3
Neat Shock 12K protein: hspl0
*formal_name thermophilic bacterium PS-3
%-Sep-1993 *sequence_revision 30-Sep-1993 *text_change
J12 Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSRENCE JU1479, WITT Tano, H.; Bauto, K.; Hayashi, H.; Tano, H.; Hauthors Hamamoto, T.; Kagawa, Y. Hamamoto, T.; Kagawa, Y. Hournal Biochem, Biophys. Res. Commun. (1993) 191:550-557 #tutle Heat shock promoter of thermophilic chaperonin operon. Ecross.refine-ecrs. MUD:93213292
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Pred. No. 2.30e-62;
3: Mismatches 3: Indexs
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the nucleotide sequence is not complete
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**HoleCule_type DNA
**residues :-94
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**molecule_type DNA
**molecule_type DNA
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1.89 **labe; XU2

**roxperimental_source C-125 strain 9724

VT This protein plays a role in protein folding by broding to the complex of an unfolding peptide and GroEL protein
                                                                                                                  ##molecule_type DNA ##label XDA ##residues 1-88 ##label XDA ##residues 1-88 ##label XDA ##residues 1-88 ##label XDA ##residues 1-80 ##label XDA ##label XDA ##label ##
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Acta Microbiol. Sin. (1996) 36;241-249
Phylogeny of molecular chaperone 50 proteins
PC6023
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Matches 8: Communication
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Jun 19 16:07:40 2000: MasPar time 3.67 Seconds 141:095 Million cell updates/sec Inbular output not generated. Run 05:

>US-09-142-524A-8 (1-:7) from US09142524A.pep 114 ! EEYLILSARDVLAVVSK :7 Description: Perfect Score: Sequence:

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

83857 seqs, 30454973 residues

Searched

Database:

swiss-prot38 l:swissprot

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis or the total score - stribution.

Mean 29.618: Variance 37,117; scale 0.798

Statistics:

Check			20			SUMMARIES				
14 100.0 99 1 CHIO_MYCTU 10 KD CHAPERDNIN PRCI 9.22e-14 100.0 99 1 CHIO_MYCTU 10 KD CHAPERDNIN PRCI 9.22e-160.0 99 1 CHIO_MYCTU 10 KD CHAPERDNIN PRCI 9.22e-160.0 100.0 99 1 CHIO_MYCTU 10 KD CHAPERDNIN PRCI 1.94e-170 100.	Result No.	Score	Query	Length		15	Descr	ription		
114 100.0 99 1 CHIQ_MYQLE 10 KD CHAPERONIN PROT 9.22e-		4	100.0			CHIO_MYCTU		•	. ~	.22e-1
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MEDLINE: 89016584.
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"The Mycobacterium tuberculosis BCG-a protein has horology with the
                         P09521;
01:MAR-1989 (Rel. 10, Created)
01:MAR-1989 (Rel. 10, Last sequence update)
15:FEB-2000 (Rel. 39, Last annotation update)
15:FEB-2000 (Rel. 39, Last annotation update)
10 KD CHAPERONIN (PROTEIN CPNIO) (PROTEIN GROES) (BCG-A HEATSHOTK WORDEN OR GROES OR CPNIO OR RV3418C (R MICY78.11)
MODB OR GROES OR CPNIO OR RV3418C (R MICY78.11)
Mycobacterium tuberculosis.
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MEDLINE: 89160258.
Shinnick T.M., Plikaytis B.P., Hyche A.D., van Landingham R.M.,
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Gordon S.V., Elqumeler K., Gas S., Barry C.E. III. Tekala E.,
Gordon S.V., Elqumeler K., Gas S., Barry C.E. III. Tekala E.,
Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bayles R., Davila K., Kredh A., McLean J., Moule S., Murphy L.,
Hornsby T., Jadels K., Kredh A., McLean J., Moule S., Murphy L.,
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01-MAY1992 (Rel. 21. Created)
15-DEC-1998 (Rel. 37. Last sequence update)
15-DEC-1998 (Rel. 37. Last sequence update)
10 KD CHAPERONIN (PROTEIN CPNIO) (PROTEIN GROES) (10 KD ANTIGEN).
MAPB CK SPEES OR CHPA OR B1620_C3_227 OR B229_C3_247.
Mycobacterium leprae.
Bacteria: Firm.cutes. Actinobacteria; Actinobacteridae;
Actinomycetales: Corynebacterineae: Mycobacteriacee; Mycobacteriam.
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-!- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SCHERESHS
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-!- SUBLIARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
Mehra V.I., Bloom B.R., Bajardi A.C., Grisso A.C., Sieling P.A., Alland D., Convit J., Fan X., Hunter S.W., Brennan P.J., Res T.H., Modlin R.L., Tan Z., Horter S.W., Brennan P.J., Res T.H., Andlin R.L., Tell antigen of Mycobacterium leprae is a 10-kD Best Sinck Cognate protein."; Exp. Med. 175:275-284(1992).
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15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (10 KD ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                    Thole J.E.R.:
"Mycobacteria contain two groß! genes: The second Mycobacter: unleprae groß! gene is arranged in an operon with großs."

Mod. Microbiol. 6:1995-2007(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ġ
                                                                                                                                                                                                                                                                                                           Hermans P.W.
                                                                                                                                                                                                                                       SECUENCE FROM N.A.
MEDILINE, 2374850.
MEDILINE, BERBİLE S., USJALICA V. MIKO I.L., Hermans P.W
Van, Scolingen D., Drijthout J., Schoeningh R., Janson A.A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114: DB 1: Length 99:
Pred. No. 9.22e-13;
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/Genbank/UDBS databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 AA; 10669 MW; 602BBB9833F7FDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: XS9413: -; NOT_ANNOTATED_CDS.
EMBL: 0206015: AAGAT31...1. NOT_ARNOTATED_CDS.
EMBL: 0206015: AAGAT31...1. -
PIR: JR0556: JR0556.
PIR: 255180: 825180.
PGB: 12.07A.9.7. CHARPENINIL.
PRINTS: PRIO257: CHARPENINIL.
PRINTS: PRIO257: CHARPENINIL.
PRINTS: PRIO257: CHARPENINIL.
PRINTS: PRIO257: CHARPENINIL.
PRINTS: PRIO256: CPRIO5: 3.
Chapelone: Antigen: Heat shock: 30.91010...
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Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leprae.";
Science 271:203-207(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 EEYLILSARDVLAVVSK 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 96138402.
Mande S.C., Mehra N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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CH10_MYCAV
O86017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .:
C
                                                                                                                                                             SECTION N.A. STRAIN-485 TYPE 21: SPECIES G.: Crefici G.: Crefici G.: Species-M.N.UWH: STRAIN-485 TYPE 21: Species G.: Sequence of the GroßL operon of Mycobacterium avium comprising the GroßL operon of Mycobacterium avium comprising the gene encoding the cpn10 protein and a portion of the gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duchene A.M., Kieser H.M., Hopwood D.A., Thompson C.J., Mazodier P., "Characterization of two groEL genes in Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-M PARATUBERCULOSIS, M.AVIDM: STRAIN-ATCC 19696, ATCC 25291; Cobb A.J., Frothingham, R.:

The Cobb A.J., Frothingham, R.:

The Santigens of Mycobacterium and Mycobacterium paratuberculosis.

Paratuberculosis.

10.00(1989)

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                           Mycobacterium avium, and Mycobacterium paratubercuiosis.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinorycetales: Corynebacteringae: Mycobacteriaceae: Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICSTRC STANDARD: PRT; 102 AA.
P40172:
P40172:
P40172:
C1-FEB-1995 (Rel. 31, Last sequence update)
C1-FEB-1995 (Rel. 31, Last sequence update)
10 ED CHAPERONIN (PROTEIN CPNIC) (PROTEIN GROES).
GROES CR SC64.39:
Steptomyces coelicolor, and Streptomyces lividans.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae: Actinobacteriaes: Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 9.22e-13;
C. Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6B0A4497405310C2 CRC64:
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SPECIES-S.COELICOLOR: STRAIN-A3(2) / J1501;
MEDLINE; 94299177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
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PRINTS: PR02297; CHAPERONINIC.
PROSITE: PS00681; CHAPERONINS_CPN10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaperone: Antigen: Heat shock.
INII_MET 0 0 9 BY
SECUENCE 99 AA: 10617 MW: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AF079544: AAC31921.1: -. EMBL: AF071829: AAD23277.1; -. EMBL: AF071828; AAD23275.1; -.
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Best Local Similarity 100.0%;
Matches 17; Conservative
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SEÇUENCE FROM N.A.
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 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
SPECIES-S.COELICOLOR; STRAIN-A3(2); Saunders D., Harris D., Parkhill J., Barrell B.G., Rajandream M. Submitted (AUG-1998) to the EWBL/GenBank/DDBJ databases.
 ö
 SECUENCE FROM N.A.
SPECIES-S.LIVIDANS:
MEDLINE; 98048481.
de Loop P., Marco S., Isiegas G., Marina A., Carrascosa J.,
Mellado R.P.;
 92.1%: Score 165: DB 1: Length 103: 82.4%: Pred: No. 1.94e-10: Artive 2: Misratches 1: Indels attive
 Stroptonyoes albus G.
Banteria: Firmicutes: Actinobacteria: Actinobacteridae:
 102 AA: 10946 MW: 6DF9FA68014AC8CC CRC64:
 MEDLINE: 92041639.
Mazodier P., Guglielmi S., Davies J., Thompson C.J.
 Cl.APR-1993 (Rel. 25, Created)
Cl.APR-1993 (Rel. 25, Last Sequence undate)
Cl.APR-1995 (Rel. 43, Last sequence undate)
U. EBF-1995 (Rel. 43, Last entotation grant)
U. MC CHAFEPONIN (PRIEIN THUL) (FPC CHAFEPONIN (PRIEIN THUL)
 102 AA
 EMBL: X75206; CAA53018.1; ...
EMBL: ALG31317; CAA20417.1; ...
EMBL: X9590; CAA65224.1; ...
PIR: X37565; S37565.
PRINTS; PRO0297; CHAPERONING.
PROSITE: PS00681; CHAPERONING.
 : RT :
 Best Local Similarity 82.48;
Matches 14; Conservative
 86 EEYLVLSARDVLAIVEK 102
 STANDARD;
 PFAM; PF00166; cpn10; 1.
 SEQUENCE FROM N.A.
 CH10_STRAL
200769:
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CONFLICT
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 Matches
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 ö
 "Molecular cinning, expression, and characterization of chaperonin-50 and chaperonin-10 from a thermophilic balterium, Thermus thermophilus HBB.";
 Gaps
 ..
C
 MEDLINE: 96064154.
Amada K., Yonda M., Odaka M., Endo I., Ishii M., Taguchi H.,
Yoshida M.,
 Thermus aquatious (subsp. thermophilus).
Bacteria: Thermus/Deinococcus group: Thermus group: Thermus.
 Lenath 102:
 udery Maich
Hest Local Similarity 76.5%: Pred. No. 6.236-10:
Matches 13: Conservative 3: Mismatches 1: Indels
 Erbezoik M., Joachimiak A.:
Submitted (JEC-1995) to the EMBL/GenBack/DDBJ databdses.
 102 AA: 10987 MW: 5788F55954CFB283 CRC54:
 CHICHETH STANDARD, PRT: 100 AA. P45747; GE0017: 01-NOV-1995 (Rel. 32, Created) 01-NOV-1996 (Rel. 33, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 10 KC CHAPERONIN (PROTEIN CPNIC) (PROTEIN GROES).
 -> K (IN REF. 3).
 or send an email to license lish-sib.ch).
 CHAPERONINS_CPN10; 1.
 EMBL: M76657; ARA26752.1; -.
PRINTS: PR00297; CHAPERONINIO.
PROSITE: PS00601; CHAPERONINIS_CPNIC;
Chaperone.
 EMBL: C45880; BAAC8298.1; -.
EMBL: U29483; AAA83440.1; -
PIR: B35313, B39313,
PRINTS: PR00297; CHAPERCNINIO.
PROSITE: PS03681; CHAPERONINS_
 Biochem. 118:347-354(1995)
 85 HEYLVLSAREVLATIEK 102
 1 EEYLLISAROVLAVVSK 17
 PFAM: PF00156; cpn10: 1.
Chaperone.
INIT_MET
CONFLICT 19 19
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SECUENCE OF 1-23
 SIRAIN=HB8
 STRAIN-HBB
 SEQUENCE
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 Segre
 Synechococcus sp. (strain Pr. 1942) (Anacystis nidulans R2)
Bacteria: Cyanobacteria: Chima incrales: Synechococcus.
 Length 1000
 Score But Os 1: Length 1: v. gred. No. 2:13e-04: 7: Mismatches 1: Indels
 ore 80% DB 1% Length 100% of No. 2.13e-04; Mismatches 1% Indels
 ... SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
13EE -> APRRI (IN REF. 2)
452F3DD9CCCBC0FA CRC64)
 89 - £7195F515952E CPCh4,
 Synechococcus sp. (strain FG: 6301).
Bacteria: Cyanobacteria: Chr. coccales: Synechococcus.
 01-AUG-1988 (Rel. 08, Created)
C1-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1996 (Rel. 33, Last amoutation update)
10 KD CHAPERONIN (PROTEIN PROTE)
 .ence ipdate)
tation update)
) (PRUTEIN GROES).
 PIR: A36721; A36721;
PRINTS: PRG0297; CHAPERONINI:
PROSITE: PSG0681; CHAPERONIN: CPN:0; 1;
 01-A06-1991 (Rel. 19, Create: 01-A06-1991 (Rel. 19, Last s. C. FEB-1996 (Rel. 33, Last s. 10 M.D. CHAPERONIN (PROTEIN CI
 10865 MW
 103 AB: 10742 MG
 EMBL; M58751; AAA27313.1; -
 Query Match
Best Local Similarity 50.0%:
 70.2%;
|larity 73.3%;
|Conservative
 Conservative
 88 DDYVLLSEKDILAVVA 103
 | EEYLILSARDVLAVVS 16
 SIANDARD;
 STANDARD:
 PFAM; PF00166; cpn10; 1.
 85 EEYVILSERDLLAVL 99
83
100 AA:
 Local Similarity
nes 11: Conserv
 SEQUENCE FROM N.A. MEDLINE; 87311713.
 CH10_SYNP6
PC7889;
 CH10_SYNP7
P22880;
 Chaperone.
SEQUENCE
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 CHO_MYCBO STANDARD: FRI. 99 AA.
P15020.
P15020.
O1-APR.1990 (Rol. 14, Created)
O1-ACG.1991 (Rol. 19, Last sequence update)
15-FBR-2000 (Rol. 39, Last annotation update)
10 KB CHAPERONIN (PROTEIN CPNID) (PROTEIN GROES) (IMMUNOSENIC PRUTEIN MPS7).
 "The organization and sequence of the genes for ATP synthase subunits in the cyanobacterium Synethococcus 6301. Support for an endosymbiotic origin of chloroplasts.";

J. Mo.. Biol. 194:359-383(1987).
 -:- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES THE ATPASE ACTIVITY OF THE LATTER.
-:- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING
 -!- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MO-ATP AND SUPPRESSES THE ATPASE ACTIVITY OF THE LATTER.
-!- SCBUNIT: HEPTAMER OF 7 SCBUNITS ARRANGED IN A RING (BY SIMILAPITY).
 Gaps
 Actinomycetales: Corynebacterineae: Mycobacteriaceae: Mycobacterium
 MEDLINE: 8936672.

COOKSON M.J., Baird P.N., Hall L.M., Coates A.R.M.;
Chookson for two unknown reading frames in Synechococous 6301
as homologues of the 10k and 65k antigen genes of Mycobacterium
tubercilosis and related heat shock genes in E. coll and Coxielia
 "Imminogenic protein MPB57 from Mycobacterium bovis BCG: molecular cloning, nucleotide sequence and expression."; FEBS Lett. 240:115-117(1988).
 ö
 MEDLINE: 89052868.
Yamaguchi R., Matsuo K., Yamazaki A., Nagai S., Terasaka K.,
 Length 103;
 Score 80: DB 1: Length 103.
Pred. No. 2.13e-04;
7: Mismatches 1: Indels
 (BY SIMILARITY).
-!- SIMILARITY: BELCNGS TO THE GROES CHAPERONIN FAMILY.
 Mycobacterium bovis.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 -:- SIMILARITY: BELCNGS TO THE GROES CHAPERONIN FAMILY.
 103 AA; 10811 MW; FFEDIDESF515952F CRC54;
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-20
 PRINTS: PR00297: CHAPERONIN10.
PROSITE: PS00681: CHAPERONINS_CPN10: 1.
 Nucleic Acids Res. 17:6392-5392(1989).
 EMBL. X05925; CAA29361.1; -.
 Query Natch
Best Local Similarity 50.0%;
Matches 8: Conservative
 88 DDYVLLSEKDILAVVA 103
 SIMILARITY TO CHAPERCNINS
 Cozens A.L., Walker J.E.;
 PFAM: PF00166; cpm10; 1.
Chaperone.
 PIR: S10836; BVYCGS
 MOPS OR GROES
 STRAIN-BCG
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connected entities requires a license itrement (See http://www.isp-sib.ch/ancoince/or send an email to licenseisb-sib.ch).
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 Tanaka N., Hiyama T., Nakamoto H.;

"Cloning, characterization and functional analysis of groess openor."

"Cloning, characterization and functional analysis of groess. from thermophilic cyanobacterizan Syndechococcus vulcanus.";

Biochim. Biophys. Acta 1345,335-446(1997).

"THE ATPASE ACTIVITY OF THE LATTER.
"THE ATPASE ACTIVITY OF THE LATTER.
"SUGUNIT: HEPTAMER OF 7 SUBHNITS ARRANGED IN A BIN3.
"EN SIMILARITY: BELLANDE OF HE CHARLES HARBER OF SEMILARITY."
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O
 Score 79: DB 1: Length 99:
Pred. No. 3.58e-04:
"...marches 0: Indels
 Length 102;
 1: Indels
 INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 1C2 AA: 10783 MW; B7CC3617298BFF67 CRC64;
 Bacteria: Cyanobacteria: Chroscoccales: Synechococcus
 99 AA: 10819 MW: IDCD5E2199447AF7 CRC64:
 15-DEC-1998 (Rel. 37, Created; IS-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 10-DE CHAPERONIN (PROTEIN CPNIC) (PROTEIN GROES).
 Score 78; DB 1; Le
Pred. No. 5.00e-04;
 7; Mismatches
 PRINTS: PRO0297; CHAPERONING.
PROSITE: PSC0681; CHAPERONINS_CPN16: 1.
 PIR; S01784; BVMY7B,
PRINTS: PR00297; CHAPERONIN.0.
PROSITE; PS00681; CHAPERONINS_CPN10;
 PFAM: PFC0166; cpn10: 1.
Chaperone, Antigen: Heat shock.
 EMBL; X13970; CAA32149.1; -. EMBL; M35389; AAA25365.1; -
 Query Match
Best Local Similarity 84.5%.
And III Conservative
 Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative
 69.3%;
84.6%;
 EMBL; D78139; BAA23816.1:
 87 EDYVLLSEKDILAIVG 102
 STANDARD;
 1 EEYLILSARDVLAVVS 16
 Synechococcus vulcanus.
 PFAM; PFG0166; cpn10;
 83 EEYLILSARDVVG 95
 1 EEYLILSARDVLA 13
 SEQUENCE FROM N.A.
 98094212
 CH10_SYNVU
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 STRAIN LBSSS / PRINGSBERN:
Stliewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.C.
 CHILLEBIN STANDER: FE DA. CHILL STANDER: F
 Ballard S.A., Segers R.P., Bloumick-Pluym N.M., Fyfe J.A.M., Fairc S., Adler B., Molecular analysis of the hsp (grob) operon of Leptospira intercedars servar copenhagen. (1)
 Bukaryota: Glauchystophyceae, Cyanophoraceae, Cyanophora
 Score 78: DB 1: Denuth 103: Pred. No. 6:00e-04: 7: Assmatches 1: Indels
 11240 MW: PF768479C0A90520 FR164;
 Leptospira interrogans.
Bacteria: Spirochaetales: Leptospiraceae: Leptospira
 LT ...
03776...
03776...
01-NV-1997 (Rel. 35, Created)
01-NV-1997 (Rel. 35, Last sequence update)
01-NV-1997 (Rel. 35, Last sequence update)
01-NV-1997 (Rel. 35, Last annomation update)
0 KO CRAPPORTIN (PROTEIN OPNIO) (PROTEIN GHOES)
0 KO CRAPPORTIN (PROTEIN GHOES)
0 KO CRAPPORTIN (PROTEIN GHOES)
 EMBL: 030821: AAA8173.1: -:
EMBL: 030821: AAA81293.1: -:
PRINTS: PROUG97: CHAPERONING.
PROSTIE: PSOC681: CHAPERONING.
 SEÇUENCE FROM N.A.
STRAIN-SEROVAR COPENHAGENI / WIJNBERG.
 58.482
 SEQUENCE FROM N.A.
STRAIN-SEROVAR LAI / HY-1;
Kim M.J., Ahd B.Y.;
 Rest Local Similarity 50.0%:
Matches 8, Conservative
 88 EEYVIISEKDILAIIA 103
 TEEYLIUSARDVIAVYS 16
 PROSITE: PS00681: CHAPPERA: PFAM: PF00166: cpn10:
 Chaperone, Cyanalie.
SECTENCE 103 AA:
 93323752.
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Schmidt A. Schlosskadt M. Variket N. Gerket M. Schmann E. Colone of A. Colone and Schmidt M. Schmann E. C. Colone and Control of the Schmidt M. "Clouing and characterization of the groSSL operon from Bacillus subtille ".
 MEDLINL, 93129852.

Tozawa Y., Yoshkawa H., Kaw Tura F., Itaya M., Takahashi H.:
"Isolation and characterization of the groES and groEL genes of Bacillus subtills maburg."

56.1995-2002(1992).
 STRAIN*168 / MARBURG;
MEDLINE; 97246038.
Sadaie Y., Yata K., Fujita M., Sadai H., Itaya M., Kasahara Y.
 4: 1m3: 1s
 Match 66.7%; Score 76; DE 1: Length 95; Local Similarity 62.5%; Pred. No. 1.67e-03; es 10; Conservative 2; Mismatches 4; Indils es
 -62850807908FD467 CR0543
 Bacillus subtilis.
Bacteria: Firmicutes: Bacillus/Clostridium
 group: Bacillus
 EMBL: 114682: AAA71991.: -
EMBL: AF032910: AAB96964.1: -
PIR: S34937: S34937: S38937: PRINCES PRONOSTE: F600287: CHAPERONING.
PROSITE: F60068: CPHO PRONOSTE: F600166: CPHO PRONOSTE: CPHO PRONOSTE: F600166: CPHO PRONOSTE: CPHO PRONOSTE: F600166: C
 Bacteriol, 174:3981-3592(1992).
 10562 MW:
 81 EYLIIRESDILAVVKK 96
 2 EYLILSARDVLAVVSK 17
 Bacillus/Staphylococcus
 SEQUENCE FROM N.A.
STRAIN 168 / MARBURG:
 STRAIN-168:
MEDLINE: 92283753.
Li M., Wong S.L.;
 96 AA:
 SECUENCE FROM N.A.
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 "Heat shock promoter of thermophilic chaperonin operon.":
Blochem. Blophys. Res. Comm : 191:550-557(1993).
-:- FUNCTION: BINDS TO CPN6. IN THE PRESENCE OF MG-ATP AND SUPPRESSES
THE AIPASE ACTIVITY OF THE LATTER.
 SECURNAL 9194309.
MEDIANE, 9194309.
Tamada H., Ohta I., Humanoto I., OtawatarHumanoto Y., Yanaji M.,
Hiralwa H., Hirata H., Kapawa Y.,
Hiralwa H., Hirata H., Kapawa Y.,
"Gene structure of heat shock proteins 61kDa and 12kDa (thermophilic chaperonias) of thermophilic bacterium PS3.":
Biochem. Blophys. Res. Commun. 179:565-571(1991).
 01-MAY-1992 (Rel. 22, C 'ed)
01-MAY-1992 (Rel. 22, La sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
10 KD CHAPERONIN (PROTEIN CPN:0) (PROTEIN GROES) (HEAT SHOCK 12 KL
 MEDLINE: 93213292.
Ohta T., Honda K., Saito K., Hayashi H., Tano H., Hamaroto i.,
 Score 75: DB 1: Length 94: Pred. No. 2.77e-03:
 -! - SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 -:- SUBCNIT: HEPTAMER OF 7 SUBCNITS ARRANGED IN A RING (BY SIMILARITY).
 94 AA; 10241 MW; 88732A0C42114821 CRC64;
 Bacteria, Firmicutes, Bacillus/Clostridium group:
Bacillus/Staphylococcus gr. 900 Bacillus.
 94 AA
 Bacillus PS3 (Thermophilic bacterium PS-3)
 PRINTS: PRO0297; CHAPERONINIO.
PROSITE: PSO0681; CHAPERONINS_CPN10; 1.
PFAM; PF00166; cpn1C; 1.
 PRT:
 Match 65.8%; Local Similarity 60.0%; nes 9; Conservative
 EMBL; L10132; AAA22751.1: -
 STANDARD:
 8C EYLILRESDILAVIG 94
 2 EYLILSARDVLAVVS 16
 Chaperone, Heat shock SEQUENCE 94 AA; 10
 SEQUENCE FROM N.A.
93224474
 CH10_BACP3
P26210;
 Kadawa Y.;
 PROTEIN).
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 MEDINE: 9634562,
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MEDINE: 9634562,
Grammon P., Schroeder K., Schmid R., Marahiel M.A.;
Grammon P., Schroeder K., Schmid R., Marahiel M.A.;
J. Bacteriol. 178:4612:4619(1996).
J. Bacteriol. 178:4612:4619(1996).
J. FUNCTION: BINDS TG CPNGO IN THE PRESENCE OF MG-ATP AND SUPPRESSES
THE ATPASE ACTIVITY OF THE LATTER.
J. SCHONIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING
 STRAIN-168 / MARBURG:
MEDLINE: 98116660.
Rasahara Y... Nakai S.. Coasawara N.. Yata K.. Sadaie Y.;
"Sequence analysis of the groESL-cuta region of the Bacilius subtilis
genome. containing the restriction/modification system genes.";
DNA Res. 4:335-339(1997).
 Gaps
 "Nucleotide sequence and analysis of the phoB-rrnE-groESL region of the Bacillus subtilis chromosome.";
The Bacillus subtilis chromosome.";
Microbiology 143:1861-1866(1997).
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 Score 75: DB 1: Length 94: Pred. No. 2.77e-03: 3: Mismatches 3: Indexs
 (BY SIMILARITY).
--- INDUCTION: BY HEAT SHOCK.
--- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 10176 MW: B25C835957B16251 03064:
 007270:
01-007-1994 (Rel. 30, Created)
01-007-1994 (Rel. 30, Last sequence update)
01-007-1996 (Rel. 33, Last annotation update)
10 KD CHAPERONIN (PROIEIN CPNIO) (PROTEIN GROES).
 Bacteria: Firmicutes; Bacillus/Clostridium group:
Bacillus/Staphylococcus group: Bacillus.
 94 AA
 EMBL: M8132: AAA2502.1: ...
EMBL: D10972: BAA27218.1: ...
EMBL: D98802: BAA1725.1: ALT_INIT.
EMBL: ABC07637: BAA27246.1: ALT_INIT.
EMBL: A96907: CAB14421.1: ALT_INIT.
PIR: A41884: A41884.
PIR: JC1771: JC1371.
SUBTILIS: P800297: CHAPERONINS_CPNIO: 1.
PROSTIE: P800597: CHAPERONINS_CPNIO: 1.
 Bacillus stearothermophilus.
 EMBL: M84965; AAA22530.1: -.
 query Match
Best Local Similarity 60.0%;
 Conservative
 SEQUENCE OF 5-94 FROM N.A.
 STANCARD;
 PFAM: PF00166; cpn10: 1.
Chaperone: Heat shock
 80 EYLILRESDILAVIG 94
 2 SYLILSARDVLAVVS 16
 SEQUENCE FROM N.A. STRAIN=NUB36;
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EMBL: S57424: CAB31564.1: ALT_SEQ.
PRIS. JQ1194: JQ1194.
PRIS. JQ1197: CHAPERONINIO.
PROSITE: PS00581: CHAPERONINIO.
CHAPECOITE: PS00581: CHAPERONINS_CPNIC: 1.
Chaperone.
SEQUENCE: 94 AA; 10340 MM: 2A9A4954AE0B457C CRC64:
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Release 1.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburch, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Non Jun 19 16:87:11 2000: MasPar time B.85 Seconds 133:146 Million cell updates/sec Ring on:

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Minimum Match 0% Listing first 45 summaries Post-processing:

225878 seqs. 69334122 residues

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sptremb112 Database:

issp\_archea\_z:sp\_bacteria\_3:sp\_fungi\_4:sp\_human\_s:sp\_invertebrate\_6:sp\_mammal\_7:sp\_mhc\_8:sp\_organelle\_9:sp\_pinge\_10:sp\_plant\_il:sp\_rodent\_12:sp\_unclass:fied\_il:sp\_vertebrate\_14:sp\_vi\_us\_

Mean 28.205; Variance 39.500; scale 0.713 Statistics:

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|          |                                  | ALIGNMENTS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |      |             |                |                                     |           |
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| 5 130-00 | HEMCLYSIN.<br>THYMHOYTAND KINASE | m v<br>von<br>oor                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 10 C | 3.5 114     | 61<br>51<br>51 | so or                               |           |
|          | HYPOTHETICAL 44.8 KD P           | រោ<br>ក                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |      | ₩.          | 2 5            | 7                                   |           |
|          | X-LIKE 1 PROTEIN.                | £00.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>1 |      | .3 302      | e<br>س         | 9                                   |           |
|          | PUTALIVE ALCOHOL DEHYS           | 7:34                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |      | .3 62       | 3 5            | Ś                                   |           |
|          | NEGATIVE ALIPHATIC AMI           | 0.4380                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      | £.          | 3              | 77                                  |           |
|          | ADH-UBIQUINONE                   | 60226                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      | .3 33       | 3 5            | Ę                                   |           |
|          | 32 KDA-CELL WALL SYMBI           | 042628                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      | .3 25       | 3 5            | 7                                   |           |
|          | 10 KD CHAPERONIN (PROT           | 051831                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      | m.          | 3              |                                     |           |
|          | IMILAR TO GROE                   | 066221                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      | .a          | 3 5            | 0                                   |           |
|          | IMILAR TO GROE                   | 74.6227                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |      | . s         | 3 5            | S.                                  |           |
|          | IAPERON                          | 268308                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ~    | 5           | 5              | 8                                   |           |
|          | ROES (FRAGMEN:)                  | .5.587                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      |             | e,             | 7                                   |           |
|          | YPOTHETICAL 17.8 KL              | 13.3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |      | .0 15       | 5              | 9                                   |           |
|          | IMILAR TO GRUES PROT             | -191                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |      | .0          | 5 5            | S                                   |           |
|          | IMILAR TO GROES PROT             | -197                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |      | .0          | 5 5            | 4                                   |           |
|          | IMILAR TO GROES PROT             | . 209                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      | 0.          | 5 5            | 3                                   |           |
|          | MILAR TO                         | 65213                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      | .0          | 5 5            | 7                                   |           |
|          | IMILAR TO GROES PROT             | 056207                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |      | 0.          | 5 5            | 1                                   |           |
|          |                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |      |             |                |                                     |           |

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SEQUENCE FROM N.A.
STRAIN-485 TYPE 21.
CREIT W. PIETROBONO R., FAILURINI ELL ORREFICI G.:
"Sequence of the Groest operation of Mycobacterium avium compilising the gene encoding the conformation of the general process.
 SECTION ERGY, N.A.
STELLES AND PARTIDENCOLOSIS, STAINHAID THEFFE, ALLY 1914 FOR THORMAN AND THE STAINHAID THE STORES AND THEFFE STAINHAID THE STAINHAID AND THEFFE STAINHAID AND THEFFE STAINHAID THE STAINHAID THE PRESENCE OF MG-AIP AND SUPPRESS THE AIPASE ACTIVITY OF THE LATTER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae: Mycobacterium
 Ouery Match 100.0%; score 114; DB 2; Length 130; Best Local Similarity 100.0%; Pred, No. 2.76e-11; Matches 17; Conservative 0; Mismatches 0; Indels
 GROES.
Mycobacterium avium, and Mycobacterium paratuberculosis.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
 01-NOV-1999 (TrEMBLE). 08. Last Sequence update)
01-NOV-1999 (TrEMBLE). 12. Last annotation update)
10 KD CHAPERONIN (PRCTEIN CPNIO) (PRCTEIN GRUES).
 0C4954DA CRC32;
 EMBL: AF079544: AAC31921.1; EMBL: AF079544: AAC31921.1; EMBL: AF071829: AAD23277.1; EMBL: AF071829: AAD23277.1; EMBL: AF071829: AAD23276.1; PROSTITE: PS00681: CHAPERONINS_CPN10: 1: PFAM: PF00166: Cpn10: 1. PFNTS: PF00297: CHAPERON N10. Chaperrone: Heat shock: SEQUENCE 100 AA: 10748 M: 0C49545A CI
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STRAIN-LH212;
 Chaperone.
 Query Match
 Query Match
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068323;
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 Best Loca
Matches
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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-NKBGO91660:

MEDLINE, 99295590

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MEDLINE, 99295590

MEDLINE, STRAIN-NKBGO91660:

"UV-A-induced expression of Groel in the UV-A-rosistant marine
of anobacterium. Scriitatoria sp. NKBG 091600.";

Microbiology 145:07-060:

"I-FUNCTION BIANS TO CPN60 IN THE PRESENCE OF NG-AIP AND SUPPRESS

"I-FUNCTION BIANS TO CPN60 IN THE PRESENCE OF NG-AIP AND SUPPRESS

"I-FUNCTION BIANS TO THE LATTER (BY SIMILARITY)

"I-SIMILARITY"

 WIVE MOBANASHIES, KUDG T.:
"MOLECULAR CLORING and BUCLEOLIDE Sequence of the groEL gene from the alkaliphilic Bacillus sp. strain C.125 and reactivation of thermally inactivated alpha-glicosidase by recombinant GroEL.":
Blosci. Blotechol. Blockem. 60:1637-1636(1996).

EMBL: D556:0; BAA09493.:-..
 Gaps
 Gaps
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 Score 76: DR 2: Length 103;
Pred. No. 8:15e-03;
3: Mismatches 2: Indels
 Score 73: DB 2: Length 88;
Pred. No. 3.27e-02;
4; Mismatches 5: Indels
 Oscillatoria sp. NKBG091600.
Bacteria, Cyanobacteria: Oscillatoriales: Oscillatoria
 Last sequence update)
Last annotation update)
 O. NOV-1999 (TrEMBLFG). 12. Created; O. NOV-1999 (TrEMBLFG). 12. Last sequence update) 01-NOV-1999 (TrEMBLFG). 12. Last annotation update) 10 KB (HAPEKNIK (PRIFIN CPNIG) (PROTEIN GROES).
 Bacteria: Firmingres: Pacilius/Clostridiom group
 103 AA: 10845 MW: 77E0DA0F CRC32.
 88 AA; 9580 MW; 30000528 CRC32;
 103 AA
 88 AA
 Bacillus/Staphylococcus ercip/ Becillus
 053304:
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-MAY-1999 (TrEMBLrel. 10, Last and
GROES (FRAMENT).
Bacillis Sp.
 PR
 STRAIN-C-125;
MEDLINE: 97141316.
XU Y., KOBAYASHI E., KUDG T.:
 query Match
Hest Local Similarity 66.7%;
Matches 10; Conservative
 cuery Match
Mest Local Similarity 53.3%;
Matches 8; Conservative
84 EEYLILSARDVLAVVSK 100
 | FEYLLSARDVLAVSK 17
 SEYVLLSXXDILAVV 102
 PRELIMINARY
 1 SEYLILSARDVLAVV 15
 PRELIMINARY
 74 EYLILRESDILATIG 88
 SEQUENCE FROM N.A.
 Chaperone.
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 THORDLESDOTTIR E.T.T., MACKMAN V.M., BUINDAL T.,
THORDLESDOTTIR E.T.T., MACKMAN V.M., BUINDAL T.,
THORBLARNAROOTTIR S.H., PALEBOITER A., HAUKSUCITIR H.,
THORBLARNOOTTIR S., EGGERTSSON G.
"Heat shock in Rhodothermus marinus: Cloning and sequence analysis of the groesl, dnak and dnaJ genes."

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

HE ATRACE ACTIVITY OF THE LATTER OF MG-ATP AND SUPPRESS THE ATRACE ACTIVITY OF THE LATTER (BY SIMILARITY).
 Gaps
 Lacrobacilius helveticus.
Bactelia: Elmmiculvs: Bacilius/Clustridyum group: Lachobaciliaceus:
 60
 SNGABENI J.R., OBERG C.J., WEI L.;
SUBTILLED (OCT.1997) to the EMBL/GenBark/CDBJ databases.
SUBTILLED (OCT.1997) to the EMBL/GenBark/CDBJ databases.
I- FUNCTION: BINDS TO CDMG. IN THE PRESENCE OF MG-AIP AND STAFF APPASE ACTIVITY OF THE LATTER (BY SIMILARITY).
I- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING (BY SIMILARITY).
I- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
EMBL. AF011929: AAC29003.1:
PROSITE: PS00682: CHAPERONINS_CPN10. 1.
PROSITE: CPN10: 1.
 'Match
Local Similarity 45.7%; i ed. No. 1.27e-01;
tes 7; Conservative 5; Misratches 3; Indels
 / Match 59.6%; Score 68: DB 2: Length 94; Local Similarity 50.0%; Pred. No. 3.10e-01; nes __7; Conservative _4; Mismatches _3; Indels
 Bacteria: Cytophagales: Rhop thermus group: Abodothernus
 SIMILARITY).

-1. SIMILARITY).

-1. SIMILARITY: BELONGS TO THE GRAES CHAPERAIN FAMILY.

BENELL AF145525.

PROSITE: PS00681: CHAPERONIUS_CPNIO. 1.

Heat Shock: Chaperone.

Fromience 100 Aa: 11089 HW E456CE99 CRC22.
 01-NOV-1999 (TrEMBLrel. 12, Created)
CL-NOV-1999 (TrEMBLrel. 12, Last sequence update)
CL-NOV-1999 (TrEMBLrel. 12, Last annotation update)
IO KD CHAPERONIN (PROTEIN C: 10) (PROTEIN GROES).
GROES.
 01-AUG-1998 (IrEMBLrel, 07, Greated)
01-AUG-1998 (IrEMBLrel, 07, Last sequence update)
01-NOV-1999 (TEMBLrel, 12, Last andotation update)
10 KD CHAPERONIN (PROTEIN GRNID) (PROTEIN GROES).
GROES.
 94 AA: 10208 MW; 7505B102 CRC32;
 4. AA
100 AA
 PRT :
 PRELIMINARY:
PRELIMINARY;
 82 EEYLIMRETDILGII 95
 79 EKYLVLHEKDILAI 92
| ! .: | :|:| :
 Rhodothermus marinus
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Lactobacillus.
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Sans

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Indels

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Pred. No. 4.81e-01;
3; Mismatches 2;
 Xenopus laevis (African clawed frog).
 01-MAY-1999 (TrEMBirel, 10, Created)
 PRT;
 PR3.
 Match
Leal Similarity 69.2%:
es 9; Conservative
 Query Match
Best Local Similarity 69.2%:
Matches 9; Conservative
Best Local Similarity 61.5%;
Matches 8; Conservative
 PRELIMINARY;
 PRELIMINARY;
 248 ILLARDVMVVVSR 260
 251 ILDARDVMVVSR 263
 304
 83 YLVMSEDEVLAVV 95
 3 YLILSARDVLAVV 15
 5 ILSARDVLAVVSK
 11 .11: :.1:
5 ILSARDVLAVVSK
 SEQUENCE FROM N.A.
 SEQUENCE
 Query Match
 Xenopus.
 LI 8
C9W634
C9W634;
 Xenopus.
 LT 10
094889
094889;
 Matches
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 MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
The complete genome of the hypertherrophilic bacterium Aquifex
aeclicus.
 STRAIN-VES.
SERENT G. WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GEARMA D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHCRI J.M., OLSON G.J., SWANSON R.V.;
SUDMILLED (JUL.1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AE000777; AAC07898.1; -
PERM: PF00166; cpn10; ..
PRINTS; PR02297; CHAPERONIN10.
SEQUENCE 122 AA; 13639 MW: A4227AAB CRC32;
 Gaps
 Bacteria: Firmicutes: Bacilus/Clostridium group: Lactobacillaceae:
Lactobacillus:
 0:
 58.8%; Score 57; DB 2; Length 122;
 Score 67: DB 2: Length 93: Pred. No. 4.81e-01: 7: Mismatches 2: Indels
 032846:
01-JAN-1998 (TEMBLERL 05, Greated)
01-JAN-1998 (TEMBLERL 05, Last sequence update)
01-NOV-1999 (TEMBLERL 12, Last annotation update)
10 KD CHAPERCNIN (PROTEIN CPNIC) (PROTEIN GROES).
 Last sequence update)
Last annotation update)
 93 AA: 10040 MW: 3F9F4871 CRC32:
 Aquifex aeolicus.
Bacteria: Aquificules: Aquiticaceae: Aquifex
 122 AA
 y3 AA.
 Created)
 PRT;
 01-A0G-1998 (TrEMBLrel, 07, 01-A0G-1998 (TrEMBLrel, 07, 01-NOV-1999 (TrEMBLrel, 12,
 Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
 Nature 392:353-358(1998)
 PRELIMINARY;
 PRELIMINARY:
 79 CDYLVLHEKDIMAI 92
 1 EEYLILSARDVLAV 14
 1 SEYLILSARDVLAV
 SEQUENCE FROM N.A.
 Lactobacillus zeae
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-VF5
 Chaperone.
 SECUENCE
 Query Match
 067942
067942:
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RESULT

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 Saps
 Sing
 Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Amphibia.
Patrachia, Amura, Mesoballachia, Pipologa, Pipidae, Men podibae.
 Xenopus borealis (Keryan clawed frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Amphibia:
Batrachia: Amura: Mesobaliachia: Pipoidea: Pipidae: Xenopodinae:
 SEQUENCE FROM N.A.
MEDILNE: 99167356.
YAMADA Y., HAGIMARA Y., SHICKAWA K., SAKAKI Y., ITO T.:
YAMADA Y., HAGIMARA Y., SHICKAWA K., SAKAKI Y., ITO T.:
Spatiotemporal, allelic, and enforced expression of Ximpact,
Xenopus homolog of mcuse imprinted gene impact.?,
Bloochem, Bloophys, Res. Commun. 256:162-169(1999).
SEMBL: AB02319; BAA76409...
SEQUENCE 312 AA, 35640 WW; QC250754 CRC32;
 3
 YAMADA Y.:
"Xenopus borealis homoloque of mouse implinted gene impact.
Submitted (DEC-1998) to the EMSL/GenBank/DDBJ databases.
EMBL; AB021258; BAA78421.1: -.
 Score 67: DB 13: Length 312:
Pred. No. 4.81e-01:
2: Mismatches 2: Indels
 Score 67; DB 13; Length 304,
Pred; No. 4.81e-01;
2; Mismatches 2; Indels
 09W625 PRELIMINARY; PKT: 312 AA. 09W625. 01-NOV-1999 (TrEMBLrel. 12. Created) 01-NOV-1999 (TrEMBLrel. 12. Last sequence update) 01-NOV-1999 (TrEMBLrel. 12. Last annotation update) XIMPACT.
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MKNA, PARTIAL CDS, SIMILAR 10 MOUSE IMPRINTED
GENE IMPACT (FRAGMENT)
 364 AA: 34661 MW: D94F43B1 CRC32:
 465 AA.
304 AA
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MEDILIN: 99397487.
MEDILIN: 99397487.
MEDILIN: 99397487.
MEDILIN: 99397487.
KCTANI H., NeWDRA N., GRAMA G.;
Prediction of the coding sequences of unidentitied human genes. XI.
Prediction of the coding sequences of unidentitied human genes. XI.
The complete sequences in VI.00 Cock CDNA Glones from brain which code for large protests in VI.00 Cock CDNA Glones from brain which code CNA Res. 5.277-286(1998).
EMBL: ABC1839: BAA34515.1: -.
SEQUENCE 465 AR: 51392 MM; D51F9266 CRC32;
 Squa
 Gabs
 Bacteria: Proteobacteria: garma subdivision; Enterobacteriaceae;
Enterobacter:
 Serratia rubidaca.
Bacteria: Proteobacteria: qamma subdivision: Enterobacteriaceae:
Serutia.
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 ŝ
 Hono Sabiens (Human).
Bukaryota, Metazoa: Chordata: Craniana; Vertebrata; Mammalia;
Butheria: Primates: Catarrhini: Hominidae: Hono.
 Length 465;
 4. Indels
 Prod. No. 1.140-00;
8: Mismarches 3, Indels
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TREMBLRel. 10, Last annotation update)
KIAAUT45 PROTEIN (FRACMENI).
 01-AUG-1948 (TEBMBLTEL, 07, Oreated)
01-AUG-1958 (TEBMBLTEL, 07, Last sequence update)
01-MAY-1999 (TFBMBLTEL, 10, Last annotation update)
SIMILAR TO GROES PROTEIN (FRAGMENT).
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
10-AUG-1999 (TrEMBLrel. 13, Last annotation update)
SIMILAR TO GROES PROTEIN (FRAGMENI).
 Score 66; DB 4; L0
Pred, No. 7.43e-01;
4; Mismatches 4;
 NON_TERM 1 1 SEQUENCE 94 AA; 9210 MW: 25PR656 DR032;
 88 AA
 38 AA
 SEQUENCE FROM N.A.
STRAIN-JCM 1240:
HARADA H., SHIKAWA H.;
J. Gen. Appl. Microbiol. 43:355-561(1997);
EMBL: ABOOBI4: BAAA5218 :: -..
PFAM: PFCC166: cpn10: 1.
 PRT
 PRT;
 Query Match
Best Local Similarity 52.9%;
 Usery Match
Rest Local Similarity 60.0%:
Matches 9: Conservative
 9: Conservative
 65 EEFLALPLEDVLELVSR 81
 1 FEYLILSARDVLAVVSK 17
 PRELIMINARY:
 cpni3: 1.
 PRELIMINARY:
 72 EBVLIMSESDILAIV 86
 1 EEYLILSAMEVLAVV 15
 SEQUENCE FROM N.A.
STRAIN-JOM6051;
HARADA H., ISHIKAWA H.:
 SEQUENCE FROM N.A.
 RESULT 11. 066201. 066201. 066201. 01. AUG-1. AUG-
 11 12
066189
056189;
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 066193 PRELLMINARY: PRI: 88 AA.
066193.
01-AUG-1948 (TERMILLE), 37 "Teated)
Al-AUG-1948 (TERMILLE), 37 "Teated)
Al-AUG-1948 (TERMILLE), 37 "Teated)
Al-AUG-1948 (TERMILLE), 38 "STATION OF GRAIN D. 13

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0.403-1998 (TENBLrel, 07, Created)

01-AC3-1998 (TENBLrel, 07, Last sequence update)

01-AC3-1998 (TENBLrel, 07, Last sequence update)

81-AC3-1998 (TENBLrel, 10, Last annotation update)
 ÷
 ::
 Score 65: DB 2: Length 84: Pred. No. 1.140*00; 3: Mismatches 3: Indeis
 Score 55: DB 2: Length 88;
Pred. No. 1.14e+00;
3: Mismatches 3; Indels
 Clab.
 Score 55, 08.2; Length 58-
Pred. No. 1.14e-00;
 AA510400 CK132:
 CBE048F0 CRC32;
 2E974CEU CRC32;

 Mismatches

 SEQUENCE FROM N.A.
STRAIN-JOH 725;
STRAIN-JOH 725;
J. Gen. Appl. Microbiol, 4::355-361(1497);
EMBL: AB008148; BAA22228:1;
PEMA: PF00166; Cpn10:1.
 SEQUENCE FROM N.A.
STRAIN-JOHN 1243
STRAIN-JOHN 1243
J. GEO. Appl. Microbiol. 43:355-361(1997).
EMBL. ABOÚR139: BAAZÉZIO.1; -.
PFAM. PFOOLG6: CPNIO? 1.
J. Gen. Appl. Microbiol. 48:355-361(1997).
EMBL: ABC08137: BAA25206.1: -.
PPAM: PFC0166: cpn16: 1.
NON IEC.
SEQUENCE 88 AA: 9254 MW: UBE046F0 CRC.
 SEQUENCE 88 AA; 9239 MW;
 Ouery Match
Best Local Similarity 60.0%:
Matches 9; Conservative
 Query Match
Best Local Similarity 60.0%;
Matches 9: Conservative
 NON_TER 1 : SEQUENCE 88 AA; 9212 MW.
 Ouery Match
Best Local Similarity 60.0%;
Matches 9; Conservative
 72 SEVLIMSESDILAIV 85
 72 ELVLIMSESDILAIV 86
 1 EEYLLISARDVLAVV 15
 72 EEVLIMSESDILAIV 85
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HESULT 15

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protein - protein database search, using Smith-Waterman algorithm M:srch_pp

Mon. Jun 19 16:05:10 2000; MasPar time 2.59 Seconds 82.425 Million cell updates/sec Rin on:

Tabular output not generated.

>US-09-142-524A-7 (1-9) from USC9142524A.pep 64

Description: Perfect Score: Sequence:

Search completed: Mon Jun 19 15:65:22 2000 Job time : 12 secs.

1 FIKRVSNVI 9 Sming table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Maximum DB seq length 9

a.geneseg35 Cutabase

scale 0.362 Variance 46.25 Mean 16.765: Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Residues 189-117 of Cr 1.25e+08 Description 9 1 WS7751 wilt Query
No. Score Match Length DB ID 64 100.0 Sesult

ALIGNMENTS

Note: Post-processor removed 44 summaries from list due to search parameters chosen.

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ESULT

D WASTS: standard: peptide: 9 AA.

MSTS: standard: peptide: 9 AA.

11-SEP-1998 (first entry)

E Residues 109-117 of Cry %:

R Cry 1 1: Japanese cedar pollen antigen: allergy: immunotherapy:

R Cryptomeria Japonica.

S Cryptomeria Japonica.

N WO9622902-AY.

S Cryptomeria Japonica.

S Cryptomeria Japonica.

N WO9622902-AY.

S Cryptomeria Japonica.

N WO9622902-AY.

S Cryptomeria Japonica.

S Cryptomeria Japonica.

N WOF 1996: JP 302053.

MR WELP ) WELLY WILL RRCD (2) LTD.

MR WPI: 96-2976:726.
                    COMMENS SERVICE
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PT Peptides derived from Japanese cedar polien antigens are immunotherapeutic agents - useful for allergy treatment and typing PT HLA class II molecules in allergy sufferers

Claim 12: Page 26: 50pp; Japanese .

Claim 20: Page 26: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64: DB 1: Length 9:
Pred. No. 1.25e+00:
C: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FIKRVSNVI 9
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| FIKRVSNVI 9
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Release 3.1A John F. Collins, Biocomputing Rusearch Unit. Copyriah: (c) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd

Tie Jun 20 13:39:14 2000; MasPar time 2.19 Seconds 59.362 Million cell updates/sec R.10. On:

protein - protein database search, using Smith-Waterman algorithm

Mesrch_pp

Jubular output not generated.

>US-09-142-524A-7 (1-9) from US03142524A.pep 64 Description: Perfect Score: Sequence:

1 FIKRVSNVI 9

145341 seqs, 14437480 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 9 Post-processing:

a-issued i:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Database:

Moan 15.775; Variance 46.625; scale 0.338 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description pred No. 91 Result Query No. Score Match Length Ds

No matches found.

Search completed: Tue Jun 20 13:39:17 2000 Job time : 3 secs.

		(TM)
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Release 1.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Extord Molecular Ltd

protein i protein database search, using Smith-Waterman algorithm W.srch_pp R .:: On:

Mon Jun 19 16:08:54 2000; MasPar tire 13.59 Seconds 65.727 Million cell updates/sec

Tubular output not generated.

>CS-09-142-524A-7 (1-9) from US09142524A.pep 64 1 FIKRVSNVI 9 Title: Description: Perfect Score: Sequence:

721208 segs, 100765575 residues PAM 150 Gap 15 Sourched:

Scoring table:

Minimum Match 0% Listing first 45 summarles Maximum DB seq length 9 Post-processing:

Cutabase

a-pending l:FCT 2:06 3:060 4:07 5:080 5:081 7:082 8:083 9:084A lc:0848 ll:085 l2:086 l3:08 l4:08E l5:089 16:090 l7:091 l8:092 l9:093 20:094 21:095 22:NEWP 23:NEWU60 24:NEWU8 25:NEWU9

Mean 18,575; Variance 43,933; scale 0.423 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description $\ddot{\cdot}$ sult Query No. Score Match Length DB Result

8

Pred.

No matches tound.

Smarch completed: Mon Jun 19 16:09:17 2000 Jub time : 23 secs.

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MPsrch_pp protein protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:04:38 2000; MasPar time 4.43 Seconds 95.841 Million cell updates/sec Jabular output n t generated. Rish on:

>US-09-142-524A-7 (1-9) from USC9142524A.pep 64

Title: Description: Po:fect Score: Sequence:

1 FIKRVSNVI 9

142080 segs, 47172406 residues Searched

PAM 150 Gap 15

Sporing table:

Pust-processing:

Minimum Match O% Listing first 45 summaries Maximum DB seq length 9

Mean 23.798; Variance 28.919; scale 0.823 Statistics:

pir62 lipir1 2:pir2 3:pir3 4:pir4

Cutabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No 11 sult No. Score Mainh Length DB Rosult

No matches found.

Search completed: Mon Jun 19 16:04:53 2000 Job time : 15 secs.

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protein : protein database search, using Smith-Waterman algorithm Mon Jun 19 16:03:40 2000; MasPar time 3.37 Seconds 81.234 Million cell updates/sec MPsrch_pp

Tabular output not generated.

R :: 10 on :

>US-09-142-524A-7 (1-9) from USC9142524A.pep 64 1 FIKRVSNVI 9

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

83857 segs, 30454973 residues Searched:

Minimum Match O% Listing first 45 summaries Maximum DB seq length 9 Post-processing:

Sutabase:

Mean 24.343; Variance 25.165; scale 0.967 swiss-prot38 l:swissprot S'atistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No Result Owery
No. Score Match Length DB 13

ç

No matches found.

Search completed: Mon Jan 19 16:03:47 2000 Jub time : 7 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Jun 19 16:04:03 2000; MasPar time 8.30 Seconds 75.200 Million cell updates/sec

Run on:

Tabular output not generated.

>US-09-142-524A-7 (1-9) from US09142524A.pep 64 1 FIKRVSNVI 9

Intie: Description: Perfect Score: Sequence:

225878 seqs, 69334122 residues PAM 150 Gap 15 Scoring table: Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 9

sptrembil2
l:sp_archea 2:sp_bacteria 3 sp_fugqi 4:sp_human
5:sp_invertebrate 6:sp_marmal 7:sp_mic 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Dulabase:

Mean 23.348; Variance 25.366: scale 0.920 Statistics pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

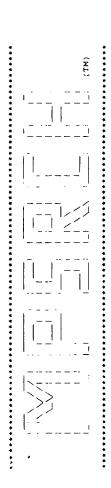
Description G Result Query No. Score Match Length DB

Pred. No

No matches found.

Search completed: Mon Jun 19 16:04:22 2000 Job time : 19 secs.

US-09-142-524A-9.rag



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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:10:20 2000; MasPar time 3.31 Seconds 107:475 Million cell updates/sec Tabular output not generated. R ... On :

>US-09-142-524A-9 (1-15) from US09142524A.pep 106 Description: Parfect Score: Sequence:

1 KSMKVIVAFNQFGPN 15

PAM 150 Gap 15 Souring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

188963 seqs, 23686106 residues

Searched:

d-deneseq35 l:geneseqp Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Variance 56.349; scale 0.328

Mean 18,458;

Statistics:

SUMMARIES

	Pred. No.		.38e-0	.38e-0	8.38	8.38e-0	8.38e-0	.38e-0	.38e-0	٣.	.38e-0	.38e-	٣.	. 38e-	.38e-	.38e-	.38e-	.38e-	8.38e-05	.38e-	٣.	8.38e-05	8.38e-05	.38e-
	Description	Japanese cedar pollen	Residues 211-225 of Cr	llergen p	T-cell epitope peptide	1 Japane	Cry j I pollen allerqe	j i pollen ali	J I polien all	j I pollen all	j i pollen all	j I pollen all	j I polien all	j I pollen a	j I pollen all	all epitope ;	ď	inese cedar	len al	ē	Ω		Cry j I pollen allerge	nese cedar
	1 1	929	W57755	34	W42144	251	R45563	59	559	4559	559	59	558	558	മ	5	4558	R75388	ထ	W42121	W04344	4	3	R6C166
	DB	r-1	, 4	. 1	، ا	4	- 1	٠,	۲,	-	_	-	,,	-	-	-	-	~	-	-1	-	٦	٦	
	Length	15	15	17	20	20	20	25	26	56	28	28	28	30	30	30	36	353	353	354	354	367	374	374
æ	Opery Match			S	100.0	00.	100.0	100.0	000	0.001	00		100.0		100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	106	106	106	106	106	106	501	106	106	106	105	30€	106	106	106	106	106	106	106	106	106	706	105
	Result No.	1	7	٣	4	'n	တ	7	ത	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

00000000000000000000000000000000000000	6.24e-02 6.24e-02 1.82e-01 2.49e-00 2.49e-00 6.90e-00
Vaapane Pricope appricope apricope apprico	Sugi allergen protein Sugi allergen protein Zinna elegans perdate Cry ji Japanese Gedar Treell epikope feptude Cry ji I pollen allerge Residues 214-222 of Gr
######################################	WR0357 WB0352 W97846 R82511 W42143 R45562
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00000000000000000000000000000000000000	2007 4000 4000 4000 4000 4000 4000 4000
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ALIGNMENTS

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20-0CT-1993: 262626.
37 20-0CT-1993: 262626.
38 20-0CT-1993: JP-262626.
39 P. 20-0CT-1993: JP-262626.
30 PETAL MILK PROD CULID.
30 PETAL MILK PROD CULID.
31 PETAL MILK PROD CULID.
32 PS-203834/27.
33 PS-203834/27.
34 PPI: 95-203834/27.
35 PS-203834 is and invertigation of Japanese cedar pollenosis provention, treatment and invertigation of Japanese cedar pollenosis.
35 PS-20388 is the Japanese cedar pollen allergen Cryl I. from which the CC T-cell epitope peptides R89747-R89295 were derived The peptides.
35 Can be used for the prevention and treatment of cryitoreria.
36 Sequence 15 AA:
                                                       12-MAR/1996 (first entry)
Japanese cedar pollen allergen Cryj I derived T-celi epitope puptide
Japanese cedar; pollen allergen Cryj I: T-cell epitope, peptides,
prevention; treatment: cryptomeria pollenosis.
JCTPtomeria japonica.
                    R89293 standard: peptide: 15 AA.
                                          R85293;
```

Saps ö Score 106: DB 1: Length JU. Pred. No. 8:38e-05: Ouery Match Best Local Similarity 100.0%; Matches 15; Conservative

.. O

1 KSMKVTVAFNQFGPN 15 ද ςy W57755 standard: peptide; 15 AA.
W57755 standard: peptide; 15 AA.
W57757 (first entry)
Residues 211-225 of Cry j 1.
Cry j 1; Japanese cedar pollen antígen: allergy; immunotherapy:
HLA class II molecule.
Cryptomeria japonica.
W08820902-AI. 22-MAY-1998.
112-NOV-1999; J04129.
113-NOV-1996; JP-302053.
(MEIP) MEIJI MILK PROD CO LTD.
Daithi K, Kino K, Kume A, Sone T;
WPI; (3-297617/26.

```
Peptides derived from Japannese cedar pollen antiquens are immunotherapeutic agents - useful for allergy treatment and typing flat and lass in molecules in allergy sufferers.

Into class in molecules in allergy sufferers claim 12, page 28: 50pp Japannese is a peptide of the invention. The peptides are derived from Japannese cedar police antices, and are issed as immunotherapeutic agents in treatment of allergy. The pertides can be used for identification and treatment of allergy. The pertides can be used for identification and typing of the particular MiA class II molecules in an allergy sufferer, and also for peptide immunotherapy of an allergy to the requirements the individual patient, allowing more effective treatment of an allery, including those patients for whom treatment with a conventional immunotherapeutic agent is ineffective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W80339-58 represent epitopes for T cells, derived from the sudi allergen proteins Civil (W80379-44) W80350-53 and W80355-58) and Cryj2 (W80345-49 and W80354-45). The peptides are useful for the treament of sugimpolitions is, an allergic reaction of the body to pollen. Sequence: 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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T-cell epitope peptide 24 from Japanese cypress pollen antigen Chaol.
Japanese cypress pollen, antigen: T-cell epitope: Claol: Chao2;
diagnosis: aliergy: spring tree pollen disease: pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.JAN-1999 (tirst entry)
Sugi allerden protein Cryj2 derived epitope for T cells.
T cell epitope: Sudi allerden proteins Cryj1: Cryj2: treatment:
sugirpollinosis; allergic roaction; poilen.
Synthetic.
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Claim 7: Page 18: 21pp: Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105: DB 1; Length 15:
Pred. No. 8.38e-05:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred, No. 8.38e-05;
0; Mismatches 0;
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29-SEP-1998
22-DEC-1996: JP-343441
(HAXB.) HAYNSHIBMRA SEIBUTSU KASAKU.
(SANY.) SANKYO CO. LTD.
WPI: 98-577037/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W42144 standard: peptide: 20 AA.
W42144:
16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W80349 standard: peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-30N-1997; 032031.

14-40N-1996, UP-153527.

(MEIP.) MELLI MILK PROD CC LTD.

DAIRIRE K, KING K.

WPI: 96-052242/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuery Match
Best Local Similarity 100.0%:
Matches 15; Conservative
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Hest Local Similarity 160.0%:
Matches
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WO9747648-Al.
18-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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WPI 95-36691/47.

Modified Cryptomeria japonica (Cry j) ; peptide(s) - useful for treating allergy to japanese cedar polien allergen or treating allergy to japanese cedar polien allergen or mimunologically cross reactive allergens

Disclosure Figure 2: 60pp; English

Novel peptides of cry j) ; have been modified as a part of a preformulation scheme to develop an optimised drow product for theraperity treatment of humans siterily from allery to japanese cours policy allergen or an allery manner of immunication of the product to the product formulation when it is defined better allery product formulations. Such them princely recess reactive allery product formulations. Peptide fragments of Cry j, modified and unmodified and unmodified, are given in REA49; RRE555. This peptide fragment corresponds to anino acids 21:-230 of the allergen mature
                                                        Claim 1. Page 27-28: 71pp: Japanese.

Claim 1. Page 27-28: 71pp: Japanese.

Claim 2. Page 27-28: 71pp: Japanese.

Claim 3. Page 27-28: 71pp: Japanese.

Claim 4. Page 27-28: 71pp: Japanese.

Cypress pollen antigen Chao! The present invention describes profiters which correspond to the Tree! epitope sites on Japanese cypress pollen antigens. Chao! and Chao2. The peptides can be used as a reasont for the diagnosis of allergy to Japanese cypress pollen, and as an activient in the treatment and prevention of spring tree pollen disease in which in pollinosis involves reactivity to Japanese cypress pullen.
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Cry i I: Japanese cedar poli : allergen. modified: drug production.

Blergy: Crytpomeria japonic.

Crytpomeria japonica.

W09527786-A1.
   police antigens
of spring tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 6
R45563 standard; Protein; 20 AA.
R4553.
R45563.
R45563.
R45654.
R45654.
R45654.
R45663 standard; peptide CJI-22.
Sapanese cedar; detection; allergy; treatment; diagnosis; reciprope; sensitivity.
Cryptomeria japonica.
R09461566-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0: Indels
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r-cell epitope peptide portion of Japanese cypress Chaol and Chao2 - used for diagnosis and treatment
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Pred. No. 8.38e+35;
0: Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105; DB 1, 1
Pred. No. 8.38e-05;
0: Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R82512 standard; Protein: 20 AA R82512;
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06-ARF-1995; UG4249.
06-APF-1994: US-226248.
06-DEC-1994: US-350225.
(IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%:
Matches 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Gaps

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Sequence

Matches

allerqy Claim 1:

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The sequence is that of us collect peptide of the languese redar police allerges Cry [1]. The pertide, CJI-43.12, can be ised for the treatment and disancess of alterates associated with Jaranese cedar police. It has enhanced therapeutic properties but reduned side effects compared to naturally occurring allergens.
15-JAN-1993; UC0139.
UC-JUL-1992; WO-JUS-56.
UC-SEP-1992; US-938990.
(IMMU-) IMMULOGIC PHARM CORE.
(IMMU-) IMMULOGIC PHARM CORE.
WPI: 94-035066/04.
Antigens derived from Japanese codar pollen alleigen GTY:::-
contain at least two 7 cell epitope(s), used to treat or diagrose
                                                                                                                                                                                                                                                           allergy

Claim 76. Fig 18: 137pp: Enables

The sequence is that of a. 1913 Hd peptide of the Japanese cold:

pollen allergen Cry 3 in The Peptide, C31-43.9, can be used for
the treatment and diagnosis allergues associated with Japanese
cedar pollen. It has enhanc therapeutic properties but indiana
side effects compared to na ally occurring allergues.
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Japanese cedar: detection: allergy: treatment: diagnosis: T cell epitope; sensitivity.
Cryptomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i3-JUL-1994 (first entry)
Cry } I pollen allergen peptide CJI-43.12.
Japanese cedar; detection: allergy: treatment; diagnosis;
I cell epitope; sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 100.0%; ore 106; iB 1; Length 26; iCal Similarity 100.0%; F. vd. No. 8.36e-05; nes 15; Conservative 0; Mismatches 0; Indels
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15-JAN-1993: UCC139.
01-SEP-1992: WO-U05661.
01-SEP-1992: US-938990.
(IMMU-) IMMULGGIC PHARM COR:.
WHU-) GARMAN RD, GRIEffit: :3, Kuo M, Poliock J; WPI: 94-035066/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 76: Fig 18: 127pp: Es lish.
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R45594 standard; Protein: 26 AA.
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13-JUL-1994 (first entry)
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WC9401560-A.
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15-JAN-1993; U00139
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Hes 15; Conser
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Matches
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                                                                                                                                                                                                                                                                                                                    claim!; Fig 13: 137pp: English.
The sequence is that of an isolated peptide of the Japanese cedar pollen allergen Cry j I (amino acids 21:123). The spetide, CJI-22, can be used certhe treatment and diagnosis of allergies associated with Japanese cedar pollen. It has enhanced therapetic properties but reduced side effects compared to naturally occurring allergens.
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01-SEP-1992: US-938990.
01-SEP-1992: US-938990.
01-SEP-1992: US-938990.
01-SEP-1992: US-938990.
Bond JF. Garman RD, Griffith IJ, Kuo M, Pollock J:
WPI: 94-0330966/24.
Antiques derived from Japanese cedar pollen alleryen Cry j I -
contain at least two I cell epitope(s), used to least or diagnose
                                                                                                                                                                                                                             Antiqens derived from Japanese cedar pollen allergen {\rm Cry} \ j i contain at least two i cell epitope(s), used to treat or diagnose
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Cry ) I pollen allergen peptide CJI-43.9.
Japanese cedar: defection: allergy: treatment; diagnosis; I cell epicope: senativity.
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Japanese cedar: detection: allergy: tre 'ment: diagnosis:
T cell epitope: sensitivity.
Cryptomeria japonica.
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                                                               10-JUL-1992: WJ-U05661.
01-SEP-1992: US-91899C.
01-MUC-) IMMULOSIC PHARM CORP.
BOND TO Garman RD, Griffith IJ, Kup M, Pollock J:
WPI: 94-035066/04.
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R45592:
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Hest Local Similarity 100.0%;
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             20-JAN-1994.
15-JAN-1993:
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WC-005661.
US-938990.
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10-JUL-1992; WC-0056
01-SEP-1992; US-9389
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                                                                                                                                                 allergy.

Claim 76: Fig 18: 137pp: Enalish.

The sequence is that of an isolated peptide of the Japanese cedar polien alteren by 1. The peptide, CJI-43.8, ran be used for the treatment and diagnosis of altergies associated with Japanese cedar poller. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring altergens.
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Claim 70: Fig. 181 187 pp. English.

Claim 70: Fig. 181 187 pp. English.

The segment is that of an isolated peptide of the Japanese codar police, allerance 187 i. The peptide, CJT-43.11, he isolated police, allerance 187 i. The peptide, CJT-43.11, he isolated the cedar police, it has enhanced therapeutic properties but reduced side effects out alleranced therapeutic properties but reduced side effects outside to naturally occurring allerance.

Sequence 28 AA.
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                                                            Bond JF, Garman RD. Griffith IJ, Kuo M, Pollock J:
WPI 94-330065/74
Antidons derived from Japanese cedar pollon allergen Cry J I -
contain at least two T coll epitope(s), used to treat or diagnose
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Pred, No. 8.38e-05;
"''marrhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cry j f pollen allergen peptide CJI-43.7.
Japanese cedar: detection: allergy: treatment: diagnosis:
T cell epitope: sensitivity.
                                                                                                                                                                                                                                                                                                                                              Score 106: DB 1; Length 28, Pred. No. 8,38e-05; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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WPI: 94-035066/04.
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R45589 standard; Protein; 28 AA.
R45589;
·13-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R45593 standard; Protein; 28 AA. R45593:
10-JUL-1992: WO-U05661.
01-SEP-1992: US-938950.
(IMMU-) IMMULGGIC PHARM CORP.
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10-JUL-1992: WO-UCS651.
01-SEP-1992: US-938990.
(IMMU-) IMMULGGIC PHARM CORP.
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est Local Similarity 106.0%;
atches 15; Conservative
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Best Local Similarity 100.0%:
Matches 15: Conservative
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15-JAN-1999: 000139.
10-JUL-1992: WO-J05661.
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WO9401560-A.
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W09401560-A.
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01-SEP-1992; US-938990.
(IMMU-) IMMULOGIC PHARM CORP.
(IMMU-) IMMULOGIC PHARM CORP.
MPI: 94-035056/04.
Antigens derived from Japane - cedar pollen allergen (19 ): contain at least two T cell (pitope(s), used to treat or diddn so
                                                                                                                                            dilergy
Claim 76: Fig 18: 137pp; Eng 'sh.
The sequence is that of an isolated peptide of the Japanese reda:
polier allergen Cry 1 1. The peptide, CJI-43.7, can be used for
the treatment and diamosts of allergies associated with Japanese
cedar pollen. It has enhanced therapeutic properties but reduced
side effects and an additional transfer occurring allergens.
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He sequence is that of an iscard population the Japanese refus policy allotype fry [1]. He politice of the Japanese from the treatment and diamons is a letter associated with Tiplese.
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Japanese cedar: detection; allergy: treatment; diagnosis; T cell epitope; sensitivity.
Cryptomeria japonica.
W09401550-A.
                                                                                                                                                                                                                                                                                                                                                                      Length . 9.
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15-JAN-1993; U00139.
10-JUL-1992; WC-10566;
01-SEP-1992; US-938990;
(IMMU-) IMMULDGIC PHARM CORP.
WPI: 94-035056/V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105; 08 1; 1
Pred. No. 8.38e-05;
0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 1; PPred. No. 8.38e-05; 0: Mismatches 0
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R45588 standard: Protein; 30 AA.
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R45587 standard; Protein: 30 AA.
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Matches 15; Conservative
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Best Local Similarity 160.0%;
Matches 15; Conservative
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13-JUL-1994 (first entry)
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completed: Mon Jun 19 16:10:31 2000 Te : 11 secs.

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MFsrch\_pp protein - protein database search, using Smith-Waterman algorithm Rin cn: Tic Jun 20 13:35:56 2000: MasPar time 2.65 Seconds 81.869 Million cell updates/sec

Tubular output not generated. Title: >US-09-142-524A-9 Describion: (1-15) From ES0914-524A peo

Title: >US-09-142-524A-9
Description: (1-15) from US-09142524A.pep
Porfect Score: 106
Sequence: 1 KSMKVŢVAFNQFGPN 15

Scoring table: PAM 150 Cap 15 Searched: 145341 segs, 14437480 residues

Post-processing: Minimum Match 3% Listing first 45 summaries Database: a .issued 1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfiles1 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 17.411; Variance 53.947: scale 0.323

Statistics:

SUMMARIES

|            | Pred. No.             | 2.10e-01     | 2.10e+01   | 2.10e+01                    | ٠.      | 3.43e+01     | 3.43e+01   | 3.43e-03   | 3.43e+01     | 3.43e+01   | 4.37e-01     | 4.37e+01  | 4.37e+01     | 5.57e+01   | 5.57e+01     | 5.57e+01   | 7.09e+01   | 7.09e+01   | 7.09e+01   | 7.09e+01    | 7.09e+01   | 7.09e+01   | 7.09e+01   | 7.09e+01    |
|------------|-----------------------|--------------|------------|-----------------------------|---------|--------------|------------|------------|--------------|------------|--------------|-----------|--------------|------------|--------------|------------|------------|------------|------------|-------------|------------|------------|------------|-------------|
|            |                       | Applicati    | Applicati  | Applicati                   |         |              |            | Applicati  | Applicati    | Applicati  | Applicati    | Applicati | Applicati    | Applicati  | Applicati    | Applicati  | Applicatio | Applicatio | Applicatio | Applicatio  | Applicatio | Applicatio | Applicatio | Applicatio  |
|            | Description           | Sequence 75, |            | Sequence 75,                |         | Sequence 59, |            |            | Sequence 74, | ~          | Sequence 72, | 7         | Sequence 72, | •          | Sequence 78, | 78,        | 4          | 4          | 7          | Sequence 4, | 5.         | ۲,         | 7          | Sequence 6, |
|            | ۵.                    | US-08-175-   | US-08-290- | <b>US-</b> 58- <b>29</b> 0- | -08-50n | .08-08-280-  | US-08-175- | US-08-290- |              | US-08-175- |              |           | US-08-175-   | US-08-175- | US-08-29C-   | US-08-290- | US-08-436- | PCI-US95-0 | PCI-US95-0 | US-08-436-  | PCI-US95-0 | CS-08-436- | US-08-436- | US-08-687-  |
|            | DR                    | -            |            | -                           | ٦.      | -            |            | ٦          | ٦            | 7          | , -ı         | -         | , ,          | 3 1        | 3            | ,- f       | 3 2        | ~          | 3 4        |             | ••         |            | 6 2        | 2           |
|            | -engt)                | 397          | 397        | 397                         | 391     | 393          | 39;        | 396        | 398          | 398        | 387          | 387       | 387          | 383        | 38           | 38         | 33,        | 333        | 33.        | 333         | 336        | 336        | 336        | 44          |
| y <b>s</b> | Overy<br>Match Length | ~            | ω.         | 53.8                        | . ;     |              |            |            |              |            |              |           | 90.05        |            | 50.0         |            | 49.1       | 49.1       | 49.1       | 49.1        | 49.1       | 49.1       | 45.1       | 49.1        |
|            | Score                 | 5.7          | 53         | 57                          | 55      | S            | 55         | 52         | 55           | 55         | 54           | t)        | 54           | 53         | 53           | S<br>S     | 25         | 25         | 52         | 52          | 52         | 25         | 52         | 25          |
|            | Fesult<br>No.         | -            | 7          | m                           | 4       | ഗ            | φ          | 7          | æ            | 6          | 0.7          | 11        | 12           | 13         | 14           | 15         | 15         | 17         | 18         | 13          | 20         | 21         | 22         | 23          |

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| e contractor de la cont | Sednence    |
| 0.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | -669-80-80  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 7           |
| 2000 100 100 100 100 100 100 100 100 100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 1481        |
| ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 46.2        |
| N N N N N N N N N N N A 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | <b>4</b>    |
| 45000000000000000044444440000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4 5         |

### ALIGNMENTS

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 1atches
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 Gaps
 APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Trorunn
APPLICANT: Rafnar, Trorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHVE & COCKFIELD
SIREET: 60 State Street, suite 510
 ö
 Score 57: DB 1: Length 397;
Pred. No. 2.19e+01:
1; Mismatches 5: Indels
 Score 57; DB 1; Length 397;
Pred. No. 2.10e-61;
1; Mismatches 5; Indels
 STATE. Massachusetts
CUNTRY: USA
21P: C2136-1875
CCMPUTER READABLE FORM:
MBDICH INTER: ELEMPTORY disk
COMPUTER: IRM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0. Version #1.25
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.444A
 397 AA.
 NAME: Amy E. Mandrogouras
REGISTRATION NUMBER: 36.207
RESERRENCE/DOCKET NUMBER: IMI-018CN
TELECCHMUN:CATION INFORMATION:
TELEPRIONE: (617)227-7400
TELEPRIONE: (617)227-75941
INFORMATION FOR SEQ IO NO: 76:
 P.R.
 MOLECULE TYPE: protein
SEQUENCE 397 AA, 42947 MW, 781425 CN:
LENGTH: 397 animo acids
TYPE: animo acid
TOPOLOGY: linear
MellEDUE TYPE: protein
SEQUENCE 397 AA: 42947 WW: 781425 CN:
 Seguence 76, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: ROGERS, Bruce
 Sequence 76, Application US/38290449A
 STANGARD;
 SEGUENCE CHARACIERISTICS:
LENGIH: 397 amino acids
TYPE: amino acid
 Substance Similarity 60.0%;
Best Local Similarity 60.0%;
Matches 9; Conservative
 53.8%:
50.0%:
 Guery Match
Best'Local Similarity 60.0%:
Matches 9: Conservative
 256 KGMLATVAFNMFTDN 270
 1 KSMKVTVAFNUFGPN 15
 linear
 Boston
 US-08-290-448A-76
 TOPOLOGY:
 xxxxxx
 RESULT
 S
 X \times X \times X
 2002
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 Saps
 Sequence 76, Application US/OBL90448A
Patent No. 5698204
GENBALICANI
APPLICANI
APPLICA
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::
 53.8%: Score 57: DB 1: Length 397:
60.0%: Pred. No. 2.10e-01;
ative 1: Mismatches 5: Indels
 391 AA
 397 AA
 FILING DATE: May 29,
APPLICATION NUMBER: C: //325.465
FILING DATE: MARCH 1: #95
ATTORNEY/AGENT INFORMATION
NAME: Amy E. Mandradoutas
REGISSRATION NUMBER: 46.207
REFERENCE/CONGRET VANDER: 181:181N
IELEPHONE: (61.)227.7401
 ADDRESSEE: LAHIVE & CUCKFIELD
STREET: 60 State Street, suite 510
 PRT
 TOPCLOGY: linear
MOLECULE TYPE: protein
JENCE 397 AA: 42947 MW: 781425 CN:
 Sequence 75, Application US/08290448A
 STANDARD:
 397 amino acids
 STANDAR
 INCOMMATION FOR SEQ 1D N
SEQUENCE CHARACTERISTICS:
 Massachusetts
 ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Local Similarity 60.0%;
 9: Conservative
 256 KGMLATVAFNMFTDN 270
 amino acid
 1 KSMKVIVAFNOFGPN 15
 STREET: 60 State CITY: Boston STATE: Massach
 USA
 RESULT 4

ID US-08-290-448A-59

XX XXXXX

AC XXXXX

XX XX

XX XX

XX XX
US-08-290-448A-76
 TOPCLOGY:
 COUNTRY:
 SEQUENCE
 Query Match
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Gabs

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256 KOMLATVAFNMETON 270

US-09-142-524A-9.rai

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Sequence 59, Application US/08175069A
Patent No. 5776761
GENERAL INFORMATION:
APPLICANT: Roper, Bruce
APPLICANT: Rapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Ruo, Mei-chang
TILLE OF INVENTION: Allergemic Proteins From Raqweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
 Query Match 51.9%; Score 55: DB 1: Length 39):
Best Local Similarity 66.7%; Pred No. 3.436-01:
Matches 8: Conservative 1: Mismatches 3: Indels
 CURRENTING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: August 15, 1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 7/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 97/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 97/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 97/525,365
FILING DATE: MARCH 1 1989
APPLICATION NUMBER: US 97/525,365
FILING DATE: MARCH 1 1989
APPLICATION NUMBER: 36,267
RECISTRATION NUMBER: 36,267
RECISTRATION NUMBER: 36,267
RECISTRATION NUMBER: 36,267
RECOMMUNICATION INF. AMAIGN:
FELECOMMUNICATION INF. AMAIGN:
 ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
 754045 CN:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1.sk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DGS
 COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERAIING SYSTEM: PC-DCS/MS-DCS
 Sequence 59, Application US/08175069A
 CHENDARIS
 TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS
LENGTH: 391 amino aci is
 MOLECULE TYPE: protein
ENCE 391 AA; 42854 MW
 STATE: Massachusetts
COUNTRY: USA
 STATE: Massachusetts
CCUNIRY: USA
ZIP: 02109-1875
CORRESPONDENCE ADDRESS:
 amino acid
 250 KGMLAIVAFNMF 261
 1 KSMKVTVAFNOF 12
 STREET: 60 S:
CITY: Boston
 STREET: 60 St
CITY: Boston
 RESULT 6
ID US-18-175 (69A-59
 TOPOLOGY:
 SEQUENCE
 xxxxxx
 q
 ö
 ö
 Sequence Patent No 5676954

Patent NFORMATION: Rogers, Bruce APPLICANT: Riapper, Lavid G. APPLICANT: Riapper, Lavid G. APPLICANT: Rainar Thorunn CC APPLICANT: Ruo, Mei-chang CC APPLICANT: Ruo, Mei-chang CC NUMBER OF SEQUENCES: 93

CC CORRESPONDENCES: 93

CC CORRESPONDENCE ADDRESS: COCKFIELD STREET: 60 State Street, suite 510
 Sequence 59, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION:
APPLICANT: Righper, Bruce
APPLICANT: Righper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Ruo, Mei-chang
TILE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
 S
 COMPTER FALSASTEFORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPTER: Lab PC compatible
COMPTER: Lab PC compatible
OPERATING SYSTEM: PO-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US./08/290.448A
FILING DATE: May 29, 1990
APPLICATION NUMBER: US.07/529.95;
FILING DATE: May 29, 1990
APPLICATION NUMBER: US.07/325,365
FILING DATE: March 17, 1989
ALTORNAY/AGENT INDORMATION:
NAME: Amy E. Mandragouras
RESTSTRATION NUMBER: 36,207
REPERSON NUMBER: 36,207
REPERSON OF COMPANION: (617)227-740C
TELEPHONE: (617)227-740C
TELEPHONE: (617)227-740C
TELEPHONE: (617)227-740C
TELEPHONE: (617)227-740C
TELEPHONE: (617)227-740C
TELEPHONE: CHARACIENTICS:
 Match 51.9%, Score 55: DB 1: Length 391:
Local Similarity 66.7%; Pred. No. 3.47e+01:
Les 8: Conservative 1: Mismatches 5: Lodels
 391 AA
 PRT:
 MOLECULE TYPE: protein
JENCE 391 AA: 42864 MW: 754045 CN:
 Sequence 59, Application US/08290448A
 Sequence 59, Application US/08290448A
 STANDARD;
 : 391 amino acids
amino acid
 250 KGMLATVAFNMF 261
 US-08-290-448A-59
 TOPOLOGY
 LENGIH:
 SEQUENCE
 Juery Match
 xxxxxx
 RESULI
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REGISTRATION NUMBER:
 TOPOLUGY: linear
MOLECULE TYPE: protein
 257 KGMLATVAFNMF 268
 1 KSMKVTVAFNOF 12
 US-08-290-448A-74
 SEQUENCE
 XXXXXX
 ò
 .:
O
 Gaps
 Sequence 74, Application US/0829:0448A
Patent No. 1676994
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Klapper, cavid G.
APPLICANT: Klapper, cavid G.
APPLICANT: Kan and Continua APPLICANT: Roo, Northon APPLICANT: APPLICANT
 ..
SCETWARE: Patentic Release #1.0. Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175.069A
FILING DATE: December 29. 1993
PRIOR APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29. 1993
APPLICATION NUMBER: US 07/229,951
FILING DATE: May 29. 1993
APPLICATION NUMBER: US 07/225,865
FILING DATE: March 17, 2969
APPLICATION NUMBER: US 07/225,865
FILING DATE: March 17, 2969
APPLICATION NUMBER: 36,207
REFERENCE/COCKET NUMBER: 36,207
REFERENCE/COCKET NUMBER: 36,207
REFERENCE/COCKET NUMBER: 1M:018CV
TELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION SEQ 120.00
SEQUENCE DARACTER/STICS:
LENGTH: 39] amino acids
 COUNTRY: USA
ZIP: 02109-1875
CUMPUIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPOTER: IBM PC compatible
OMPOTER: IBM PC COMPA: DS SOFTWARE: Patentin Release #1.C, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29/46A
FILM DATE: Aquest 15, 1994
APPLICATION NUMBER: US 27/529,95;
FILM CATE: May 29, 1990
APPLICATION NUMBER: US 37/325,365
FILM CATE: March 1989
ATIORNEY/ARRY INFORMATION:
NAME: Amy E. Manch agours
 query Match
Fest Local Similarity 66.7%: Pred. No. 3.436-01:
Matches 8: Conservative 1: Mismatches 3: Indels
 398 AA
 PRI
 MOLECULE TYPE: protein
JENCE 391 AA: 42864 MW; 754045 CN:
 Sequence 74, Application US/08290448A
 STAMBARD:
 : 391 amino acids
amino acid
 CITY: Moston
STAIE: Massachusetts
 linear
 250 KGMLALVAFNMF 261
 : RSMKVTVAENOF 12
 US-08-290-448A-74
 TOPOLOGY
 SEQUENCE
 xxxxx
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 Sequence 74, Application US/0829445A
Patent No. 569824
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kiapper, Lavid G.
APPLICANT: Kiapper, Lavid G.
APPLICANT: Kaffarr, Thoron:
APPLICANT: Ko. Mai-chaid
IIILE OF INVENTION: Alleraenic Proteins From Madward and Dans NUMBER OF SEQUENCES:
ADURESSEE: LAHIVE & CANKFIELD
STREET: EQ. STATO SILVEL: STIVE 'E.
 Ouery Match 51.9%, Soure 55, DB 1, Length 698, Best Local Similarity 66.7%, Pred. No. 3.44e-01. Matches 8: Conservative 1, Mismatches 9; indeix
 COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
DOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rejedse #1.0. Version #1.25
CURRENT APPLICATION DATA:
SPELICATION NUMBER: 75/08/299,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
 FILING DATE: May 29, 197529,931
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/225,365
FILING DATE: March 17, 1989
ATTORNEY/AGENI INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: IMI-018CN
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 IMI - 018CN
 TOPOLOGY: Linear
MOLECCLE TYPE: protein
JENCE 398 AA: 43654 KW: 779005 CN:
 Sequence 74, Application US/08290448A
 REFERENCE/DOCKET NUMBER IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
16.207
 TELEFAX: (6.7)227-594:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS
LENGTH: 398 amino acids
IYPE: amino acid
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 74:
 STANDARD:
 ZIEL (ZIS FINE)
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
 STREET: CO State Str
NITY Puston
STATE: Rassarh setts
NORTHY SA
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Matches
RESULT
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 Gaps
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Riapper, Journal G.
APPLICANT: Raffar, Thorunn
APPLICANT: Kuo, Mei-chang
TILLE CF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
 0
 Score 55; DB 1; Length 398;
Pred. No. 3.43e+01;
1; Mismatches 3; Indels
 Lengt. 398;
 3; Indels
 COMPUTER: Eloppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COERAIING SYSTEM: PC-DOS/MS-DS SCFTWARE: Patentin Release #1.0, Version #.25 SCFTWARE: Detentin Release #1.0, Version #.25 CURRENT APPLICATION DATA: DS.09/28/175.069A FILING DATE: Detentin DATA: PROJECTION DATA: PS.01/28/23 PROJECTION NUMBER: US.01/28/23 PS. FILING DATE: MAY 24, 1990 APPLICATION NUMBER: US.01/28/23/55 FILING DATE: MARCHIT, 1989 ATTORNEY/AGENT INFORMATICN: NAME: ATTORNEY/AGENT INFORMATICN: NAME: ATTORNEY/AGENT NUMBER: 36,207 PREGISTRATION NUMBER: ATTORNEY PREGIST
 398 AA
 Score 55; DB 1: Louis Dred. No. 3.43e+01; 1; Mismatches 3
 REFERENCE/DOCKET NUMBER: IMI-018DV TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
 ADDRESSE: LAHIVE & COCKFIELD, LLP STREE: 60 State Street
CITY: Bosson
STATE: Massachusetts
 PRT:
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 398 AA: 43664 MW: 779006 CN:
198 AA; 43664 MW: 779006 CN;
 Sequence 74, Application US/08175069A
Patent No. 5776761
 Sequence 74. Application US/08175069A
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 74:
 STANCARD;
 SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
 51.98:
 CCMPUTER READABLE FORM:
 Query Match
Best Local Similarity 66.7%:
Matches 8: Conservative
 Query Match
Rest Local Similarity 66.7%:
Matches 8; Conservative
 COUNTRY: USA
21P: 02109-1875
 257 KGMLATVAFNMF 268
 US-08-175-069A-74
 SEÇUENCE
 xxxxxx
 RESULT
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 g
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APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Klapper, David G.
APPLICANT: Rannar, Thorung.
APPLICANT: Ruo, Mei-chany
IITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
ADDRESPENDENCE ADDRESS:
ADDRESPENDENCE ADDRESS:
 Score 54: DB 1; Length 387: Pred. No. 4.37e+01; 2: Mismatches 5; indels
 ¥
 387 AA
 E: LAHIVE & COCKFIELD
60 State Street, suite 510
 PRT:
 MOLECULE TYPE: protein
SEQUENCE 387 AA; 41660 MW; 736967 CN;
 COUNTRY: USA
ZIP: 02109-1875
COMPOTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 72, Application US/38290449A Patent No. 5698204 GENERAL INFORMATION:
 Sequence 72, Application US/08290448A
Patent No. 5676954
 Sequence 72, Application US/38290448A
 Sequence 72, Application US/U8290448A
 STANDARD;
 : 387 amino acuds
amino acid
3%: linear
 STANDARD:
 TELEFAX: (617)227-594' INFORMATION FOR SEQ ID NO:
 SECUENCE CHARACTERISTICS
 50.9%;
53.3%;
 STREET: 60 State Stre
C.TY: Boston
STATE: Massachusetts
 8: Conservative
 246 RGMLATVAFNTETDN 260
 1 KSMKVIVAFNOFGPN 15
 RESULT 11
US-08-290-448A-72
XX
AC XXXXXX
DT
XX
XX
DE Sequence 72, Applica
XX
CC Sequence 72, Applica
CC Sequence 72, Applica
 Local Similarity
US-08-290-448A-72
 LENGTHE
 Query Match
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SEQUENCE
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 Cars
 Sequence 72, Application US/08175069A
Patent No. 577670.
GENERAL INFORMATION
APPLICANT: Rogers, Bruce
APPLICANT: Riaper, David G.
APPLICANT: SEQUENTION: 311ergenic Proteins From Ragweed and Uses NUMBER OF SEQUENCE: 93
 APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Klapper, David G.
APPLICANT: Kuo, Mei-chang
AFFLICANT: Kuo, Mei-chang
AFFLICANT: Kuo, Mei-chang
ATTLE OF INVENTION: Allergenic Proteins From Hugweed and Uses
COPRESPONDENCE ADDRESS:
 ö
 CITY:
STATE: Mass...
COMPUTER: DOS...
COMPUTER FEADABLE FCRM:
REDIUM TYPE: Floppy disk
CCRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
PRING DATE: May DATA:
FLING DATE: May DATA:
FLING DATE: May DATA:
FLING DATE: May DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May DATA:
APPLICATION NUMBER: US 07/325,365
FILING DATE: May DATA:
APPLICATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
FERNCE/DOCKET NUMBER: MAY-018GN
TATAIN NUMBER: MAY-018GN
TATAIN NUMBER: MAY-018GN
TATAIN NUMBER: MAY-018GN
TERROCE/DOCKET NUMBER: MAY-018GN
TATAIN NUMBER: MAY-018GN
TATAIN NUMBER: MAY-018GN
 Score 54; DB 1; Length 387;
Pred. No. 4.37e+C1;
2; Mismatches 5: 1.36.s
 387 AA
 REFERENCE/DOCKET NUMBER: IM1-018CN TELECOMM'NICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION F:8 SEQ ID N: 72.
SEGUENCE CHRARCTERRISICS:
IENGIH: 397 amigo acids
 ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 60 State Street
 ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
 PRT:
 MOLECUSE TYPE: protein
JENCE 357 AA: 41660 MW: 736967 CN:
 Sequence 72, Application US/08175059A
 STANDARD;
 Query Match
Best Local Similarity 53.3%;
Mitches 8; Conservative
 246 RGMLATVAFNTFTDN 269
 1 KSMKVIVAFNOFGPN 15
 TYPE: amino acid
 linear
 SENERAL INFORMATION:
 STREET: 50 S:
CITY: Boston
 US-08-175-069A-72
 SEQUENCE
 XXXXXX
 5
```

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Sape
 APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Klapper, David G.
APPLICANT: Kafnar, Thorunc
APPLICANT: Kuo, Mel-chang
TILLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABHIVE & COCY IELD, LLP
STREET: 60 State Street
CITY: Boston
 Ü
 MEDICAL TYPE: FLOOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORPATING SYSTEM: PC-5-XX8-10-5
SOFTWARE: Patentin Release #1.5. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/175.054
FILING DATE: December 29, 1993
APPLICATION NUMBER: US 07/225.455
FILING DATE: MARCH 29, 1995
APPLICATION NUMBER: US 07/225.455
FILING DATE: MARCH 27, 1989
APPLICATION NUMBER: US 07/225.455
FILING DATE: MARCH 27, 1989
APPLICATION NUMBER: US 07/225.455
FILING DATE: MARCH 27, 1989
AFFORMEY/OBCKET NUMBER: 1MI-018DV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 Score 54: CB.1 Lebath 347
Pred. No. 4.37e+011
2: Mismatches 5: Indels
 COUNTRY: USA

ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/175,069A
FLING DATE: December 29, 1993
 ir.
 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 387 AA: 41660 MW: 736967 CN:
 Sequence 78, Application US/UE1750A9A
Patent No. 5776761
GENERAL INFORMATION:
 Sequence 78, Application US/LKI75UNIA
 TELEPHONE: (617)227-7400
TELEFAX: (617)227-7400
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACIER:STICS:
LENGTH: 387 amino acids
TYPE: amino acid
 STANDARD:
 Massachusetts
Massachusetts
 COMPUTER READABLE FORM:
MEDICM TYPE: Floppy
 Query Match
Best Local Similarity 53.3%;
Matches 8: Conservative
 246 RGMLAIVAFNIFIDN 260
 1 KSMKVIVAFNOFSPN 15
 RY: USA
02109-1875
 LT 13
US-C8-175-C69A-78
 COUNTRY:
 CITY: E
STATE:
```

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Sequence 78, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION
APPLICANT: Rainar, Thorund
APPLICANT: Roy Mei-Chais
IITLE OF INVENTION
AID: Genue CESS
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE 6: FIELD
STREET: 60 State Str. suite 516
CITY: Boston
CITY: Boston
CITY: Boston
 50.0%; Score 53; DB 1; Length 383; 53.3%; Pred. No. 5.57e+01;
 Score 53: DB 1: Length 383: Pred. No. 5.57e+01; 2: Mismatches 5: Indels
 383 AA
 NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REPEROEC/DOCKET NUMBER: IMI-618CN
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
 PRT;
 TOPOLOGY: linear
MCLECULE TYPE: protein
JENCE 383 AA: 41852 MW; 738971 CN;
 MOLECULE TYPE: protein
SEQUENCE 383 AA; 41852 MW; 738971 CN;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floepy disk
CMDUTER: ISM PC (computed):
OPENATING SYSJEM: PC-LV-S/MS-F: S
 Sequence 78, Application US/08290448A
 INFORMATION FOR SEQ ID NU: 78: SEQUENCE CHARACTERISTICS:
 (617)227-7400
(617)227- 41
 STANDARD:
 LENGTH: 383 amino acids TYPE: amino acid
 : 383 amino acids
amino acid
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 53.3%:
Matches 8; Conservative
 243 RGMLCTVAFNKFTDN 257
 1 KSMKVIVAFNOFGPN 15
 linear
 COUNTR: USA
ZIP: 02109-1875
 Query Match
Best Local Similarity
 LT 15
US-08-290-446A-78
 TOPOLOGY:
 LENGIH:
 SEQUENCE
 XXXXX
 RESULT
 888888888
 õ
 ö
 Gaps
 APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thounn
APPLICANT: Rub Annar, Thounn
TITLE OF INVENTION: Allergenic Proteins From Rupword and Uses
NUMBER OF SEQUENCES: 93
CORRESSENCE ADDRESS: LANING & COCKFIELD
STREET: 60 State Street, suite 510
 ö
 CITY: Poston
STATE: Massachusetts
CONTRY: USS
CONTRY: USS
CONTRY: USS
CONTRY: USS
COMPUTER READABLE FORM:
MEDIUM TYPE: F.Ceppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release 41.0, Version #1.25
CONTRYING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 41.0, Version #1.25
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/290.448A
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/525,365
FILING DATE: May CONTROL MUMBER: US 07/525,365
 Score 53: DB 1: Length Just
Pred. No. 5.57e+01:
""mairches 5: Indels
 383 AA.
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951
FILING :ATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNAYAGENT INFORMATION:
NAME: AMPERICATION NUMBER: IMI-0180V
REFERENCE/DOCKET NUMBER: IMI-0180V
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227,7400
TELEFANCE: (617)227,7400
 NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REGISTRENCE/DOCKET NUMBER: IMI-018CN
IELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
 PRT:
 MCLECULE TYPE: protein
SEQUENCE 383 AA: 41852 MW; 738971 CN;
 Sequence 78, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
 Sequence 78. Application 08/08290448A
 LENGULH: 383 amino acids
TYPE: amino acid
TOPOLOSY: Incore
 STANDARD:
 Match 50.0%;
Local Similarity 53.3%;
es 8; Conservative
 243 RGMLCTVAFNKFIDN 257
 1 KSMKVIVAFNOFGPN 15
 RESULT 14
ID US-08-290-448A-78
 Query Match
 xxxxxx
 *atches
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0:

Gaps

Ö :::de:: Š 2; Mismatches Matches 8; Conservative 

Swarch completed: Tue Jun 20 17:16:01 2000 Jcb time: 5 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:26:01 2000; MasPar time 14.94 Seconds 101:202 Million cell updates/sec Rug on:

Tabular output not generated.

>US-09-142-524A-9 (1-15) from US09142524A.pep 106 1 KSMKVIVAFNQFGPN 15 Title: Description: Perfect Score: Segmence:

Sporing table:

721208 seqs. 100765575 residues PAM 150 Gap 15 Searched:

Minimum Match 0% Listing first 45 summaries Pust-processing:

a-pending 1:PCT 2:06 3:U6C 4:U7 5:UF 5:U8L 7:U82 8:U83 9:U84A 10:U84B 11:U8S 12:U86 13:C 7 14:U89 15:U89 16:U9O 17:U91 18:U92 19:U93 20:U94 21:U5L 22:NEWP 23:NEWU6O 24:NEWU8 25:NEWU9 5utabase:

Mean 20,537; Variance 53,151; scale 0 386 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| July Score Match Length DB 1D Description Pred No. Score Match Length DB 1D Description Pred No. 19 10 US-08-467 Sequence 227, Applicat 4.81e-05 3 156 100:0 2 4 05-07-938 Sequence 227, Applicat 4.81e-05 4 05-07-938 Sequence 230, Applicat 4.81e-05 106 100:0 2 10 US-08-467 Sequence 230, Applicat 4.81e-05 106 100:0 2 10 US-08-467 Sequence 231, Applicat 4.81e-05 10 US-08-467 Sequence 231, Applicat 4.81e-05 10 US-08-467 Sequence 231, Applicat 4.81e-05 10 US-08-468 Sequence 231, Applicat 4.81e-05 11 US-08-468 Sequence 83, Applicat 4.81e-05 12 US-08-468 Sequence 83, Applicat 4.81e-05 13 US-08-467 Sequence 83, Applicat 4.81e-05 12 US-08-467 Sequence 83, Applicati 4.81e-05 12 US-08-467 Sequence 84, Applicati 4.81e-05 12 US-08-467 Sequence 83, Applicati 4.81e-05 12 US-08-467 Sequence 83, Applicati 4.81e-05 12 US-08-467 Sequence 84, Applicati 4.81e-05 12 US-08-467 Sequence 83, Applicati 4.81e-05 12 US-08-467 Sequence 84, Applicati 4.81e-05 12 US-08-467 Sequence 84, Applicati 4.81e-05 12 US-08-467 Sequence 81, Applicati 4.81e-05 12 US-08-467 Sequence 8 |          |       | æ     |        |          | SOLUMINOS  |           |       |           |          |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|-------|-------|--------|----------|------------|-----------|-------|-----------|----------|
| Score Match Length DB ID   Description   Pre-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Result   |       | Onery |        |          |            |           |       |           |          |
| 106 130.0 19 10 GS-08-467- Sequence 227, Applicat 4, 106 130.0 23 10 GS-08-467- Sequence 227, Applicat 4, 106 130.0 20 10 GS-08-36. Sequence 230, Applicat 4, 106 130.0 20 10 GS-08-36. Sequence 230, Applicat 4, 106 100.0 20 10 GS-08-467- Sequence 231, Applicat 4, 106 100.0 21 10 GS-08-467- Sequence 231, Applicat 4, 106 100.0 21 10 US-08-467- Sequence 231, Applicat 4, 106 100.0 24 10 US-08-468- Sequence 231, Applicat 4, 106 100.0 26 10 US-08-468- Sequence 33, Applicat 4, 106 100.0 26 10 US-08-468- Sequence 86, Applicat 4, 106 100.0 26 10 US-08-468- Sequence 87, Applicat 4, 106 100.0 26 10 US-08-468- Sequence 87, Applicat 4, 106 100.0 26 10 US-08-468- Sequence 87, Applicat 4, 106 100.0 26 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 26 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 26 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-467- Sequence 87, Applicat 4, 106 100.0 28 10 US-08-468- Sequence 87, Applicat 4, 106 100.0 20 US-08-468- Sequence 87, Applicat 4, 106 100.0 20 US | No.      | Score | Match | Length | <u>න</u> | QI.        | Descripti | on    |           |          |
| 155 100.0 19 8 US-G8-350- Sequence 227. Applicat 4. 156 100.0 2 4 US-G8-350- Sequence 230. Applicat 4. 156 100.0 2 4 US-G7-938 Sequence 47. Applicat 4. 156 100.0 2 0 10 US-G8-467- Sequence 230. Applicat 4. 156 100.0 2 110 US-G8-467- Sequence 231. Applicat 4. 156 100.0 2 110 US-G8-467- Sequence 231. Applicat 4. 156 100.0 2 110 US-G8-468- Sequence 231. Applicat 4. 156 100.0 2 110 US-G8-468- Sequence 231. Applicat 4. 156 100.0 2 10 US-G8-468- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-468- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-468- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-468- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-468- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 331. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 10 US-G8-467- Sequence 341. Applicat 4. 156 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100.0 2 100. | ٦        | 106   | 0.001 | 19     | 0.7      | US-08-467- | Seguence  | 227,  | Applicat  | 4.81e-05 |
| 106   100   2   10   US-G8-467   Sequence   230   Applicat   4   106   100   2   4   US-G9-938   Sequence   230   Applicat   4   106   100   2   2   4   US-G9-938   Sequence   230   Applicat   4   106   100   2   10   US-G8-467   Sequence   231   Applicat   4   106   100   2   10   US-G8-467   Sequence   231   Applicat   4   106   100   2   10   US-G8-467   Sequence   231   Applicat   4   106   100   2   10   US-G8-468   Sequence   231   Applicat   4   106   100   2   10   US-G8-468   Sequence   231   Applicat   4   106   100   2   10   US-G8-468   Sequence   232   Applicat   4   106   100   2   10   US-G8-468   Sequence   232   Applicat   4   106   100   2   10   US-G8-468   Sequence   233   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   2   10   US-G8-467   Sequence   234   Applicat   4   106   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   10   | €,       | 106   | 0.001 | 13     | ထ        | US-08-350- | Sequence  | 227.  | Applicat  | 4.81e-05 |
| 105 100.0 20 4 US-C7-938 Sequence 47, Applicati 4. 105 100.0 20 8 US-08-350- Sequence 47, Applicati 4. 106 100.0 20 10 US-08-467 Sequence 230, Applicat 4. 106 100.0 21 10 US-08-467 Sequence 231, Applicat 4. 106 100.0 21 10 US-08-467 Sequence 231, Applicat 4. 106 100.0 24 10 US-08-468 Sequence 233, Applicat 4. 106 100.0 24 10 US-08-468 Sequence 234, Applicat 4. 106 100.0 26 10 US-08-468 Sequence 83, Applicati 4. 106 100.0 26 10 US-08-468 Sequence 84, Applicati 4. 106 100.0 26 10 US-08-467 Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467 Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467 Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467 Sequence 83, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 Sequence 81, Applicati 4. 106 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 100.0 20 10 | ~        | 106   | 100.0 | 7      | 0.5      | US-C8-467- | Sequence  | 230.  | Applicat  | 4.81e-05 |
| 106 100.0 20 8 US-08-350- Sequence 230 Applicat 4. 106 100.0 20 10 US-08-467- Sequence 231, Applicat 4. 106 100.0 21 10 US-08-468- Sequence 231, Applicat 4. 106 100.0 21 10 US-08-468- Sequence 231, Applicat 4. 106 100.0 24 10 US-08-468- Sequence 231, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 224, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 85, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 87, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 87, Applicat 4. 106 100.0 26 10 US-08-467- Sequence 88, Applicat 4. 106 100.0 26 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 26 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicat 4. 106 US-08-467- Seq | 4        | 106   | 100.0 | 7      | 7        | US-07-938- | Seguence  | 47,   | Applicati | 4.81e-05 |
| 106 100.0 2010 US-08-467- Sequence 47. Applicati 4. 106 100.0 2110 US-08-467- Sequence 231, Applicat 4. 106 100.0 2110 US-08-468- Sequence 233, Applicat 4. 106 100.0 24 10 US-08-468- Sequence 234, Applicat 4. 106 100.0 24 10 US-08-468- Sequence 234, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 86, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 87, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 87, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 87, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 87, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 US-08-450- Sequence 81, Applicati 4. 106 US-08-450- Sequence 81, Appli | Ŋ        | 106   | 100.0 | 2 C    | œ        | US-08-350- | Sequence  | 230.  | Applicat  | 4.81e-05 |
| 106 100.0 21 10 US-08-467- Sequence 231, Applicat 4. 106 100.0 21 10 US-08-467- Sequence 231, Applicat 4. 106 100.0 21 10 US-08-468- Sequence 233, Applicat 4. 106 100.0 24 10 US-08-468- Sequence 224, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 85, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-226- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 8 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 9        | 106   | 100.0 | 20     | 10       | US-08-467- | Sequence  | 47.   | Applicati | 4.81e-05 |
| 106 100.0 2:10 US-08-467- Sequence 231. Applicat 4. 106 100.0 2310 US-08-468- Sequence 233. Applicat 4. 106 100.0 24 10 US-08-468- Sequence 224. Applicat 4. 106 100.0 26 10 US-08-468- Sequence 83. Applicat 4. 106 100.0 26 10 US-08-468- Sequence 83. Applicati 4. 106 100.0 26 10 US-08-26- Sequence 83. Applicati 4. 106 100.0 26 10 US-08-26- Sequence 83. Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84. Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84. Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84. Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81. Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81. Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81. Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81. Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81. Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81. Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 7        | 106   | 100.0 | 21     | 01       | US-08-467- | Sequence  |       | Applicat  | 4.81e-05 |
| 106 100.0 23.10 US-08-468- Sequence 233. Applicat 4. 106 100.0 24.10 US-08-467- Sequence 224, Applicat 4. 106 100.0 26.10 US-08-468- Sequence 85, Applicati 4. 106 100.0 26.10 US-08-468- Sequence 83, Applicati 4. 106 100.0 26.10 US-08-26- Sequence 83, Applicati 4. 106 100.0 26.10 US-08-467- Sequence 84, Applicati 4. 106 100.0 26.10 US-08-467- Sequence 83, Applicati 4. 106 100.0 26.10 US-08-467- Sequence 84, Applicati 4. 106 100.0 28.10 US-08-467- Sequence 81, Applicati 4. 106 100.0 20.0 20.0 20.0 20.0 20.0 20.0 20.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | œ        | 106   | 100.0 | 21     | ា        | US-08-467- | Sequence  | 231,  | Applicat  | 4.81e-05 |
| 106 100.0 24 10 US-08-467- Sequence 224, Applicat 4. 106 100.0 26 10 US-08-468- Sequence 85, Applicati 4. 106 100.0 26 10 US-08-468- Sequence 83, Applicati 4. 106 100.0 26 7 US-08-226- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-350- Sequence 81, Applicati 4. 106 US-08-350- US-08-350 | σ        | 106   | 100.0 | 23     | 10       | US-08-468- | Sequence  | 233,  | Applicat  | 4.81e-05 |
| 106 100.0 26 10 US-08-468 - Sequence 85, Applicati 4. 106 100.0 26 10 US-08-468 - Sequence 83, Applicati 4. 106 100.0 26 10 US-08-226 - Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467 - Sequence 86, Applicati 4. 106 100.0 26 10 US-08-467 - Sequence 87, Applicati 4. 106 100.0 26 10 US-08-467 - Sequence 87, Applicati 4. 106 100.0 26 10 US-08-467 - Sequence 87, Applicati 4. 106 100.0 28 10 US-08-467 - Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467 - Sequence 81, Applicati 4. 106 100.0 28 8 US-08-467 - Sequence 81, Applicati 4. 106 100.0 28 8 US-08-350 - Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 10       | 106   | 100.0 | 24     | 10       | US-08-467- | Sequence  | 224,  | Applicat  | 4.81e-05 |
| 106 100.0 26 12 US-28-468- Sequence 83, Applicati 4. 106 100.0 26 7 US-08-226- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 86, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Ľ        | 106   | 100.0 | 26     | 10       | US-08-468- | Sequence  | 86,   | Applicati | 4.81e-05 |
| 106 100.0 26 7 US-08-226- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 86, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84, Applicati 4. 105 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 105 100.0 28 8 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 12       | 106   | 100.0 | 26     | 10       | US-08-468- | Seguence  | 83,   | Applicati | 4.81e-05 |
| 106 100.0 26 10 US-C8-467- Sequence 86, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 84, Applicati 4. 106 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 106 100.0 28 10 US-08-467- Sequence 81, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4. 106 100.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 7,3      | 106   | 100.0 | 26     | ٢        | US-08-226- | Sednence  | 83,   | Applicati | 4.81e-05 |
| 106 100.0 26 1C US-08-467- Sequence 83, Applicati 4. 206 100.0 26 1C US-08-467- Sequence 84, Applicati 4. 206 100.0 26 1C US-08-467- Sequence 83, Applicati 4. 206 100.0 28 1C US-08-468- Sequence 81, Applicati 4. 206 100.0 28 10 US-08-467- Sequence 82, Applicati 4. 206 100.0 28 8 US-08-350- Sequence 81, Applicati 4. 206 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | -1       | 106   | 100.0 | 26     | 10       | US-C8-467- | Sequence  | . ,98 | Applicati | 4.81e-05 |
| 106 100.0 26 10 US-08-467- Sequence 84, Applicati 4. 105 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 105 100.0 28 10 US-08-467- Sequence 82, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 15       | 106   | 100.0 | 26     | 10       | US-08-467- | Sequence  | 83,   | Applicati | 4.83e-05 |
| 105 100.0 26 10 US-08-467- Sequence 83, Applicati 4. 106 100.0 28 10 US-08-468- Sequence 81, Applicati 4. 105 100.0 28 10 US-08-467- Sequence 82, Applicati 4. 105 100.0 28 8 US-08-350- Sequence 81, Applicati 4. 105 100.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 9:1      | 106   | 100.0 | 26     | ] C      | US-08-467- | Seguence  | 34.   | Applicati | 4.81e-05 |
| 106 100.0 28.10 US-08-468- Sequence 81, Applicati 4. 106 100.0 28.10 US-08-467- Sequence 82, Applicati 4. 106 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | r-<br>-1 | 106   | 100.0 | 26     | 10       | US-08-467- | Sequence  | 83,   | Applicati | 4.8.6-05 |
| 136 160.3 28 10 US-08-467- Sequence 82, Applicati 4. 106 160.3 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ar)      | 301   | 100.0 | 2      | 70       | US-08-468- | Sequence  | e1,   | Applicati | 4 8 e 05 |
| 105 100.0 28 8 US-08-350- Sequence 81, Applicati 4.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | e)       | 106   | 100.0 | 2      | 10       | US-08-467- | Sequence  |       | Applicati | 4.81e-05 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 20       | 105   | 100.0 | 28     | œ        | US-08-350- | Sequence  |       | Applicati | 4.8.6-05 |

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3 KSMKVIVAENQEGEN 17
 US-08-467-023-230
 SECUENCE
 Query Match
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 Sequence 227, Application US/0835025
GENERAL INFORMATION:
APPLICANT Scriffeth, IIWIN J.;
APPLICANT Scriffeth, JUNIAN F.;
APPLICANT Garman, Bichard D.;
APPLICANT Garman, Bichard D.;
APPLICANT Garman, Bichard D.;
APPLICANT Young, Signmel H.;
APPLICANT Young, Signmel H.;
APPLICANT Extey, Mark A.;
APPLICANT Extey Mark A.;
APPLICANT Ext
 ö
REGISTRATION NUMBER: 38.872
REPEROX/COURT NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNCATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION: 227-7401
INFORMATION: 227: 227-18
EUGHI: 19 amino acids
TEMPE: animo acids
TOPOLIGY: linear
M.LEOURITYRE: peptido
FRAGMENTITYRE: peptido
FRAGMENTITYRE: peptido
SEQUENCE: 19 Ami: 2156 MW: 1801 CN:
 Soure 105: Est 10; Length 19; Prod. No. 4.81e-05; C. Mismatches C. Indels
 COMPUTER: NEW RECORDS OF STEEL STEEPING STEEL STEELING STEEL STEELING STEEL STEELING . 9 AA
 PRI
 Sequence 227, Application US/08350225
 STANCARD:
 CITY: Waltham STATE: MA COUNTRY: USA ZIP: G154 COMPUTER REARABLE FORM: MEDIUM TYPE: Floppy J:
 100.0%:
Hest Local Similarity 100.0%:
Matches 15: Conservative
 1 KSMKVIVAFNOFGPN 15
 3 KSMKVTVAFNQFGPN 17
 Prisott 2

11 US-98-359-225-227

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 SEQUENCE
 88889888888888
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 Sequence 236, Application US/18467027
GENERAL INFORMATION
APPLICANT Grilleto. Twin U
APPLICANT Bools USING A
APPLICANT Garman Richald D
APPLICANT Garman Richald D
APPLICANT Woung Slummer W.
APPLICANT Woung Slummer W.
APPLICANT Woung Slummer W.
APPLICANT Woung Slummer W.
APPLICANT Braner Andrew
APPLICANT Exiey Mark A.
APPLICANT Exiey Mark A.
APPLICANT Exiey Mark A.
APPLICANT Braner. Seeven B.
ITLE OF INVENTION Allergenic Proteins And Peptides From TITLE OF INVENTION Japanese Cedar Folien
 SOFTWARE. Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DAIN.
APPLICATION NUMBER: US/06/467.023
F.LING DATE. June 6, 1995
C.ASSIFICATION NUMBER: US/06/467.023
F.LING DATE. June 6, 1995
C.ASSIFICATION DAIN.
APPLICATION NUMBER: 08/350.225
FILING DAIE. DOCEMBER 6, 1994
ATTORNEY/ACENT INFORMATION.
NAME. Jane E. Remilland.
REGISTRATION NUMBER: 38/872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (INT-D28CPD2)
IELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-746
TELEPHONE: (617) 227-75941
INFORMATION FOR SEQ. JED NO. 230:
SEQUENCE CREATERISTICS:
LENGTH: 20 amino acids
 Lendin 174
 2. AA
 Score 1(t) 78 8: 7 Pred; No. 4.81e 55
 7.
 ZIP: U2154
COMPUTER REARBLE FORM:
MELUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DVS
 Sequence 230, Application US/0846702×
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: allocat
 MOLECULE TYPE: Febtide
FRAGMENT TYPE: internal
JENCE 19 AA: 2156 MW: 1801 GN,
 STANDARD
 Obery Match
Best Local Similarity 100.0%:
Matches 15: Conservative
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1 KSMKVTVAFNQFGPN 15
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 Gaps
 APPLICANT: Griffith, Irwin J.
APPLICANT: Ground Griffith, Joanne
APPLICANT: Bodliock, Joanne
APPLICANT: Bodd Julian
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 76
CORRESPENDENCE ADDRESS:
 Ċ
 Lenath 2C:
 STATE: MA

COUNTRY: MA

COUNTRY: USA

LIP: 02109

COMPUTER FROABLE FORM:
MEDICH TYPE: Floppy disk
COMPUTER: LEW FO COMPATIBLE
OPERATION SYSTEM: PO-DOS/MS-DOS
SOFTWARE: PATENTIAN PO-DOS/MS-DOS
SOFTWARE: PATENTIAN NUMBER: US/07/938,990A
FILING:ATE: 1992'0'0'1
CLASSIFICATION: 435
CLASSIFICATION: A35
FROM APPLICATION NUMBER: 07/736,452
FILING:ATE: July 15, 1991
FROM APPLICATION NUMBER: 07/736,452
FILING:ATE: July 15, 1991
FROM APPLICATION NUMBER: July 15, 1991
FROM APPLICATION NUMBER: July 16, 1991
FROM APPLICATION NUMBER: July 16, 1991
FROM APPLICATION NUMBER: JA TORRICE/SOCKET NUMBER:
 Score 105, DB 4; Length 20;
Pred. No. 4.81e-05;
0; Mismatches 0; Indeis
 0: Indels
 20 AA
 Score 106; DB 10;
Pred. No. 4.81e-05;
0; Mismatches 0.
 PRT;
 Sequence 47, Application US/07938990A GENERAL INFORMATION:
 Sequence 47, Application US/07938990A
 E: Lahive & Cockfield
Sixty State Street
 20 AA: 2244 MW; 1852 CN;
 TOPOLOGY: linear

WOLEGULE TYPE: peptide

FRAGMENT TYPE: internal

JENCE 20 AA: 2285 MM: 2007 CN:
 INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS:
 TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
 STANDARD:
 LENGIH: 20 amino acids :YPE: AMINO ACID
 MOLECULE TYPE: peptide
FRASMENT TYPE: internal
 Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative
 Ouery Match
Best Local Similarity 100.0%:
Matches 15; Conservative
 1 KSMKVTVAFNQFGPN 15
 linear
 amino acid
 4 KSMKVTVAFNQFGPN 18
 Boston
 JT 4
US-07-938-990A-47
 ADDRESSEE:
STREET: Si
 TOPOLOGY:
 Sequence 47,
 SECUENCE
 SEQUENCE
 XXXXXX
 RESULT
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ó.
 Saps
 APPLICANT: Garman, Richard 2),
APPLICANT: Kuo, Mai-Chang:
APPLICANT: You, Mai-Chang:
APPLICANT: Exio, Mark A.:
APPLICANT: Exiov, Mark A.:
APPLICANT: Solution and Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
 ö
 Length 20;
 ZIP: 02154
COMPUTER REACABLE FOR.
MEDIUN TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERTING SYSTEM: PC-DOS/WS-DOS
SOFTHARE: Patentin Relcane *1.0, Version *1.25
SOFTHARE: Patentin Relcane *1.0, Version *1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,225
FILING DATE: Decembe: 1994
CLASSFICATION: 424
PRICATION NUMBER: US/22,246
FILING DATE: APPLICATION UNMBER: US/22,246
FILING DATE: APPLICATION NUMBER: US/22,246
APPLICATION NUMBER: US/22,246
FILING DATE: APPLICATION NUMBER: US/22,246
 0; Indels
 ADDRESSEE: Immulogic Pharmaceutical Corporation.
STREET: 610 Lincoln St
CITY: Waltham
 FILING DATE: January 15, 1993
ATTORNEY, AGENT INFORMATION:
NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-028CP2)
TELEDHONE: (617) 466-6700
 20 AA
 Score 106; DB B; I
Pred. No. 4.81e-05;
0; Mismatches 0;
 PCI/US93/00139
 PRT
 Sequence 230, Application US/08350225 GENERAL INFORMATION:
 Sequence 230, Application US/68350225
 FILING DATE: September 1, 1992 APPLICATION NUMBER: PCI/US93/0
 RMATION:
Griffeth, Irwin J.,
Pollock, Joanne;
Bond, Julian F.;
 TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA: 2285 MW; 2007 CN;
 INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
 (617) 466-6900
17) 466-604
 STANDARD
 LENGTH: 20 amino acids TYPE: amino acid
 Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative
1 KSMKVIVAFNQFGPN 15
 (617)
 USA
 COUNTRY: US
 J. 5
US-08-350-225-230
 TELEFAX:
 LENGTH:
 APPLICANT
 SEQUENCE
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4 KSMKVTVAFNQFGPN 18

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Gaps

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Application US/08467023

Griffeth, Irwin J.

Pollock Johnne Bond Juli F.; Bond Juli F.; Kuo, Mel-Chang: Yeung, Slurmel H.; Brauer, Androw, Exley, Mark A.;

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Sequence 231, Application US/08467023
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 GENERAL
 XXXXXX
ô
 Ö
 Gaps
 APPLICANT: Exley, Mark A.;
AFPLICANT: Powers. Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SECURORES: 261
CORPESPONDENCE ADDRESS:
 Ö
 ADDRESSED: Immulogic Pharmaceutical Corporation, Inc. STREET: 410 Lincoln St. CIIV: Waltham
 Score 106: DB 10; Length 20;
Pred. No. 4.81e-05;
C: Mismatches C: Indels
 REFERENCE/JONNUMBER. 78.972
REFERENCE/JONNUMBER. 025.6 FSD4 (IMI-0287P04)
TELECORMUNICATION INFORMATION: (617) 2277400
TELEFRA: (617) 2277400
TELEFRA: (617) 2277400
SEGENCE CHEBANTION FOR SEQ. 10 NO: 47:
 COMPUTER PEADABLE FORM:
MEDICH TYPE: Floppy disk
CMUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: June 6, 1995
 20 AA
 PRI:
 Sequence 47, Application US/08467697
GENERAL INFCRMATION
APPLICANT GALIffeth, Irwin J.;
APPLICANT POLICEK, Jeanne,
APPLICANT Bond, Julian F.;
APPLICANT Garmen, Richard D;
APPLICANT Kuo, Mos-Chang,
APPLICANT Func, Siummeth:
 CLASSIFITATION 424
PRIOR APPLICATION DATA
APPLICATION DATA
FILING (ATE, December 6, 1944
ATTORNEY/A SENT INFORMATION:
 LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAMENI TYPE: internal
 Sequence 47, Application US/08457697
 STANDARD;
 query Match
Best Local Similarity 100.0%;
Matches 15; Conservative
CITY,
STATE: NA
COUNTRY: USA
TP: 02154
 RESULI 6
ID US-08-467-697-47
 SEQUENCE
 XXXXX
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 Sells
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Dapan, se dedar Publen
NUMBER OF SEQUENCES: 26.
CORRESPONDENCES: 26.
CORRESPONDENCE ADDRESS:
STREET: 610 incoln St
 Ö
 Score 106; DB 10; Length 21; Pred. No. 4.81e-05; 0; Mismatches 0; Indels
 38.872
5R: 025.6 USD2 (IMI:0280EC2)
 COUNTRY: DAM
ZIP: 02154
CCMPUTER READABLE FORM:
MEDIUM TYPE: FLOPEN disa.
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D-S
SOFTARE: Patentin Release #1.0, Varsio: #1 25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: DS/C8/467,623
FILLING DATE: June 6, 1995
 21 AA
 PRT;
 APPLICATION NUMBER: 08/350.225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
 Sequence 231, Application US/08467006
 TYPE: amino acid
TOPOLGSY: linear
MOLEGULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 21 AA: 2415 MW: 2154 CN:
 REGISTRATION NUMBER: 36.872
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
 TELEFAN. (617) 227-748.
INFORMATION FOR SEQ. 12 NO. 2-41
SEQUENCE CHARACIES STITES
LENGTH: 21 amino acids
 STANDARD;
 Jane E. Remillard
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
 4 KSMKVTVAFNOFGPN 18
 1 KSMKVIVAFNOFGPN 15
 RESULT 8
ID US-08-467-006-231
XX
AC XXXXXX
DT
XX
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XX
XX
XX
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XX
XX
DE Sequence 231, Applia
 STATE: MA
 COUNTRY:
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21 AA.

PRT;

STANDARD:

RESULT 7 ID US-08-467-623-231

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APPLICANT: Garman, Rich.: D:
APPLICANT: Wido, MealCha.
APPLICANT: Yeard, Slurce. Addrew.
APPLICANT: Brauer, Andrew.
APPLICANT: Brauer, Andrew.
APPLICANT: Bray.
APPLICANT: Bray.
APPLICANT: Bray.
APPLICANT: Bray.
APPLICANT: Bray.
APPLICANT: Powers: Steven P.
ITLE OF INVENTION: Allergenic Proteins And Peptides Film.
ITLE OF INVENTION: Allergenic Proteins And Peptides Film.
APPRESPENDENCE. 25:
CORRESPONDENCE ADDRESS
ADDRESSEE: Zenualogic: immaceutical Corporation: Inc.
STREET: 610 Lincoln S:
CITY: Waltham
STREET: MA
 Query Match 100.0%; Score 105; CB 10; Length 23; Best Local Similarity 100.0%; Pred. No. 4.61e-05; Matches 15; Conservative 0; Mismatches 0; Inde's
 FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION: 424

PRIOR APPLICATION: 424

PRIOR APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

APPLICATION NUMBER: 08/266,248

FILING DATE: April 8, 1994

APPLICATION NUMBER: 07/956,990

FILING DATE: September 1, 1992

APPLICATION NUMBER: 10/93/CC13+

APPLICATION NUMBER: 10/93/APPLICATION NUMBER: 10/93/APPLICATION NUMBER: 07/96,990

FILING DATE: Aminary 15, 1993

ATTORNEY/AGENT INFORMATION:

NAME: DATIFURE A. VANSLONE

REGISTRATION NUMBER: 025.6 US (IMI-028CP2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 466-604

INFORMATION FOR SEQ ID NO: 233:
SEQUENCE CHARACTERISTICS

FORCE CHARACTERISTICS
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DUG/MS-DUS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/468,940
 24 AA
 Sequence 224, Application US/08457023
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
 Sequence 224, Application US/38467023
 MOLEGOUE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 23 AA) 2558 MW, 2764 (N)
 Griffeth, Irwin J.;
Pollock, Joanne:
Bond, Julian F.;
 STANDARD;
 amine acid
 4 KSMKVTVAFNOFGPN 18
 USA
 COUNTRY: US
ZIP: 02154
 US-08-457-023-224
 TOPOLOGY:
 XXXXXX
 RESULT
 ò
 Ö
 APPLICANT BOILOCK, Joanne,
APPLICANT BOILOCK, Joanne,
APPLICANT BOND, Julian F.,
APPLICANT BOND, Julian F.,
APPLICANT Garman, Richard D.,
APPLICANT BOUNG, Siu-mel H.,
APPLICANT Brauer, Andrew.
APPLICANT BRAIN.
APP
 Gaps
 ö
 STAIL:
COURTY: USA
ZIP: 0.2154
ZIP: 0.2154
ZIP: 0.2154
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DAILA:
APPLICATION UNMBER: US/08/467,006
FILING SATE: Junc 6, 1995
TINGS SATE: Junc 6, 1995
 Score 106: DB 10; Length 21: Pred. No. 4.81e-65; 0: Mismatches 0: Indels
 NAME: Jane E. REGALLIANG
REGISTRATION NUMBER: 38.872
REFERENCE/DOCKET NUMBER: 025.6 US 5 (IMI-028CPD6)
TELEPHONICATION INFORMATION:
TELEPHONE: (6.77) 2.27-7400
TELEPHONE: (6.77) 2.27-7400
TELEPHONE: (6.77) 2.27-5941
INFORMATION FOR SEQ ID NC: 231:
SEQUENCE: 2. aming acids
 PRT:
 Sequence 233, Application US/08468946
GENERAL INF.RMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: POLlock, Joanne;
APPLICANT: Bond, Julian F.;
 CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 38/350,225
FILLING DATE: December 5, 1994
ATTORNEY/AGENT INFORMATION:
 Sequence 233, Application US/08468940
 TYPE: amino acid
TOPOLOGY: incar
MOLECULE TYPE: peptide
FRAGMENI TYPE: internal
JENCE 21 AA: 2415 MM: 2154 CN:
 STANDARD;
 Cuery Match
Best Local Similarity 190.0%:
Matches 15: Conservative
 4 KSMKVTVAFNQFGPN 18
 1 KSMKVTVAENOFGPN 15
 J 9
US-08-468-940-233
 SEQUENCE
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Gaps

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26 AA
 Coety Match Louis viscos Socie (06) 137 [3]
Best Louis Similarity (01) % (104) No. (14) 000 Matches (15) Consentative (01) Massachus
 Sequence 83, Application US/38468940
GENERAL INFORMATION.
APPLICANT: Siffeth, Irwin 3.;
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D.;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: POWERS, Steven P.
 PRT :
 LENGTH: 26 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: pertide
FRAGMENT TYPE: internal
 Giffeth, Irwin J.;
Pollock, Joanne:
Bond, Julian F.;
Garman, Richard D.;
Kuo, Mei-Chang;
Yeung, Siurmei H.;
Brauer, Andrew;
Exley, Mark A.;
Powers, Steven P.
 Sequence 83, Application US/08458943
 TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
 STANDARD;
 COUNTRY: USA
21P: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 1 KSMKVIVAENQEDEN 15
 1 KSMKVTVAFNQEGPN 15
 US-08-468-940-83
 SEQUENCE
 XXXXXX
 ò
APPLICANT: Garman, Nichard D.
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer. Andrew.
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Brauer. Severa D.
TITLE OF INVENTION: Japanese Cedar Polien
NUMBRE OF SEQUENCES:
CRRESPONDENCE AUDRESS:
ADDRESSEE: Immunogro Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St.
COINTY: Walltham
STATE: MA
 ZIP: NO.2154
ZIP: NO.2154
ZIP: NO.2154
ZEDEN IVES FREE FORM:
MEDIUM IVES: Floppy disk
COMPUTER: TRM PC COMPATIBLE
COMPUTER: TRM PC COMPATIBLE
COMPUTER: TRM PC COMPATIBLE
COMPUTER: PACCULIN MELBASE #1.0, Version #1.25
SOFIWATE: PACCULATION DATA:
APPLICATION NUMBER: US/08/467.023
FILING LATE: Ucme 6. 1995
GLASSIE:GATION DATA:
APPLICATION NUMBER: 08/350,225
FILING CATE: December 5, 1994
ATCRNEY/ACRI INFORMATION:
NAME: Janc E. REMILIAR ERESTENCY/DOCKET NUMBER: 38/872
REFERENCY/DOCKET NUMBER: 38/872
RECENTATION SOURCE CARACTERISTICS:
LENGTH: 24/amino acids
 Score 106: DB 10; Lensth 24: Pred. No. 4.81e-05: 0: Mismatches 0: (nde)s
 26 AA
 PRT:
 equence 86, Application US/08468940 GENERAL INFORMATION:
 Griffeth, Irwin J.;
Pollock, Joanne:
Bond, Julian F.;
Garman, Richard D;
 Sequence 86, Application US/08458940
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
HENCE 24 AA: 2716 MW: 2744 CN;
 Kuo, Mei-Chang:
Yeung, Siu-mei H.;
Brauer, Andrew:
Exiey, Mark A.;
Powers, Steven P.
 STANDARD;
 udery Match
East Local Similarity 100.0%:
Matches 15: Conservative
 TYPE: amino acid
TOPOLOGY: linear
 3 KSMKVTVAFNOEGPN 17
 1 KSMKVIVAFNOFGPN 15
 iinear
 US-08-468-940-86
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 Sequence 86,
 SHOUENCE
 XXXXXX
 RESULT
 5
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3.
3.
3.
IITLE OF INVENTION: Allergenic Proteins and Peptides From TITLE OF INVENTION: Japanese Cedar Pollen NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Immulogic Patraceutical Corporation, Inc., STREET: 610 Lincoln St. CITY: Waltham
 MEDIUM TYPE: Flippy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATTON COMPATIBLE
CORRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,940
FLING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/56,225
FILING DATE: December: 1994
APPLICATION NUMBER: 08/226,248
FILING DATE: September: 08/226,248
FILING DATE: September: 08/226,248
FILING DATE: September: 1994
APPLICATION NUMBER: U7/188/990
FILING DATE: September: 1992
APPLICATION NUMBER: FCT US93/V0139
FILING DATE: September: 1993
AND DATE: JOHNAND NUMBER: FCT US93/V0139
FILING DATE: JOHNAND NUMBER: FCT US93/V0139
 NAME: Darlene A. Vanstone
RCISTRATION NUMBER: 15,729
REFERENCE/COCKET NOMBER: 025,6 US (INI-028CP2)
TELEPHONE: (617) 456-6.00
```

 $\ddot{\circ}$ 

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APPLICANT: Powers, Steven P.
TILE OF INVENTION: Allergenic Proteins And Peptides From
TILE OF INVENTION: Japanese Cedar Polien
NUMBER OF SEGIENCES: 261
CORRESPONDENCE ADDRESS:
 IIILE OF INVENTION: Alleraenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Poilen.
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immulogic Pharmaceutical Corporation: Inc., STREET: 610 Lincoin St.
 COMPTIENT TYPE: Floppy disk

COMPTIENT IBM PC COMPATIONE
COMPUTER: IBM PC COMPATIONE
COMPUTER: IBM PC COMPATIONE
COMPUTER: IBM PC COMPATIONE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/226.248A
FILING DATE: April 8, 1994
PRING APPLICATION DATA:
APPLICATION NUMBER: US/992
FILING DATE: September: 1992
APPLICATION NUMBER: PCT/059/20) 49
FILING DATE: January 15, 1993
ATTORNEY AGGNET INFORMATION:
NAME: Datlene A. Vanstone
REFERENCE/DOCKET NUMBER: 35.729
REFERENCE/DOCKET NUMBER: 35.729
REFERENCE/DOCKET NUMBER: 25.5 US (IMI-028CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
INFORMATION FOR SEQ ID NO: #3:
SEQUENCE CHARACTERISTICS:
FERTALLO SACCITED STATES
FERTENCE CHARACTERISTICS:
FERTENCE CHARACTERISTICS:
FERTALLO SACCITED STATES
 Length 26:
 1500018
 AA
 y Match 100.0%; Scure 106. LB 7; 1
Local Similarity 100.0%; Pred. No. 4.81e-05;
hes 15; Conservative U: Mishatries 0.
 3
 Sequence 86. Application US/39467697
GENERAL INFORMATION.
APPLICANT: Griffeth, Irvin J.:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard D.
APPLICANT: Garman, Richard D.
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Exley, Mark A.:
APPLICANT: Exley, Mark A.:
APPLICANT: POWNERS, Steven P.
 Sequence 86, Application US/08467697
 TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
 STANDARD
 26 amino acids
 aminc acid
 1 MSMKVTVAFNOFISHN 13
 1 KSMKVIVAFNOFOPN 15
 CSA
 02154
 J. 14
US-08-467-697-86
 LENGIH:
 SECCENCE
 Query Match
 xxxxxx
 Matches
 RESULT
 Ö
TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Gedar Polien COMPRES OF SEQUENCES: 261
CORRESPONDENCE ADDRESS: ADDRESSE: ImmuLogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoin St STREET: Maltham STATE: Ma
 Scure 106: 09 10: Depart 26:
Fred. No. 4.#1e:05:
0: Mismatches 0. Indels
 OPERALING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PREGREE #1.5, Version #1.25 CURRENT APPLICATION DATA: PC-DOS/MS-DOS SOFTWARE: PREGREE #1.5, Version #1.25 APPLICATION NUMBER: US/08/468.540 FILLS OATE: APPLICATION NUMBER: US/08/350.225 FILLNG DATE: December 6, 1994 APPLICATION NUMBER: US/324,248 FILLNG DATE: December 6, 1994 APPLICATION NUMBER: US/336,990 FILLNG DATE: September 1, 1992 APPLICATION NUMBER: US/336,990 FILLNG DATE: September 1, 1993 APPLICATION NUMBER: US/336,990 FILLNG DATE: Danuary 15, 1993 APPLICATION NUMBER: DC/JOS93/00:39 FILENG DATE: Danuary 15, 1993 APPLICATION NUMBER: 35,729 REPRENCE/OCKET NUMBER: 35,729 REPRENCE/O
 25 AA
 Sequence 83. Application US/08226248A
GENERAL INCRMATICN:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard D;
APPLICANT: Koo, Met-Crang:
APPLICANT: Koo, Met-Crang:
APPLICANT: Young, Slutmei H.;
APPLICANT: Xeung, Slutmei H.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: POWERS, Steven P.
 PRT;
 COUNTRY: USA
ZIP: 32154
CCMPUTER REDABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: 18M PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/MS-DOS
 Sequence 83, Application US/08226248A
 25 AA: 2944 MW: 2955 CN
 STANDARD:
 MALECULE TYPE: peptide
FRAGMENT TYPE: internal
 Query Match
Best Local Similarity 100 54:
Matches 15: Conservative
 amino acid
 linear
 1 KSMKVIVAFNQFGPN 15
 1 KSMKVTVAENQEGPN 15
 RUSULT 13
15 US-08-226-248A-83
 SECUENCE
 xxxxxx
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US-09-142-524A-9.rap

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ö
 Gaps
 Sequence 83. Application US/08467005
Sequence 83. Application US/08467005
SEMERAL INDRMATION:
APPLICANT: Griffet, Irwin J.;
APPLICANT: Bollock, Joanne, APPLICANT: Garman, Michard D.;
APPLICANT: Garman, Michard D.;
APPLICANT: Kuo, Mel-Chang;
APPLICANT: Kuo, Mel-Chang;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Sieven P.
IILE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCES: 261
CORRESPONDENCES: Zamulogic Pharmaceutical Corporation, Inc.
STATE: Maltham
STATE: Maltham
 ö
ADDRESSE: immulogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St
CITY: Waltham
STATE: MA COUNTRY: USA
 Score 106: DB 10: Length 26: Pred. No. 4.81e-05: 0: Mismatches 0: Indels
 MEDIUM TYPE: Floppy Jisk
COMPUTER: IBM PC corpatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release 41.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.697
FILING CATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 38/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
 NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD4 (IMI-028GPD4)
TELECOMMICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-541
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHRRACIERISTICS:
LENGTH: 26 amino acids
 25 AA.
 . .
. .
. .
 26 AA; 2944 MW; 2965 CN;
 STANDARD
 : 26 amino acids
amino acid
 TOPOLCGY: linear
MCLEGULE TYPE: peptide
FRAGMENT TYPE: internal
 ZIP: 02154
COMPUTER READABLE FORM:
REDIUM IYPE: Floppy
 Query Match
Best Local Similarity 100.0%;
Matches 15: Conservative
 1 KSMKVTVAFNQEGPN 15
 1 KSMKVIVAENOEGEN 15
 02154
 LT 15
US-08-467-006-83
 CITY: Wa
STATE: M.
COUNTRY:
ZIP: 021:
 RESULT
 ö
```

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3000
 Score 106, DB 10; Length 26, Pred, No. 4.818-05; 0; Mismatches 0, Indels
COMPUTER READABLE FORM:
MEDICH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PATENTIN Release #1.0. Version: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,005
FILING DATE: June 6, 1995
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT I
 NAME: Jane E. Remiliard
REGISTRATION NUMBER: 38,872
REFERENCE/COCKET WUMBER: 025 6 USD6 (IMI-028CPD6)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-74cc
TELEPAX: (617) 227-941
INFORNATION FOR SEQ 1D NO: 83.
 Search completed: Mon Jun 19 16:26:18 2000
Job time : 17 secs.
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 26 AA: 2944 MW; 2965 CN;
 : 26 amino acids amino acids
 Ouery Match
Best Local Similarity 100.0%;
Matches 15: Conservative
 1 KSMKVIVAFNOFGPN 15
 linear
 TOPOLOGY:
 LENGIH:
 SEQUENCE
 888888888888888888888888888888888
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|------------------------------------------------------|----------|
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| ****                                                 |          |
| *                                                    |          |
| ****                                                 | <u> </u> |

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MFsrch\_pp

MasPar time 5.32 Seconds 132.941 Million cell updates/sec Mon Jun 19 16:09:54 2000: Fun on:

Tabular output not generated.

>JS-09-142-524A-9 (1-15) from US09142524A.pep 196 1 KSMKVIVAFNQFGPN 15 Title: Description: Perfect Score: Sequence:

Scoring table:

142080 segs, 47172406 residues PAM 150 searched:

Minimum Match 08 Listing first 45 summarres Post-processing:

pir62 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 26.468: Variance 33.820; scale 0.783

Statistics:

SUMMARIES

|               |       | æ            |        |        |        |                       |           |
|---------------|-------|--------------|--------|--------|--------|-----------------------|-----------|
| Result<br>No. | Score | Cuery        | Length | e<br>G | CI     | Description           | Pred. No. |
|               | 136   | . 0          |        | . 7    | JC2124 | ergen                 | 1.14e-11  |
| 2             | 106   | $\circ$      | יח     | 7      | JC2123 | or allergen Cry       | 14        |
| 3             | 9C    | 75.5         | 404    | ~      | S12209 | te lyase (EC 4.       | 3.38e-35  |
| ₹             | 78    | $\sim$       | *      | ~•     | TC5556 | ate :yase (EC 4.      | σ.        |
| S             | 97    | _            | 4      | 7      | 100856 | te lyase (EC 4        | 2.88e-04  |
| 9             | 74    | æ            | 397    | ď      | S26211 | te lyase (EC 4.       | .24e-     |
| 7             | 74    | (Th          | 450    | 7      | 0952   | e pectate lva         | 4e-       |
| 80            | 72    | r~           | 398    | 7      | 0705   | lyase (EC 4.          | 33        |
| 5             |       | $\sim$       | 434    | ~1     | 2961   | lyase (               | .33e-     |
| 10            | 72    | 67.9         | 438    |        | S43335 | lyase (EC 4.          | ٣.        |
| 11            | 7.1   | •            | 542    | 7      | T06728 | . 4                   | 3.89e-03  |
| 12            | 7.0   | ø            | 817    |        | T07701 | te lyase (EC 4.       | 6.48e-03  |
| 13            | 68    | 4            | 374    | 7      | T05240 | lyase                 | 1.78e-02  |
| 14            | 94    | <b>9</b> .09 | 432    |        | T03949 | τ.                    | 1.27e-01  |
| 15            | 64    | 60.4         |        | 7      | 851098 | yase                  | 1.27e-01  |
| 16            | 99    | $\circ$      |        |        | T01825 | ical                  | 1.27e-01  |
| 1,7           | 59    | 'n,          |        |        | S45484 | $\mathbf{v}$          | 1.35e+00  |
| 8 1           | 58    | 4            |        |        | (4)    | omnipotent suppressor |           |
| т<br>• •      | 57    | m.           | 340    |        | 962    | yce-3                 | œ,        |
| 20            | 5.7   |              | 397    | 7      | C39099 | -                     | e,        |
| 21            | 5.7   | 53.8         | 9      | 7      | 24     | allergen Amb a 1.3 pr | 3.35e+00  |
| 22            | 57    | ۳.           | 414    | ~      | $\sim$ | ehyde-3-ph            | 3.35e+00  |
| 23            | 57    | ε.           | 571    | 7      | E64903 | arylsulfatase homolog | 3.35e+00  |

JC2123 \*type complete
major allergen Cry j I precursor (clone pCCI-2-2) - Japanese
cedar
eformal\_name Cryptomeria japonica \*common\_name Japanese cedar
14-Jul-1994 \*sequence\_revision 14-Jul-1994 \*text\_change

ORGANISM DATE

RESULT ENTRY TITLE

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| WMBPP9 Iysozyme (EC 3.2.1.1 G71678 Iysozyme (EC 3.2.1.1 G71678 Issozyme (EC 3.2.1.1 G71678 Issozyme (EC 3.2.1.1 G71678 Issozyme (EC 3.2.1.1 G71678 Issozyme GE 3.2.2.4 Gallergen Amb a 1.2 p beta galactos (assozyme (EC 3.2.1.4 Gallergen Amb a 1.2 p beta galactos (assozyme (EC 3.2.1.4 Gallergen Amb a 1.2 p probable arginine/se s 714008 Gallergen Amb a 1.4 p S50853 translation releasing A8065 Experient A8065 Experient A8065 Translation releasing A8065 Translation releasing A8065 Translation releasing A8065 Translation releasing Except Ambas a 1.4 p S50853 translation releasing Except Ambas Amb | 114010 NADH dehydrodenase su 2.940-0 | ype implete<br>n Cr. j 1 precursor (clone pCCI-15) - Japanese | Cryptomeria japonica #common_name Japaneso cedar<br> sequence_revision 14-Jul-1994   #text_change<br> | lyama. N.: Shimizu. K.: Kusakabe. I.: Morikubo. | Mys. Res. Commun. (1994) 199.619-625<br>equencing of CDNA coding for Cry ( ), a major<br>Capanese cedar pollen.<br>13234 | Cabe, SCN<br>66545; NICO44-643 ETECOTOCHOBE: EIE 26436-4<br>517-4<br>COTS described markethyddate ichdoca Sile 10:<br>peolae 1yuse LAIS9<br>pollen | signal sequence estatus predicted *late: SiGN   major allergen Cry j I (clone pCCI-15) *status rted *labe! MATN   (covalent) #status ited   major allerate (Asp) (covalent) #status ited   molecular-weight 40702 #checksum #592 |
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| 550<br>500<br>500<br>500<br>500<br>500<br>500<br>500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 355                                  | 2124<br>jor<br>ceda                                           | forma<br>4-Ju<br>25-7                                                                                 | 302123<br>Sone, I.: Kor<br>K.: Kino. K          | ကားပ ည်း                                                                                                                 | Juza<br>_type<br>feren<br>:tal.<br>#sup<br>glyc                                                                                                    | #domain s<br>#product<br>predict<br>54 #binding<br>predict<br>#length 374                                                                                                                                                        |
| 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 45 5<br>ESULT 1                      |                                                               | RGAN<br>ATE                                                                                           | REFERENCE<br>#authors                           | urna;<br>tle<br>oss-r                                                                                                    |                                                                                                                                                    | 1-21<br>22-374<br>159,191,293,3<br>SUMMARY                                                                                                                                                                                       |

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translated from GB/EMBL/DDBG
 *Superfamily perface :yase LATS9 carbon-oxygen lyase *length 434 *molecular-weight 44
 *superfamily pectate lyase LATS9 carbon-oxygen lyase *iength 455 *molecular-weight 5:
 **experimental_source cultivar Columbia
 *type complete
 TC0855 #type
pectate lyase (EC
#formal_name Arabi
 66/2: 295/3: 376/3
 12-Feb-1999 #seq
 29-Sep-1999
T00856
 37/2: 287/2
 266 KNMQVTIAFNHFG 278
 309 KKMQITVAFNHFG 321
 .3
 | | :||-||:|
| KSMKVTVAFNQFG 13
 F22K18.20
 ##status
##molecule_type DNA
 **molecule_type DNA
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 #map_position 4
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 *domain signal sequence *status predicted *label SiGN *product major allergen Cry) : (clone pCCI-2-2) *status predicted *label MATN | clone pCCI-2-2) *status *binding_site carbohydrate (Asn) (covalent) *status
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 $1259
Badelier K.A. Srith, A.G.: Gasser, d.s.
Badelier K.A. (1950) 224:183-194
Regulation of a stylar transmitting tissue-specific cene in
wild-type and transgenic tomato and tabacco.
 ö
 *#molecule_type protein
**residues 22-53;58-81:219-232:236-259:299-307:346-372 **label SO2
26-Aug-1999
JC2123: PC2065
JC2123: P
 105556 *type complete pectare lyase (EC 4.2.2.2) F22Ki8.20 - Arabidopsis thaliana protein F22Kl8.20
 ##Indiacolous_Lype mraph in the following services of the following se
 **.esidues :-374 **.abel SON
**cross-references GB:D26544, NID:g493631; PID:d1006086; PID:g493632
**experimental_source pol:en
reession PC2065
 the authors described carbohydrate binding site for residue 279
*superfamily pectate lyase LATS9
alycoprofein; pollen
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 predicted # #molecular-weight 40645 #checksum 2920
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 whery Match 100.0%; Score 106: DB 2: Length 374: Bost Local Similarity 100.0%; Pred. No. 1.14e-11: Matches 15; Conservative 6: Mismatches 6: Indels
 Clery Match 75.5%: Score 80: DB 2: Length 404: best Local Similarity 76.9%: Pred. No. 3.38e-05; Matches 10: Conservative 2; Mismatches 1; Indels
 *cross-reterences MCID:91117185
 ##molecule_type mRNA
 232 KSMKVTVAFNOFGPN 246
 T KSMKVIVAFNQEGPN 15
 262 KGMCVTVAFNHFG 274
 1 KSMKVTVAFNQFG 13
 $12209
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 158, 191, 293, 354
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Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, P.; Hobersel, Bevan, M.; Wedler, E.; Wambutt, P.; Hobersel, Selveller, C.
Submitted to the Protein Sequence Database, February 1999-170556
 ipsis thalland *common_name mouserear
*formal_name Arabidopsis thallana *common_name mouserear
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 'e_revision 12-Feb-1999 *text_Change
 ##MOLOCUIE_Lipro D.m.
##residues 1-455 ##Label ROU
##cross-references EMBL/RC02521: N.ID:92947056: PIDN:AAC05456.1:
##cross-references EMBL/RC02521: N.ID:92947069
 Rounsley, S.D.: ... X.: Ketchum, K.A.: Crosby, M.:
Brandon, R.C.: Sykes, S.M.: Kaul, S.: Mason, T.M.
Kerlavago, A.E.: Adams, M.D.: Sometville, C.R.: V
 *molecular-weight 44495 #checksum
 #molecular-weight 51257 #checksum
 submitted to the EMPL Lata Library, March 1978. Arabidopsis thailiana our mostero ti BAC 12.5% or sequence.
 ##residues 1-404 ##label BEV
##cross-references EMBL:AL035356
##experimental_source cultivar Columbia: BAT clone F22K15
 Query Match 73.6%: Score 78: DB 2: Length 404: Best Local Similarity 69.2%: Pred. No. 3.926-05. Matches 9: Conservative 3: Mismatches 1: Indels
 Query Match 71.7%; Score 76; 58 2; Length 455; Best Local Similarity 69.2%; Pred. No. 2.88e-04; Matches 9; Conservative 2; Mismatches 2; Indels
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1 KSMKVIVAFNOFG

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RESULT
 *accession $26212
**molecule_type mRNA
**residues 119-155, C7.157-188,190,'G7,191-199,'D7,200,'R7.203-248,
**residues NV.256,381 **label RC2
**cross-references EMBL:X67159
 ö
 ::
 ##cross-references EMBL:X61102; NID:q19981: PIDN:CAA43414.1: PID:q19982
 ESSIONS S26213: S21933: S22753; S22754 S26212: S21933: S22753; S22754 S26212: S21933: S22753; S22754 S26212: S21933: S22753; S22754 S26212: S26212: S21933: S22754 S22754 S26212: S26212: S21943-552 S62493-552 S624012: S219412: S2194312: S2194312: S2194312: S2194313:
 not complete
pectate lyase (EC 4.2.2.2) - common tobacco *formal_name Nicotiana tabaccu *formal_name Sequence_revision 12-Feb-1993 *text_change
 10.554
privable pentais hyase (0.6.2.2.2) - aifalta
privable pentais hyase (0.6.2.2.2) - aifalta
#formal_came Medicago Sativa #common_name aifalta
16.701-1999 #sequence_revision 16.7u1-1999 #text_change
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 *checksum 3091
 ##rosidues 1-397 ##label ROG ##Cross-reterences EMBL:X67158; NID:q19907: PIDN:CAA47630.1:
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 6
 cutalyzes cleavage of pectate to oligosaccharides ksuperfamily pectate lyase LATS9 carbor-converse lyase carbor-converse lyase sength 450 *molecular-weight 50155 *checksum 3*
 sednence is
 **status preliminary; translated from GB/EMBL/DDBJ##molecule_type DNA ##residion
 Query Match 69.8%; Score 74; DB 2; Length 450; Best Local Similarity 69.2%; Pred. No. 8.24e-04; Matches 9; Conservative 2; Mismatches 2; Indels
 Score 74: DE 2: Length 397:
Pred. No. 8.24e-04:
4: Mismatches 1: Indels
 Lonsdale, D.M. submitted to the EMBL Data Library, July
 *molecular-weight 44351
 Erickson, L
 translation of the nucleotide
 *Superfamily pectate lyase LAIS9 carbon-oxygen lyase *length 397 *molecular-weight 44
 Wu, Y.; Qiu, X.; Du, S.; Er
submitted to the EMBL Data
 query Match
Hest Local Similarity 61.5%
Matches 8: Conservative
 26-Aug-1999
T09524
 254 KDMKITLAYNHFG 266
 309 KIMQIIVAFNHFG 321
 I KSMKVTVAFNOFG 13
 ##molecule_type DNA
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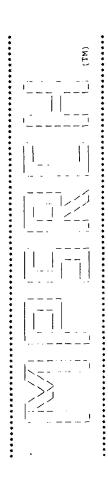
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**cross-references EMBL:217328; NID:919450; PIDN:CAA78975.1; PID:9:9451 **experimental_source cv. Nellie White, mature flower CLASSIFICATION *superfamily pectate lyase LAT59
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 Kim, S.; Finkel. D.J.: An, G.
Submitted to the EMBL Data Library, October 1992
Aundanced to the Table Data Library, October 1992
Aundance patterns of lily pollen cDNAs: characterization
three pollen-preferential cDNA clones.
 $29612 *type complete
pectate lysse (FC 4.2.2.2) - trumpet lily
#formal_name_Lili.um iongiflorum #common_name_trumpet_lily
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_Change
 *formal_name Lycopersicon esculentum *common_name tumatu
30-Apr-1999 *sequence_revision 30-Apr-1999 *text_change
29-Sep-1999
107038; SC8382
115896
 ##residues 1-24,'F',26- 4,'K',51-61,'RCGG',66,'L',69-114,'R'
118-141,'E. 143-166,'SNSGYCIYRS',177-349,'NVLH'
354-355,'IW' ##Label MIW
##Cross-references EMBD:X15500
 z.
 #length 434 #molecular-weight 48457 #checksum 6432
 S.K. Grsin.
 #molecular-weight 44563 #checksum
 Wing, R.A.
submitted to the EMRL Data Library, September
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 Scire 72: DB 2: Length 398:
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6: Missurines 0: Inbels
 Wing, R.A.: Yama.uchi. J.: Larabell.
McCormick, S.
Plant Mol. Biol 989) 14:17-28
 translated from GB/EMB1/DDBJ
T07058 *type complete pectate lyase (E 4.2.2.2) LAT56
 *superfamily pectate lyase LAIS9 carbon-oxygen lyase
 ##experimental_source strain VF36; author NOCE $08383
 1-434 **label KIM
 carbon-oxygen lyase
 preliminary
 Query Match
Best Local Similarity 53.8%:
Matches 7: Conservative
 29-Sep-1999
S29612
 19471: 29472
 *length 398
 protein P56
 255 ROMKILLAYNBEG 267
 1 KSMKVIVAFNUFG 13
 **molecule_type mRNA
**residues 1-434
 **molecule_type DNA **residues [-3
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 234 KLMOVTIAYNHFG 246
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| KSMKV:VAFNQFG 13
 280 GMQVTIAFNHFG 291
 ##molecule_type DNA
 2 SMKVTVAFNOFG 13
 **molecule_type DNA
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Flant Mol. Biol. (1997) 23:1061-1065
Flant Mol. Biol. (1997) 23:1061-1065
isolation and characterization of police specific maize genes
with sequence homology to ranweed altergens and pectate
 Ouetier, F.: Choisne, N.: Robert, C.: Brottier, P.: Wincker, P.: Cattolico, L.: Artiguenave, F.: Saurin, K.: Wolssenbach, J.: Salanoubat, M.: Mewes, H.W.: Mayer.
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 K.F.X.; Schuciler, C. submitted to the Protein Sequence Database, April 1999 [06728]
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 ##Cross-reterences EMBL:L2C140; NID:q4C5534; PIDN:AAA16476.1;
PID:q4C5535
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 *Superfamily pectate lyase LAT59
carbon-oxygen lyase
#length 542 *molecular-weight 58573 *checksum
 ##residues 1-542 ##label CUE
##cross-reterences EMBL:AL049655
##experimental_source cultivar Columbia: BAC clone F28Pl0
 i: Indels
 Score 72; DB 2; Lendth 438;
Pred. No. 2,33e-03;
 uery Match
Fest Lond Similarity 66.7%: Prod. No. 3.89e-03:
Matches 8: Conservative 3: Mismatches i: Indels
Score 72: DB 2: Length 434: Pred. No. 2.33e-03; i: Mismatches 1: Indels
 1; Indels
 ##status nucleic acid sequence not shown ##molecule_type DNA_
 1; Mismatches
 46/2: 346/3: 413/2: 480/2
 1-438 ##label TUR
 *cross-references MOID:94083558
 Cuery Match
Hest Local Similarity 81.8%:
Matches 9; Conservative
 Unery Match
Best Local Similarity 81.8%:
Matches 9: Conservative
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 **molecule_type DNA
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 Bevac, M.: Weber, N.: Stueniquer, D.: Schmidbein, T.:
Bancroft, I.: Newes, H.W.: Mayer, K.F.X.: Schueller, G.
submitted to the Protein Sequence Catabase, February 1999
 #formal_came Arabidopsis thallaca #corros_care mousered:
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 Bevan, M.; Pohl, I.; Weizenesder, I.; Sancroff,
H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, May
107701
 carbon-oxygen lyuse
#length 416 #molecular-weight 45251 #chenksum
 **experimental_source cultivar Columbia: BAC clone Fi7N18
 ##residues 1-374 ##label BEV
##cross-references EMBL:AL035528
##experimental_source cultivar Columbia: BAC clone F18A5
 # Match 66.0%: Score 70. UR i, Length 418:
Local Similarity 61.5%: Pred. No. 6 48e-UN:
nes 8: Conservative 3: Mismatches 2: Indels
 Query Match 64.2%; Score 68: 38.2; Length 374:
Best Local Similarity 61.5%; Pred. No. 1.78e-02;
Matches 8: Conservative 3: Mismatches 2; Indels
 23-Apr-1999 #sequence_revision 23-Apr-1999 23-Jul-1999
 26/2: 49/2: 264/3: 295/2: 345/3
F17N18.100
*Superfamily pectate lyase LAT59
 *superfamily pectate lyase LAT59
 intron positions not resolved F18A5.100
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 carbon-oxygen lyase
#length 374 #cherksum 1983
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submitted to the EMBL Data Library, October 1997
Arabidopsis thaliana BAC T3F12 from chromosome IV.
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 ##res:dues 1-449 ##label WIN ##cross-references EMBL:X15499; NID:919270; PIDN:CAA33523.1; PID:919271
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 From All Large Lycopersicon esculentum #commun_name tomato 12.Peb-1993 #sequence_revision 12.Peb-1993 #text_change 29.88pp.1995 #sequence_revision 12.Peb-1993 #text_change 27.7098; Sep-1999 # Sequence_revision 12.Peb-1993 #text_change 27.7098; Sep-1999 # Managuchi, J.: Larabell, S.K.: Ursin, V.M.; WoOdmick, S.
 T00949 *type complete
hypothetical protein T3F12.10 · Arabidopsis thaliana
*iormal_name Arabidopsis thaliana *common_name mouse-ear
 Gaps
 #journal Plant Mol. (1989) 14:17-28
#title Molecular and genetic characterization of two
pollan-expressed genes that have sequence similarity pectate 1yases of the plant pathogen Erwinia.
 Gaps
 #.ength 432 #molecular-weight 46471 #checksum 3230
 #map_position 3 #17/2 #introns 67/2: 177/2 #introns 67/2: 177/2 #Sintrons #superfamily pectate lyase LAI59 #EYWORDS carbon-oxygen lyase SUMMARY #length 449 #molecular-weight 50893 #checksum 506
 .;
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 residues 1-432 **!abel GNO *cross-reterences EMBL:AC002983; NID:q2443899; PID:q2565009
 Query Match 60.4%: Score 64: DB 2: Length 432: Best Local Similarity 70.0%: Pred. No. 1.276-91; Matches 7: Conservative 3: Mismatches D: Indels
 Subery Match 60.4%; Score 64; DB 2; Length 449; Best Local Similarity 63.6%; Pred. No. 1.27e-01; Matches 7; Conservative 3; Mismatches 1; Indels
 S27698 *:ype complete
pectate lyase (EC 4.2.2.2) LAT59 - tonato
protein P59
 translated from GB/EMBL/DUBJ
 121/3; 296/2; 329/3; 351/2; 385/3
T3F12.10
#accession S27098
##molecule_type_DNA
 ##molecule_type DNA
 309 MOITLAFNHFG 319
 | :|:|||:||
3 MKVIVAFNQFG 13
 216 VIVPFDHFGP 225
 #map_position 4
#intross 12
#note T3
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Search completed: Mon Jun 19 16:10:02 2000
Job time : 8 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

MPsrch\_pp protein protein database search, using Smith-Waterman algorithm

Mcm Jun 19 16:08:52 2000: MasPar time 3.45 Seconds i32.343 Million cell updates/sec ลิน:: on:

Tabular output not generated.

>US-09-142-524A-9 (1-15) from US09142524A.pep 106 1 KSMKVIVAFNQFGPN 15 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

83857 segs, 30454973 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Statistics:

Pred. No. if the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 27.102; Variance 30.545; scale 0.884

SUMMARIES

| Score Match Length DH   1D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |               |         | d              |        |            | ST TURE S  |                        |            |
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| 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Result<br>No. | Score   | Ouery<br>Match | Length | HO         | 91         | Description            |            |
| 90 75.5 404 19612_LYCES SITLE_DEVELOMBENT-SPEC 3 72 67.9 397 1 PEL_LYCBAC PECTATE_LYASE_PRECURSO 1 72 67.9 434 1 PEL_LILOBAC PECTATE_LYASE_PRECURSO 1 67.9 434 1 PEL_LILLO PECTATE_LYASE_PRECURSO 3 65.7 416 1 PEL_LILLO PECTATE_LYASE_PRECURSO 3 58 94.7 419 1 PEL_LILLO PECTATE_LYASE_PRECURSO 3 58 94.7 415 1 G3PA_GRAVE GLYCERALDEHYDE 3-PHOSP 1 58 94.7 435 1 ERFI_ARATH EUKARYOTIC_PEPTIDE_CHA 6 57 53.8 414 1 G3PA_CROCR GLYCERALDEHYDE 3-PHOSP 1 58 19 40 1 G3PA_CROCR GLYCERALDEHYDE 3-PHOSP 1 58 10 258 1 LYCV_BPPL2 LYSOZYME (EC 3.2.1.17) 2 55 51.9 486 1 YAMB_SCHPO PULEN_ALLERGEN_AMB A 2 55 51.9 486 1 YAMB_SCHPO PULEN_ALLERGEN_AMB A 2 56 51.9 396 1 MP12_AMBAR POLLEN_ALLERGEN_AMB A 2 57 50.9 396 1 MP12_AMBAR POLLEN_ALLERGEN_AMB A 4 58 50.9 396 1 MP12_AMBAR POLLEN_ALLERGEN_AMB A 4 59 50.9 396 1 MP12_AMBAR POLLEN_ALLERGEN_AMB A 4 50 396 1 MP11_AMBAR POLLEN_ALLERGEN_AMB A 4 50 396 1 MP11_AMBAR POLLEN_ALLERGEN_AMB A 4 51 50.9 396 1 MP11_AMBAR POLLEN_ALLERGEN_AMB A 4 52 50.9 396 1 MP11_AMBAR POLLEN_ALLERGEN_AMB A 4 53 50.0 250 1 MP11_AMBAR POLLEN_ALLERGEN_AMB A 4 54 50.9 396 1 MP14_AMBARCE (C 3.2.1.18 7 55 50.0 340 1 MP14_AMBAR POLLEN_ALLERGEN_AMB A 4 54 50.9 396 1 MP14_AMBAR POLLEN_ALLERGEN_AMB A 4 55 50.0 340 1 G3PLARCEC GLYCERALDEHYDE 3-PHOSP 7 56 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |               | 105     | 100.0          | 374    |            | SBP_CRYJA  | BASIC                  | 1.90e-13   |
| 74 69.8 397 1 PEL_TOBAC PECTATE LYASE PRECURSO 1 2 67.9 398 1 PES_LIYCES PROBABLE PECTATE LYASE 3 7 2 67.9 4 398 1 PES_LIYCES PROBABLE PECTATE LYASE 3 6 6.4 449 1 PES_9 LYCES PROBABLE PECTATE LYASE 2 5 5 5 7 436 1 G3PA_GRAVE GLYCERALDEHYDE 3-PHOSP 3 5 7 435 1 ERFI_ARATH GUYGERALDEHYDE 3-PHOSP 5 7 53.8 340 1 G3PA_CRAVE GLYCERALDEHYDE 3-PHOSP 5 7 53.8 414 1 G3PA_CRAVE GLYCERALDEHYDE 3-PHOSP 5 7 5 1.9 258 1 LYCV_BPPA POLLEN ALLERGEN AMB A 1 1 G3PA_CRAVE GLYCERALDEHYDE 3-PHOSP 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 7             | 80      | 75.5           |        |            | 9612 LYCES | STYLE DEVELOPMENT-SPEC | 3.02e-06   |
| 72 67.9 39B 1 PE56_LYCES PROBABLE PECTATE LYASE B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ٣             | 74      | 59.8           |        | ٠ ٦        | PEL_TOBAC  | PECTATE LYASE PRECURSO | 1.05e-04   |
| 72 67.9 434 1 PELLILO PECTATE LYASE PRECURSO 3 (2.14 449) 1 PELLILO PECTATE LYASE 2 (2.14 449) 1 PELLILO PELLINO PERUNDI PELLINO PELLINO PELLINO PELLINO PELLINO PELLINO PELLINO PERUNDI PELLINO PERUNDI PERUND | 4             |         | 67.9           | 39B    | - 1        | PES6_LYCES | PROBABLE PECTATE LYASE | 3.346-04   |
| 64 60.4 449 : PE59_LYCES PROBABLE PECTATE : YASE 2 5 5 7 416 : G3PA_GRAVE GLYCERALDEHYDE 3.+HOSP 3 6 9 5.7 416 : G3PA_GRAVE GLYCERALDEHYDE 3.+HOSP 3 6 1 G3P2_BACSU GLYCERALDEHYDE 3.+HOSP 1 5 3.8 340 1 G3P2_BACSU GLYCERALDEHYDE 3.+HOSP 1 5 5 5 1 8 414 1 G3PA_CHOCK GLYCERALDEHYDE 3HOSP 1 5 5 5 1 9 258 1 LYCV_BPP2 LYSOZYME (EC 3.2.1.17) 2 5 5 1 9 388 1 MP12_AMBAR POLLEN ALLERGEN AMB A. 2 5 5 1 9 388 1 MP12_AMBAR POLLEN ALLERGEN AMB A. 2 5 5 1 9 488 1 YAMB_SCHPO HYPOTHETICAL 53.9 KD P 2 5 5 1 9 348 1 TRD_SYNY 3 ANTHRANILATE PHOSPHORI 4 5 4 50.9 348 1 TRD_SYNY 3 ANTHRANILATE PHOSPHORI 4 5 5 5 0 0 171 1 SCRC_SCHJA SYCLIN ALLERGEN AMB A 4 5 5 5 0 0 171 1 SCRC_SCHJA SYCLIN BACK GLYCHOME P450 1 1 (2710_LMBAR POLLEN ALLERGEN AMB A 5 5 0 0 171 1 SCRC_SCHJA SYCLIN SYCLIN BACK GLYCHOME P450 1 1 (2710_LMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 0 0 300 300 300 300 300 300 300 300 3                                                                                                                                                                                                                                                                                                                                                                                                                | 'n            | 7.2     | 67.9           | 434    | ~          | PET TILLO  | PECIATE LYASE PRECURSO | 3.346-04   |
| \$ 5.7 416 : G3PA_GRAVE GLYCERALDEHYDE 3-PHOSP B 54.7 435   ERF1_ARATH EURARYOTIC PERTIDE CHA 6 57 53.8 397   MPI3_AMBAR GLYCERALDEHYDE 3-PHOSP B 57 53.8 397   MPI3_AMBAR POLLEN ALLERGEN AMB A 1 6 7 7 2 2 5 1.9 2 5 1.9 2 5 1.9 2 5 1.9 2 5 1.9 2 5 1.9 398   MPI2_AMBAR POLLEN ALLERGEN AMB A 2 5 5 1.9 486   YAMB_ACHPO LYCOZYME (EC 3.2.1.17) 2 5 5 1.9 486   YAMB_ACHPO POLLEN ALLERGEN AMB A 2 5 6 1.9 396   MPI2_AMBAR POLLEN ALLERGEN AMB A 2 6 1.9 346   TRPD_SYNY3 ANTHRANILATE PHOSPHORI 4 5 6 1.9 396   MPI2_ARRD BETA-GALACIOSCDASE (EC 5 6 1.9 396   MPI2_ARRD BETA-GALACIOSCDASE (EC 5 6 1.9 396   MPI2_ARRD BETA-GALACIOSCDASE (EC 5 6 1.9 396   MPI2_BARB POLLEN ALLERGEN AMB A 4 5 5 5 1.9 396   MPI2_BARB POLLEN ALLERGEN AMB A 4 5 5 5 1.9 396   MPI2_BARB POLLEN ALLERGEN AMB A 4 5 5 1.0 3 1.1   SORC_SCHAP SCHOWE P450   A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 9             | 94      | ()             | 449    |            | PES9_LYCES | PROBABLE PECTATE :YASE | 2.82e-02   |
| \$ 54.7 435   ERFI_ARATH EUKARYOTIC PEPTIDE CHA 6 1 63P2_BACSU GLYCERALDEHYDE 3-PHOSP 1 57 53.8 414   G3PA_CHOCR GLYCERALDEHYDE 3-PHOSP 1 57 53.8 414   G3PA_CHOCR GLYCERALDEHYDE 3-PHOSP 1 55 51.9 258   LYCV_BPPLA   LYSOZYME (EC 3.2.1.17) 2 55 51.9 398   MP12_AMBAR POLLEN ALLERGEN AMB A 2 55 51.9 486   YAMB_SCHPO POLLEN ALLERGEN AMB A 2 54 50.9 396   MP12_AMBAR POLLEN ALLERGEN AMB A 2 54 50.9 348   TRPD_SYN 3 ANTHRANILATE PHOSPHORI 4 54 50.9 396   MP12_AMBAR POLLEN ALLERGEN AMB A 4 54 50.9 396   MP12_AMBAR POLLEN ALLERGEN AMB A 4 54 50.9 396   MP12_AMBAR POLLEN ALLERGEN AMB A 4 54 50.9 396   MP12_AMBAR POLLEN ALLERGEN AMB A 4 54 50.0 370   CP11_DICLA   CYTOCHROME P450 1A1 (E 4 50.9 36.0 171   SORC_SCH3 SCHOLN   C 4 50.0 340   MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340   MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340   MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 340 340 340 340 340 340 340 340 34                                                                                                                                                                                                                                                                            | ۲-            |         | 55.7           | 416    |            | G3PA_GRAVE | GLYCERALDEHYDE 3-PHOSP | m.         |
| 57 53.8 346 1 G3P2_BACSU GLYCERALDEHYDE 3-PHOSP I                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | œ             |         | 54.7           | 435    | -          | ERF1_ARATH | EUKARYOTIC PEPTIDE CHA | ė.         |
| 57 53.8 397 1 MP13_AWBAR POLLEN ALLERGEN AMB A 1 1 GPA_CHOCK GLYCERALDEHYDE 3-PHOSP 15.5 51.9 258 1 LYCV_BPP2 LYSOZYME (EC 3.2.1.17) 2 25 51.9 258 1 LYCV_BPP2 LYSOZYME (EC 3.2.1.17) 2 25 51.9 398 1 WP12_AMBAR POLLEN ALLERGEN AMB A 2 2 2 2 1 3 3 1 MP12_AMBAR POLLEN ALLERGEN AMB A 2 2 2 2 3 3 1 MP12_AMBAR POLLEN ALLERGEN AMB A 3 2 2 2 3 3 2 3 2 3 3 3 3 3 3 3 3 3 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | თ             | 57      | 53.8           |        | -1         | G3P2_BACSU | GLYCERALDEHYDE 3-PHOSP | 1.04e-00   |
| 57 53.8 414 1 G3PA_CHOCR GLYCERALDEHYDE 3_PHOSP 1 55 51.9 258 1 LYCV_BPPL2 LYSOZYME (EC 3.2.1.17) 2 55 51.9 398 1 LYCV_BPPL2 LYSOZYME (EC 3.2.1.17) 2 55 51.9 486 1 YAMBAR POLLEN ALLERGEN AMB A . 2 54 50.9 348 1 TRPD_SYNT3 ANTHRANILATE PHOSPHORI 4 54 50.9 348 1 TRPD_SYNT3 ANTHRANILATE PHOSPHORI 4 54 50.9 396 1 MP11_AMBAR POLLEN ALLERGEN AMB A 4 54 50.9 396 1 MP11_DICLA CYTOCHROWE P450 IAI (E 4 50.9 30.0 171 1 SORC_SCHJA SYROLIN ALLERGEN AMB A 4 50.0 370 1 MP14_AMBAR ROLLEN ALLERGEN AMB A 4 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 5 50.0 340 1 G3P_ARCFC GLYCERALDEHYDE 3-PHOSP 7 53 50.0 340 1 G3P_ARCFC GLYCERALDEHYDE 3-PHOSP 7 50.0 340 1 G3P_ARCFC GLYCERALDEHYDE 3-PHOSP 7 50.0 340 1 G3P_ARCFC GLYCERALDEHYDE 3-PHOSP 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 340 1 MP14_AMBAR POLLEN AL | 10            | 57      | 53.8           |        | ٦          | MP13_AMBAR | POLLEN ALLERGEN AMB A  | 1.04e+00   |
| 55 51.9 258 1 LYCV BPPH2 LYSOZYME (EC 3.2.1.17) 2 5 5 1.9 258 1 LYCV_BPPA LYSOZYME (EC 3.2.1.17) 2 5 5 1.9 258 1 LYCV_BPPA LYSOZYME (EC 3.2.1.17) 2 5 5 1.9 258 1 LYCV_BPPA POLLEN ALLERGEN AMB A D D D D D D D D D D D D D D D D D D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::            | 57      | œ.             | 414    | - 1        | G3PA_CHOCR | GLYCERALDEHYDE 3-PHOSP | ٦          |
| 55 51.9 258 1 LYCV_BPPZA LYSOZYME (EC 3.2.1.17) 2 55 51.9 398 1 MP12_AMBAR POLLEN ALLERGEN AMB A . 2 55 51.9 398 1 MP12_AMBAR POLLEN ALLERGEN AMB A . 2 54 50.9 138 1 BGAL_AGRRD BETA-GALACTOSIDASE (EC 4 54 50.9 346 1 TRPD_SYNY3 ANTHRANILATE PHOSPHORI 4 54 50.9 396 1 MP11_AMBAR POLLEN ALLERGEN AMB A 4 54 56.9 520 1 MP11_DIGLA CYTOCHROWE P450 IAI (E 5) 55 50.0 171 1 SCRC_SCHJA SCRCIN. 53 50.0 266 1 NANH_BACFR S.ALLDASE (EC 3.2.1.18 7 55 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 3 50.0 392 1 MP14_AMBAR POLLEN ALLERMA BA 3 50 | 12            | 55      | - 1            | 258    | <b>~</b> 1 | LYCV_BPPH2 | LYSOZYME (EC 3.2.1.17) | 2.77e-00   |
| 55 51.9 398 1 MP12_AMBAR POLLEN ALLERCEN ANB A . 2 5 5 1.9 486 1 YAMB_SCHPO HYPOTHETICAL 53.9 KD P 2 5 5 0.9 346 1 TRPJ_SYNY3 ANTHRANILATE PHOSPHORI 4 5 5 0.9 396 1 MP11_AMBAR POLLEN ALLERGEN AMB A 4 5 5 5 0.0 171 1 SORC_SCHPA SCHROWE P450 IAI (ET 10 10 10 10 10 10 10 10 10 10 10 10 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 13            | 55      | Ϊ.             |        | -          | LYCV_BPP2A | LYSO2YME (EC 3.2.1.17) | 2.77e+00   |
| 55 51.9 486 1 YAMB_SCHPO HYPOTHETICAL 53.9 KD P 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 14            | 55      | ٦.             |        | -          | MP12_AMBAR | POLLEN ALLERGEN AMB A  | . 2.77e+00 |
| \$4 50.9 138 1 BGAL_AGRRD BETA-GALACIOSIDASE (EC 4 5 6 6).9 348 1 TRPD_SYNY3 ANTHERALITATE PHOSPHORI 4 5 6 5 9 348 1 TRPD_SYNY3 ANTHERALITATE PHOSPHORI 4 5 5 5 0 1 7 1 1 SCRC_SCHJA STROME P450 1A1 6 5 5 5 0 0 171 1 SCRC_SCHJA STROME P450 1A1 6 7 5 5 5 0 0 171 1 SCRC_SCHJA STROME P450 1A1 6 7 5 5 5 0 0 392 1 NANH_BACFR S.ALIDASE (EC 3.2.1.18 7 5 5 5 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 5 5 5 0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 15            | 55      |                |        | -          | YAM8_SCHPO | ð                      | 2.77e+00   |
| 54 50.9 348 1 TRP2_SYNY3 ANTHRANILATE PHOSPHORI 4 54 50.9 396 1 MP11_AMBAR POLLEN ALLERGEN AMB A 4 54 50.9 350 1 CP11_DICLA CYTOCHROME P450_IAI_(E 53 50.0 171_I SCRC_SCHJA SCRCIN. 53 50.0 266 1 NANH_BACFR S.ALDBARE (EC 3.2.1.18 7 55 50.0 340 I G3P_ARCFC GLYCERALDEHYDE 3-PHOSP 7 53 50.0 340 I MP14_AMBAR POLLEN ALLERGEN AMB A 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 16            | 54      | 50.9           |        | -          | BGAL_AGRRD | BETA-GALACIOSIDASE (EC | 4.46e+00   |
| 54 50.9 396 1 MP11 AMBAR POLLEN ALLERGEN AMB A 4 54 50.9 520 1 CP11_DICLA CYTOCHROME P450 IA1 (E 4 50.0 171 1 SCRC_SCHJA SCRCIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 17            | 54      | 50.9           | 348    | ~          | TRPD_SYNY3 |                        | 4.46e+00   |
| 54 56.9 520 1 CP11_DICLA CYTOCHROME P450 1A1 (E 4 5 5 5 0.0 171 1 SCRC_SCHJA SCRCIN. 53 50.0 266 1 NANH_BACFR SIALIDASE (EC 3.2.1.18 7 5 5 5 0.0 340 1 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 18            | 54      | SC.9           | 396    | ~          | MP11_AMBAR | AMB                    | 4.46e-00   |
| 53 50.0 171 1 SCRC_SCHJA SCRCIN. 53 50.0 266 1 NANH_BACFR S.ALIDASE (EC 3.2.1.18 7 53 50.0 340 1 MANH_BACFC GLYCERALDEHYDE 3.PHOSP 7 53 50.0 392 1 MAN14_ANBAR POLLEN ALLERGEN AMB A 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 19            | 54      | 50.9           | 520    | ٦          | CP11_DICLA | P450 1A1               | -          |
| 53 50 0 266 1 NANH_BACFR S:ALIDASE (EC 3.2.1.18 7 53 50.0 340 1 G3P_ARCFU GLYCERALDEHYDE 3.PHOSP 7 53 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 20            | 53      | 50.0           | 171    | -          | SCRC_SCHJA | SCRCIN.                | 7.14e+00   |
| 53 50.0 340 1 G3P_ARCFU GLYCERALDEHYDE 3-PHOSP 7 53 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 21            | 53      | 50.0           | 266    | ٦          | NANH_BACFR | S:ALIDASE (EC 3.2.1.18 | 7.         |
| 53 50.0 392 1 MP14_AMBAR POLLEN ALLERGEN AMB A 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 22            | 53      | 50.0           | 340    | -          | G3P_ARCFU  | GLYCERALDEHYDE 3-PHOSP | 7.146+00   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 23            | υ.<br>Ε |                | 392    | ٦          | 4          |                        | 7.14e+00   |

| 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2   | 7.806-01               |
|-----------------------------------------|------------------------|
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|                                         | VP2_AHSV4              |
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| 00000000000000000000000000000000000000  | 7.15                   |
| 000000000000000000000000000000000000000 | 20                     |
| 45000000000000000000000000000000000000  | <b>7</b>               |

## ALIGNMENTS

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2
 PFAM; PF00544; pec_lyase: 1.
PRINTS: PR00807; AMBALLEKGEN
 EMBL: X55193: CAA38979.1: -
 Query Match
Best Local Similarity 76.9%:
 44298
 10; Conservative
 STANDARD:
 20
404
37
191
 397
 262 KGMOVIVAFNHFG 274
 1 KSMKVIVAFNOFG 13
 21 4
37
191
404 AA:
 PIR: S12209: S12209
 Lyase: Signal
SIGNAL
 RESULT 3

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 ö
 SEQUENCE FROM N A.
STRAIN-CV. VESS: 118SUE-PISTIL:
MEDILINE: 9117185.
Budeller K.A. Smith A.G. Gasser C.S.;
Budeller K.A. Smith A.G. Gasser C.S.;
Mid-type and transpenic transport tromato and tobacco.":
Molf-type and transpenic tromato and tobacco.":
Molf-type and transpenic tromato and tobacco.":
TOWTION: MAY HAVE A ROLE IN THE EVELICOPMENT OF THE TRANSMITTING
TISSUE OF THE STYLE AND/OR IN THE EVENIS RELATED TO POLLINATION
SUCH AS SOME ASPECT IN THE FACILITATION OF COMPATIBLE POLLEN TUBE
 TISSUE SPECIFICITY PREDOMINATLY FOUND IN THE PISTIL WHERE IT IS TOWND IN THE OUTER FIVE LAYERS OF THE STRANDS OF TRANSACTIING TISSUE WITHIN THE UPPER TWO-THIRDS OF THE STYLE. FOUND AT MCCH LOWER LEVELS IN THE ANTHERS AND VEGETATIVE ORGANS.

SEVELOMBENTAL STACE: MAXIMUM LEVELS ARE FOUND JURING ANTHESIS. SIMILARITY: 54% IDENTICAL TO TOWATO PROTEINS PS9 (AC P1572) AND PS6 (AC P15721).
 Saps
 Lycopersicon esrulentum (Indato).
Eskaryota viiidiplantae: Streptopita: Embryophyta: Tracheophyta:
euphyllophytes: Spermarophyta: Aggnollophyta: eudicityledons:
core eudicots: Asteridae; euasterids I; Solanaies; Solanaceae;
 0
 Length 374;
 2-13;
s 0; lndels
 SUGI BASIC PROTEIN.
L -> F (IN CRV 21-B).
L -> F (IN CRV 21-B).
S -> T (IN CRV 21-B).
C -> S (IN CRV 21-B).
C -> S (IN CRV 21-B).
K -> O (IN CRY 21-B).
K -> O (IN CRY 21-B).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-ULL-1999 (Rel. 82, Last annotation update)
STYLE beveloopming PSECIPIC HATHIN 9612 PRECIPESE
 Signal.
 Score 106; DF 1;
Pred. No. 1.8 3-13;
0; Mismatches C
 404 AA
 PFAM: PF00544: pec_lyase: 1.
PRINTS: PR00607: ANBALUSHGEN.
Allergen: Glycoprotein: Multigene family:
 AMB A I/AMB A II/CRY J I SUBFAMILY
 PRT;
 SUBCELLULAR LOCATION: SECRETED.
 ×
 EMBL: D26544: BAA05542.1; C. EMBL: D26545: BAA05543.1; C. EMBL: D34639: BAA07020.1; C. PIR; A44773: A44773.
 Cuery Match
Rest Local Similarity 190.0%:
Matches 15: Conservative
 40645
 232 KSMKVTVAFNQEGPN 246
 STANDARD:
 LIN TILL TILL
TREMKVIVAENUESPN 15
 CARBOHYD
CARBOHYD
 SECUENCE
 SIGNAL
CHAIN
VARIANT
VARIANT
VARIANT
VARIANT
VARIANT
 CARBOHYD
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 entities requires a license augement (See http://www.ist.sib.ch/augoinde/
or send an email to license(isu-sib.ch).
 ċ
 DE DEVELOPMENT-SPECIFIC PROTEIN 4612 ENTIAL
 30.5
 Rogers Hill, Harvey A., Lonson of the "Country Gene with Luminous to pectate lysee which is specifically expressed during mandrosporoseesis."
 Nicoriana tabacum (Common tobacco)
Wharyota, Vinfolplantae: Streptophyta: Embryophyta: Trachesphyta:
euphyllophytes: Spermatophyta: Madrochyta: eudiccyledons:
core eudicots: Asteridae; eua 'rids': Solanales; Solanaceae.
 DEVELOPMENT.
-!- SIMILARITY: BELCNGS TO THE POLYSACCHARIDE LYASE FAMILY DEVICED.
 l: Indels
 Length 404
 F46E0598128D8675 CRC64:
 Score 60: DB 1. D4
Pred. No. 3.02e-06:
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PECTATE LYASE PRECURSOR (EC 4.2.2.2)
 2: Mismatches
 197 AA
 POTENTIAL. PECTATE LYASE.
 ENTIAL
 P. .. ENTIAL
 78.7
1.
 SEQUENCE FROM N.A.
STRAIN-CV. SAMSUN; TISSUE-POT N;
MEDLINE: 93043039.
 EMBL: X67158; CAA47630.1; ...
EMBL: X67759; CAA47631.1; ...
EMBL: X51102; CAA434.4.1; ...
PIR; S26211; S26211; PFAM: PF00544; pec..yase: 1.
PRINTS: PR09867; AMBALLERGEN.
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US-09-142-524A-9.rsp

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 NOT THE TAKE WAN AND DOUGGOOGGOOK AND AND OOGGOOK AND AND OOGGOOGGOOGGOOK AND AND OOGGOOGGOOK AND AND OOGGOOK
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 ö
 Wing R.A., Yamuguchi J., Larabell S.K., Trsin V.M., McCormick S., "Molecular and genetic characterization of two polien-expressed genes that have sequence similarity to pectate yases of the plant pathogen Erwinia.";
 CLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-MANN-4-ENURONOSYL GROUPS
AI THEIR NON-REDUCING ENDS.
-: TISSUE SPECIFICITY: EXPRESSED IN ANTHERS AND POLLEN.
-: SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 Gaps
 Lycopersicon esculentum (Tomato).
Sukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledoms:
core eudicots: Asteridae: euasterids I; Solanales: Solanaceae:
 Wing R.A.:
Submitted (SEP-1994) to the EMBL/GenBank/DOBJ databases.
-:- FUNCTION: MIGHT BE NEEDED DURING POLLEN DEVELORMENT AND TUBE
 ::
 Score 74: DB 1: Length 397;
Pred. No. 1.05e-04;
4: Mismatches 1: Indels
 OR 22 (POTENTIAL).
PROBABLE PECTATE LYASE PS6.
POTENTIAL.
PCTENTIAL.
 PCTENTIAL.
8D676250BD8BC7C8 CRC64;
 EFCA82CESDA7643F CRC54;
 01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
PROBABLE PECIATE LYASE P56 PRECURSOR (EC 4.2.2.2).
POTENTIAL.
POTENTIAL.
SPINITAL.
SPOTENTIAL.
GS -> GG (IN MRNA).
S -> D (IN MRNA).
S -> D (IN MRNA).
H -> N (IN MRNA).
H -> N (IN MRNA).
 398 AA
 PRT;
 Lyase: Multigene family; Signal.
SIGNAL 1 27 OR
 SEQUENCE FROM N.A.
STRAIN-CV. VF36; TISSUE-ANTHER;
MEDLINE; 91322485.
 Plant Mol. Biol. 14:17-28(1990)
 STRAIN-CV. VE36; TISSUE ANTHER;
 44563 MW;
 EMBL: X1550C; CAA33524.1; -. PIR; S08383. S08383. PFAM: PF00544; pcc_lyase: 1. PRINTS: PRO0807; AMBALLERGEN.
 44351 MW;
 Query Match
Best Local Similarity 61.5%:
Matches 8: Conservative
 STANDARD:
 254 KDMKITLAYNHFG 266
 I KSMKVIVAFNOFG 13
 273
135
228
398 AA;
 222
2024
2020
2020
244
244
37
37
4A
 PESS_CYCES
 GROWTH
 REVISIONS
 ACT_SITE
CARBCHYD
 CARBCHYD
SECUENCE
 ACT_SITE
CARBCHYD
CARBCHYD
 CONFLICT
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 Sdro
 01-FEB-1995 (Rel. 31, Created)

01-FEB-1995 (Rel. 31, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)

16-DEC-1998 (Rel. 37, Last annotation update)

ECTATE LYASE PRECURSOR (EC 4.2.2.2).

Lilium longiflorum (Trumpet 11ly).

Buxaryota: Viridiplancae; Streptophyta: Embryophyta: Tracheuphyta.

Liliaceae: Lilium.
 STRAIN-CV. NELLIE WHITE; IISSUE-FOLLEN,
Kim S.R., Finkel D.J., An G.;
Submitted (JUN-1993) to the EMBL/GenBank/DUBJ databases.
-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE CLIGOSACCHARDES WITH 4-DEDXY-ALPHA-D-MANN-4-ENURONN-SYL GRUDPS
AT THEIR NON-REDUCING ENDS.
 Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta: eudicotyledons; euphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudidots; Asteridae; euarterids I; Solanates; Solanareae;
 ..
o
 -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 Length 434;
 1: Indels
 Indels
 Tength 398
 CIF3E30AD2BBDC64 CRC64;
 01-478-1990 (Rel. 14, Created)
01-478-1990 (Rel. 14, Last sequence update)
15-UCL-1999 (Rel. 38, Last annotation update)
PROSABLE PECTATE LYASE PS9 PRECURSOR (EC 4.2.2.2).
 Pred. No. 3.34e-04:
 Pred. No. 3.34e-04;
 DB 1;
 1: Mismatches
 449 AA.
 M.smatches
 POTENTIAL
PETTATE LYANE.
POTENTIAL.
POTENTIAL.
 434 AA
 ĽΒ
 POTENTIAL
 Score 72;
Score 72:

무유규 :
 434 AA; 48457 MW.
 EMBL: 217328; CAA78976.1; -
EMBL: L18911; AAA3398.1; -
PIR; S29612; S29612;
PFAM: PF00544; pec_lyaser;
 PRAM. PROGS44; pec_lysee. 1
PRINTS: PROGBCT: AMBALLEPIEN
 / Match
Local Similarity 81.8%;
67.9%;
similarity 53.8%;
7; Conservative
 9: Conservative
 STANDARD;
 STANDARD;
 24
4 34
3 12
68
97
 255 RGMKITLAYNHFG 267
 1 KSMKVTVAFNQFG 13
 296 MOVIVAFNHEG 306
 3 MKVTVAFNCFG 13
 Best Local Similarity
 SEQUENCE FROM N.A.
 23
312
68
97
 Lyase: Signal.
Signat.
 PE59_LYCES
P15722;
 LT 5
PEL_LILLO
P40973;
 ACT_SITE
CARBOHYD
CARBOHYD
SEQUENCE
 Query Match
 Query Match
 CHAIN
 CAT59
 Matches
 Matches
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 -1. CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D (ANN-4-ENURGNOSYL GROUPS AT THEIR NON-REDUCTING ENDS.
-1. IISSUE SPECIFICITY: EXPRESSED IN ANTHERS AND FOLLEN.
-1. SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASH FAMILY 1.
 ö
 Eukaryota, Rhodophyta, Florideophyceae, Gracilariales, Gracilariaceae,
Gracilaria,
 STRAIN-CV VESS: TISSUE-ANTHER:
MEDLINE; 9.322485.
Wing R.A., Yamadich; J., Larabel; S.K., Ursin V.M., McCormick S.:
"Molecular and genetic characterization of two pollen-expressed genes
that have sequence similarity to pectate lyases of the plant pathogen
Erwinia.";
 Zhou Y.H., Ragad M.A.;
"CONA cloning and characterization of the nuclear gene encoding chocoplast diversaleehyda-3-phosphate dehydrogenase from the marine curr. Genet. 23:483-489(19:3).
 Gaps
 Plant Mol. Blol. 14:17-28(1990).
-!- FUNCTION: MIGHT BE NEEDED DURING POLLEN DEVELUPMENT AND TUBE
 G3PA_GRAVE STANDARD: BWI: 416 AA
930724.
01-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 35, Last Sequence update)
15-JUL-1999 (Rel. 38, Last Sequence update)
GLYCERALDBHYDE 3-PHGSPHATE DEHYDROGENASE, CHLORAPLAST PREGURSOS
(EC. 1.2.1.12).
 Score 64: DB 1; Length 449;
Pred. No. 2.82e-02;
3; Mismatches 1: Indels
 POTENTIAL.
PROBABLE PECTAIE LYASE PS9.
POTENTIAL.
 POIENTIAL.
POIENTIAL.
POIENTIAL.
17E3AA13E173863G CRO64;
 EMBL: XIS499: CAA33523.1; -.. PIR: S27098. S27098. PPAM: PF00544: pec_lyase: 1. PRINTS: PR00807: AMBALERGEN. Lyase: Multiqene family: Signal SIGNAL.
 Query Match
Sest Local Similarity 63.5%;
 Conservative
 4 6
4 12 70
9 70 70
 309 MOITLAFNHFT 319
 Gracilaria verrucosa
 3 MKVIVAFNOFT 13
 SEQUENCE FROM N.A.
STRAIN NORWAY:
MEDLINE: 93306755.
 95042840.
 SEQUENCE FROM N A.
 GROWTH
 REVISIONS.
 ACT_SITE
CARBOHYD
 CARBOHYD
CARBOHYD
SEQUEN:
 CHAIN
 GAPA.
 Matches
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Zhou Y.H., Ragan M.A.:

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 Ċ
 CHLOROPLAST (POTENTIAL).
SUYCERALDERYDE J-PHOSPHATE DERYUR (B.NASEL)
ALYCERALDERYDE J-PHOSPHATE.
A. IVALYS THICL GROUP DOWING CATALUSIS.
(3894)7E84230B08 CROCK!
 CULT Genet. 26:79-86(1994).

-!-CATALYTIC ACTYLTY: D-GEYCERALDEHYDE 3-PHOSEMATE - TRITH PHOSEMATE.

- NADALYTIC ACTYLTY: D-GEYCERALDEHYDE 3-PHOSEMATE - TRITH PHOSEMATE.

-!-PATHWAY: CALVIN CYCLE.

-!-SUBCRIT: HOWCIETRAMER.

-!-SUBCRITULAR LOCATION: CHICKSELASI.

-!-SIMILARITY: BELONGS TO THE SLYCERALGEHYDE 3-PHOSEMATE.

DEHYDROGENASE FAMILY.
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Brown C.M., Quigley F.R., Miller W.A.;
Three edvaryold release factor one (eRVI) homologs from Arabidopsis
 ERFLAMATE STANDARD, FRED 477 AA.
P35514:
P35514:
P35514:
P35514:
P35514:
P3514:
"Cloning and characterization of the nuclear gene encoding plastif
glyceraldebyde-3-phosphate dehydrogenase from the marine red alui-
gracilaria verrucosa.":
 Eukaryota: Viridiplantae, Streptophyta: Embryophyta: Trachesphyta: euphyllophytes, Spermatophyta: Magnollophyta: eudinotylodhis: core eud cots; Rosidae, eurosids II: Brassicales; Brassicande
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA:
MEDLINE: 9798669.
Quidiey F., Dace P., Cottet A., Mache R.;
"Sequence analysis of an 81 xb contic from Arabidopsis thalland
 PFAM: PF00044; gpdh: 1.
Calvin cycle; Cxidoredictase; NAD: Transit peptide; Chloroplas;
 Score 59: DB 1: Length 416;
Pred: No. 3.83e-01;
1. Mismatches 2: Indels
 Arabidopsis thallana (Mouse-ear cress).
 (In) Plant Gene Requster PGR95-123
 44337 MW.
 Match 55.7%;
Local Similarity 75.0%;
es 9; Conservative
 78
416
233
260
 2 SMKVIVAENOFG 13
 78 SMKVRVAINGFG 89
 233 2
260 2
416 AA;
 Multigene family.
TRANSIT
 Arabidopsis.
 ACT_SITE
SEQUENCE
 Cuery Match
 BINDING
 be
 3
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Page 5

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256 KGMLATVAFNMFTDN 270
 LI 10
MP13_AMBAR
P27761;
BINDING
ACT_SITE
SEQUENCE
 MOD_RES
VARIANT
 SEQUENCE
 Query Match
 Query Match
 SIGNAL
 Matches
 Matches
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 Gaps
 15-JUL-1998 (Rel. 36, Created)
LS-JUL-1998 (Rel. 36, Last snotation update)
15-JUL-1999 (Rel. 38, Last anotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC 1.2.1.12) (GAPDH).
 ..
 DB 1: Lenath 435; 6.34e-01;
 4; indels
 49007 MW: 489D1617D5BDB34E CRC64:
 PFAM: PF00044: gpdh; 1.
Glycolysis: Oxidoreductase; NAD: Multigene family.
 Bacteria: Firmicutes: Bacillus/Clostridium group:
Bacillus/Staphyiccoccus group: Bacillus.
 Mismaiches
 340 AA
 Score 58:
Pred. No. (
 PRT;
 EMBL: AF008220; AAC00355.:.
EMBL: 299118: CAB14662.:..
HSSP: POC362: 3DEV.
SUBTILITY: B61259; GAPB.
PRINTS: PRC0078: G3PBHBGCNASE.
PROSITE: PS00071; GAPBH: 1.
 EMBL: X69375: CAA49172.1: --
EMBL: X98130: CAA66813.1: --
EMBL: X97466. CAA65118.1: --
EMBL: X97466. CAA65118.1: --
PIR: S31328: S31328.
PFAM: PF31605: RF1: 1.
 Ouery Match
Sest Local Similarity 50:0%;
Matches 7: Conservative
 DEHYDROGENASE FAMILY.
 STANDARD:
 104 KEKKVIIDFEPFKP 117
 1 KSMKVIVAFNOFGP 14
 Protein biosynthesis.
SEQUENCE 435 AA; 4
 SEQUENCE FROM N.A. MEDLINE: 98048467.
 Bacillus subtilis.
 G3P2_BACSU
034425;
 $4888888888888888
```

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 ó
 ö
 MEDLINE: 92234573.
Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.,
"Sequence polymorphism of Amb a I and Amb a II, the major allergens
 Gaps
 MEDLINE; 91093235.
Refinar T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,
Klapper D.G.;
"Cloning of Amb a I (antigen E), the rajor allergen family of short
 CAIALYSIS
 01-A06-1992 (Rel. 23, Created)
01-A06-1992 (Rel. 23, Last sequence update)
01-A06-1998 (Rel. 37, Last sequence update)
POLLEN ALLERGEN AMB A 1.3 PRECURSOR (ANTIGEN E) (ANTIGEN AMB A 1)
Ambrosia artemisifolia (Short raqweed)
Eukaryota: Viridiplandae: Streptophyta: Enkryophyta: Tracheophyta:
 euphyliophytes: Spermatophyta: Magnoliophyta: eudicotyledons:
core eudicots: Asteridae: euasterids II: Asterales; Asteraceae:
Asteroideae; Heliantheae; Ambrosia.
 .;
;
 ACTIVATES THISE GROUP DURING
 Antigen: Allergen: Signal: Multigene family: Polymorphism.
 Score 57: DB 1: Length 397;
Pred. No. 1.04e+50;
1: Mismatches 5: Indels
 Indels
CLYCERALDEHYDE 3-PHOSPHATE.
 Length 34.
 POLLEN ALLERGEN AMB A 1.3.
 C8DB41257590DD0A CRC64;
 DD1DD4BC7D633EC6 CRC64:
 DB 1: L€
1.04e-00:
 1: Mismatches
 397 AA
 Score 57;
Pred. No.
 BLOCKED.
 Biol. Chem. 265:1229-1235(1991).
 EMBL: M62961; AAA32669.1; -. EMBL: M80560; AAA32669.1; ALT_SEO. PIR; C39099; C39099. PFGAY: PF00544; pcc_lyase; 1. PRINTS: PR00807; AMBALLERGEN.
 SEQUENCE FROM N.A., AND V ANTS
 37476 MW:
 397 AA: 42928 MW;
 53.8%;
 Query Match
Best Local Similarity 72.7%;
 Local Similarity 50.0% nes 92 Conservative
 8; Conservative
 726
 3 MKVIVAFNOFG 13
 I MKVKVAINGFG 11
 340 AA;
 SEQUENCE FROM N.A.
 ragweed pollen.
 IISSUE-POLLEN;
```

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PIR: B24721: WMBPP9.
 SECUENCE FROM N.A. MEDLINE: 87106857.
 SEQUENCE FROM N.A. MEDLINE: 87117505.
PROTEIN 2).
 LYCV_BPPZA
 /iruses:
 Query Match
 Matches
g
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 Ċ
 CHLOROPLASI (POTENTIAL).
GLYCERALDEHYDE 3-PHCSPHATE DEHYDROGENASE.
GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVALES THOLO GROUP DURING CATALYSIS.
065DE62CE1064111 CRC64;
 genes encoding cytosolic and chloroplast diyecraldehyde-3 phosphate dehydrusenases from Choodius crispus. 1

2. Mol. Evol. (8:319-327,1994).

1. CALALYTIC ACTIVITY: D-SLYCERALDEHYDE 3-PHOSPHAIE + ORTHOPHOSPHAIE + NADH.

1. NAD(+) - 1.3 DIPHOSPHAIEGLYCERAIE + NADH.

1. PATHWAY: CALVIN CYCLE.

1. PATHWAY: CALVIN CYCLE.

1. SUBUNIT HOWETERAMER.

1. SUBCELLULAR LOCATION: CHLOROPLAST.

1. SUBCELLULAR LOCATION: CHLOROPLAST.

1. SUBCELLULAR LOCATION: CHLOROPLAST.

2. SIMILARITY: BECONGS ID THE GLYCERALDEHYDE 3-PHOSPHAIE

DEHYDROGENASE FAMILY.
 Gaps
 Eukaryota: Rhodophyta: Florideophyceae: Gigartinales: Gigartinaceae;
 SEQUENCE FROM N.A.
STRAIN-STACKHOUSE:
MEDLINE: 94275876.
Liadd M.-F., Valentin C., Martin W., Bouget F.Y., Kleareg B.,
Cerff R.;
The evolutionary origin of red algae as deduced from the nuclear
 EMBL: X73035; CAA51515.1; PIR. S22705; S2205; S2205; HSSP: P50362: LNUH. MSNEL T720; CHOCKOPARA: PROSITE; P50007: GAPPHERONASE. PROSITE; P50007: GAPPHERONASE. PROSITE; P50007: GAPPHERONASE. PERM: PF0044: gpdh: L. PERM: PF0044: gpdh: L. PERM: PF0044: gpdh: L. PERM: PF0044: gpdh: L. TRANSIT. TRANSIT. 76 CHICROPLASI (POTENTAL).
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHAIE DEHYDROGENASE, CHLOROPLAST PRECURSOR
 ..
..
 Score 57; OB 1; Length 414; Pred. No. 1.04e+00; 2; Mismatches 2; Indels
 2: Indels
 414 AA
 PRT
 Chondrus crispus (Carragheen)
 44459 MW;
 Cuery Match
Best Local Similarity 66.7%;
 Conservative
 STANDARD:
 1 KSMKVTVAFNCFGPN 15
 414
231
258
 76 : MKVRVAINGFG 87
 2 SMKVTVAFNCFG 13
 23;
258
414 AA:
 G3PA_CHOCR
 BINDING
ACT_SITE
SEQUENCE
 Chondrus.
 Matches
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 required for the genome encapsidation reaction. Consider the control of the genome encapsidation reaction. Consideration 1.1. FUNCTION: HELPS TO RELEAS. HE MATURE PHAGE PARTICLES FROM THE CELL WALL BY BREAKING DOWN. HE SEPTIDOGLYCAN.

-!-CATALYTIC ACTIVITY: HYDRON: 1S OF THE 1.4 -BETA-LINKAGES BETWLEN N-ACETYL-D-GLUCOSAMINE AND N-ACETYLMOPAMIC ACID IN PEPTIDOGLYCAN HEDEROPOLYMERS OF THE PROMEMANING ACID WALLS.
-!-SIMILARITY: BELONGS TO FAMILY 24 OF SLYCUSY! HYDROLARS
 Saps
 Vicek C., Paces V.; Multerliam of Bacillus phage phi 29 completes the 19,248-bp sequence of phi 29 genome. Comparison with the homologous sequence of phage PZA.":
 SEQUENCE OF 116-258 FROM N.A.
MEDLINE: 86165873.
Garvey K.J., Saedi M.S., Ito J.:
"The complete sequence of Bacilis phage phi 29 gene 16 J ptitory
 01-APR-1988 (Rel. 07, Created)
1-APR-1988 (Rel. 07, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
LYSOZYME (EC 3.2.1.17) (LYSIS PROTEIN) (MURAMIDASE) (LATE PROTEIN
 Bacteriophage PZA.
Viruses: dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
 dsDNA viruses, no RNA stage: Tailed phages: Podoviridae
 HSSE: PC0720: 265L.
PFAM: PF00959: Blader:jyscymer. |
PFAM: PF01959: Blader:jyscymer. |
PFAM: PF01476: P3_binding_n: |
Late protein: Hydrolase: 0iycosidase. Harteriolytic Hilymer ACI_SIE |
ACI_SIE |
ACI_SIE |
PR010N | OFNER (HY SIMILARITY) |
SEQUENCE | 258 AA: 28054 MM: 26AEUCID927842D8 CRC64.
 Match
Local Similarity 50.0%: Pred. No. 2.776-00;
es 7: Conservative 5: Mismatches 2: Indels
 qenes 14
 er phage lysozymes.
10008(1986)
 Garvey K.J., Saedi M.S., 110 3.:
*Nucleotide sequence of Bacilius phage phi: 29
*Nucleotide sequence of Bacilius phage lysozymes
Nucleic Acids Res. 14:1000 10038(1946).
 258 AA
 PRT;
 EMBL: X04962; CAA28632.1; -. EMBL: M14782; AAA32288.1; -. EMBL: M14431; AAA88347.1; -.
 STANDARD;
 70 KALKVSVTQNCFDA 83
 1 KSMKVTVAFNCFGP 14
 Gene 46:215-225(1986)
Bacteriophage phi-29
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STRAIN-972:
 YAM8_SCHPO
Q10063;
 SPACIES . 080
 TRANSMEM
 CARBCHYD
CARBOHYD
 CARBOHYD
CARBOHYD
CARBOHYD
 TRANSMEM
 CARBCHYD
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 SEQUENCE
 CARBOHYD
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 CARBOHYD
 MCD_RES
VARIANT
 VARIANT
 SIGNAL
 CHAIN
 Matches
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 ö
SEQUENCE FROM N.A.
MEDLINE: 87031573.
Parces V. VICER C., Urbanck P.;
Parces V. VICER C., Urbanck P.;
Aucleotide sequence of the late region of Bacilius subtillis phage
PZA, a close relative of phi 29.";
Gene 44:107-114(1986).
I. FUNCTION HELPS TO RELEASE THE MATURE PHAGE PARTICLES FROM THE
CELL WALL, BY BREATING JOWN THE PEPTIDOGLYCAN.
I. CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1.4 BETA-LINKAGES BETWEEN
N ACETYL-D-GJUCOSANINE AND N-ACETYLWURAMIC ACID IN PEPTIDOGLYCAN
HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
I. SIMILARITY: BELONGS 10 FAMILY 24 UF GLYCOSYL HYDROLASES.
 #EDLINE: 92234570.

Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.;

"Sequence polymorphism of Amb a I and Amb a II. the major allergens in Ambrosia artemisifolia (short ragweed).";
Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).
-: SUBJNIT: MCNOMER.
-:- IISSUE SPECIFICITY: POLLEN AND FLOWERS.
-:- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
-:- SIMILARITY: BELONGS IJ THE POLYSACCHARIDE LYASE FAMILY I. AMB A IZARB A IZORY JI SUBFAMILY.
 Klapper D.G.: "Clouing of Amb a I (antigen E), the major allergen family of short
 Gaps
 PRIZ. MRP12_MEAR STANDARD; PRI; 398 AA.
P27760;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
POLIEN ALLEWSEN AMB A 1.2 PRECURSOR (ANTIGEN E) (ANTIGEN AMY A 1).
Ambrosta atterisilota (Stort ragword).
Ewkaryota, Viridiplantus: Streptophyra: Embryophyra: Iracheophyra.
Eukaryota, Viridiplantus: Streptophyra: Embryophyra: Iracheophyra.
core cudicous: Asteridae: chastorids II: Asterales: Asteraceae;
 ..
 TISSUS-FOLLEN;
MEDLINE: 91093238.
Rafnar I., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,
 Score 55; DB 1: Length 258; Pred, No. 2.77 -00; 5; Mismatch 8 2; Indels
 Chem. 266:1229-1236(1991).
 Asteroideae: Heliantheae: Ambrosia.
 SECUENCE FROM N.A., AND VARIANIS.
TISSUE-POLLEN:
 EMB1: M11813: AAA88492.1: -.
 51.9%;
 Sest_Local Similarity 50.0%;
Matches 7; Conservative
 70 KALKVSVTCNOFDA 83
 1 KSMKVIVAFNOFGP 14
 SEQUENCE FROM N.A.
 ragweed pollen.
J. Biol. Chem.
 Query Match
 RESULT
 3
 3
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 between the Swiss Institute or Bioinformatics and the EMBL distation the European Bioinformatics in Structure. There are no restrictions use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and lot numerical entities requires a license agreement (see http://www.sshrsib.n./annonnee/or send an email to licenselessbib.ch).
ht. It is produced through a collaboration
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23
 Contles S., Odell C., Church T.Y. Fattell H.G., Kulandream Walsh S.V.:
 ÷
 dene family. Polymorphism
 Length 398:
 3: Indels
 Submitted (NoV-1995) to the EMBL/Octfeank/1995 databases -1. SIMILARIIY: SGME, TO YEAST MID).
 P. LEN ALLENGEN AMB A 1.2.
PI INED.
 Eukaryota: Fungi: Ascomycota: Schizosaccharomycetales:
Schizosaccharomycetaceae; Schirosaccharomyces.
 02000662D987416G CRC64;
 C1-FEB-1996 (Rel. 33, Created)
C1-FEB-1996 (Rel. 33, Last sequence update)
C1-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHERICAL 53.9 KD PROTEIN C1F5.08C IN CHROMOSCME
 Transmembrane: Glycoprotein
 Score 55: DB 1: L4
Pred. No. 2 77e+00:
1: Mismatches 3.
 486 AA
 Schizosaccharomyces pombe (Fise.on yeast).
 POTENTIAL.
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PUTENTIAL.
PUTENTIAL.
 POTENTIAL. POTENTIAL.
 ENTIAL.
 POTENTIAL
 PRT
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This SWISS-PROT entry is copy:
 PIR: B39C99: B39099.
PFAM: PF00544; pec_Lysse: 1.
PRINTS: PR00677; AMBALLERGEN
Actigen: Allergen: Signal: M:
 . .
¥
 Query Match
Best Local Similarity 66.7%;
 EMBL; M62981; AAA32666.1;
EMBL; M80559; AAA32667.1;
 43664
 EMBL: 258136; CAA92236.1;
 8; Conservative
 STANDARD;
 726
345
381
 Hypothetical protein;
 257 KGMLAIVAFNMF 268
 1 KSMKVIVAFNOF 12
 725
345
381
398 AA;
 SEQUENCE FROM N.A.
```

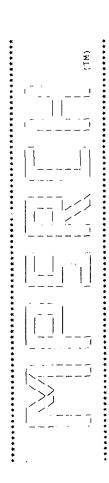
POTENTIAL

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Ö
 Saps
 03
 Substitution of 1.9%: Score 55: DB 1: Length 486: Pest Local Similarity 63.6%: Pred. No. 2.77e+00; Matches 7: Conservative 3: Mismatches 1: Indels
336 330 POTENTIAL.
341 341 POTENTIAL.
353 353 POTENTIAL.
379 379 POTENTIAL.
445 445 POTENTIAL.
466 AA: 53888 MW: 352C417356036958 CRO64:
 118 VSSAFSCFAPN 128
1: 'i:|!:
5 VIVAFNQFGFN 15
 CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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Sourch completed: Mon Jun 19 16:09:08 2000 Ach time : 16 secs.

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US-09-142-524A-9.rspt



Release 3.1A John F. Collins, Biocor uting Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

Mistch\_pp protein - protein database search. using Smith-Waterman algorithm

Mon Jun 19 16:09:25 2000; MasPar time 8.84 Seconds 117.642 Million cell updates/sec 3410 OC:

Tabular output not generated.

>US-C9-142-524A-9 (1-15) from USO9142524A.pep 196 1 KSMKVIVAFNJFGPN 15 Title: Description: Parfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match O% Listing first 45 summaries Post-processing:

Database

sptremb112 1.sp\_archel 2.sp\_bacteria 3.sp\_fungi 4.sp\_human 5.sp\_invertebrate 6.sp\_mammal 7.sp\_mhc 8.sp\_organelle 9.sp\_phage 10.sp\_bant 11.sp\_rodent 12.sp\_unclassified 13.sp\_vertebrate 14.sp\_virus

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 26,072: Variance 31,115: scale 0.838

Statistics:

|                |                       |                  |                        |                        | _                 |                        |                        |                        |                        |                        | _                 |                        |                        |                        |                | ~~                     | ۵.                     | ٠.                     | ٠.                |                   |
|----------------|-----------------------|------------------|------------------------|------------------------|-------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-------------------|------------------------|------------------------|------------------------|----------------|------------------------|------------------------|------------------------|-------------------|-------------------|
| NO.            | 02e-12                | 02e-12           | 6e-07                  | ò                      | e-07              | 87e-06                 | 96e-05                 | 96e-05                 | e-05                   | 30e-05                 | 64e-34            | 88e-04                 | 88e-04                 | 82e-04                 | e-03           | 88e-03                 | 7e-02                  | 7e-02                  | 7e-02             | ú                 |
| Fred           | 8                     | 1.02             | 1.46                   | 1.45                   | 2.67              | 2.87                   | 2.96                   | 2.96                   | 9.30                   | 9.30                   | 1.64              | •                      | 2.88                   | 8.82                   |                | 7.88                   | S                      | 6.57                   | 3                 | 1.85              |
| Description    | POLLEN MAJOR ALLERGEN | CHAO1 PRECURSOR. | PECTATE LYASE LIKE PRO | PECTATE LYASE LIKE PRO | F12F1.22 PROTEIN. | PECTATE LYASE (EC 4.2. | PUTATIVE PECTATE LYASE | PECTATE LYASE PRECURSO | PUTATIVE PECTATE LYASE | PUTATIVE PECTATE LYASE | TIGIL, 7 PROTEIN. | PECTATE LYASE (EC 4.2. | PECIATE LYASE HOMOLOG. | POLLEN SPECIFIC PECIAT | PECTATE LYASE. | PUTATIVE PECTAIE LYASE | PUTATIVE PECTAIE LYASE | PUTATIVE ZINC-FINGER P | T15F16.7 PROTEIN. | F13F21.9 PROTEIN. |
| Ω              | Q92NU7                | 096385           | 065457                 | 065456                 | 065388            | 043783                 | 023667                 | 024554                 | 064513                 | 023665                 | C23017            | 004084                 | 040319                 | 043862                 | 024416         | 023668                 | 024:6:                 | ~                      | 081463            | Q9X;B4            |
| 508            | 9.                    | 0.1              | 0.1                    | C                      | 011               | ر.                     | C                      | 10                     | 0.                     | 0                      | 10                | :                      | 10                     | 10                     | 10             | 10                     | 10                     | 0                      | 0,                | 3.0               |
| Length         | ري                    | Γ.               | 394                    | 364                    | 390               | Φ                      | 2                      | 401                    | 455                    | S                      | ٠,                | 263                    | r)                     | 438                    | 0              | 227                    | Γ,                     | (T)                    | 461               | -                 |
| Query<br>Match | 100.0                 | 100.0            | 82.1                   |                        | 81.1              |                        | 73.6                   | 73.6                   | 71.7                   | 71.7                   |                   |                        | 6.8                    | 67.3                   |                | 64.2                   | 60.4                   | <b>9</b> .09           | 60.4              | 58.5              |
| Score          | 40                    | 106              | 0,<br>7.               | 8.7                    | 86                | 82                     | ۱۰.<br>80              | 3.6                    | 7.5                    | 76                     | 45                | 74                     | <del>1</del>           | 72                     |                | 89<br>49               |                        | **                     | 79                | 62                |
| sult<br>No.    | ,                     | (7               | ٣                      | 77                     | 'n                | 9                      | 7                      | œ                      | თ                      | 10                     | -1                | 12                     | 33                     | 7.                     |                | 9                      |                        |                        |                   |                   |

|                                                                                                                                             | 2,326+01<br>2,326+01<br>2,326+01<br>2,326+01<br>2,326+01                                                        |
|---------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|
| - напочн - хараанохни - <b>к</b> а<br>- яндехманххния - омично                                                                              | MYELOBLAST KIAA0246 PK<br>MSF16 PROJEIN.<br>NADH CHHYDOGENASE SYB<br>HYPOTHETICAL 52.3 KD P<br>F40F9.6 PROJEIN. |
| 001966<br>0037174<br>0037174<br>0037174<br>003207<br>003207<br>003744<br>003744<br>00374<br>00374<br>002233<br>002233<br>0020237<br>0020237 | 093072<br>092V50<br>037447<br>009579<br>020239                                                                  |
| 110 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                     | 400000                                                                                                          |
| 28233<br>28233<br>28233<br>3550<br>2868<br>3550<br>3550<br>3550<br>3550<br>3550<br>3550<br>3550<br>355                                      | * + 00 tO tO O                                                                                                  |
| <ul><li>*** ** *** *** *** *** *** *** *** ***</li></ul>                                                                                    | 00000                                                                                                           |
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## ALIGNMENTS

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3 MKVTVAFNOFGP 14
 SEQUENCE FROM N.A.
 F12F1.22 L.OTEIN.
F12F1.22.
 01-AUG-1998
01-AUG-1998
 BEVAN M., WE
SCHUELLER C.
 01-NOV-19:
F12F1.22 1.40
 Arabidopsis
 SEQUENCE
 SEQUENCE
 Query Match
 043783;
 043783
 T 5
065388
065388;
 Lyase
 Matches
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 a
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 ن
 ö
 MEDLINE: 96265194.
SCZUKI M., KOMIYAMA N., ITCH M., ITCH H., SONE I., KUNG K., TAKAGI I.,
 OHTA N.:
*Purilication, characterization and molecular cloning of Cha o 1, a major allergen of Chamaecyparis obtusa (Japanese cypress) pollen."; Man of Chamaecyparis obtusa (Japanese cypress) pollen."; Man of Chamaecyparis obtusa (Japanese cypress) pollen."; Man of Chamaecyparis obtuse (1996).

EMBL: D45404; BAC8246.1;

MENDEL: 7456; Chamboli099:7626.

PRAM: PP00544; PeC_1956: 1.

PRINTS: PR00807; AMBALLERSEN.
 Gaps
 Gaps
 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: euphyllophytas: Spernatophyta: Magnollophyta: eudicotyledons: core eudicots; Rosidae: errosids II: Brassicales: Brassicaceae;
 SECUENCE FROM NIA.
BEVAN MIL WEDGER HIL WAMBOTT RIL BANCKOFT III NEWES HIWI, MAYER KI
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 Score 106: DB 10: Length 375; Pred. No. 1.02e-12; 0: Mismatches 0: Indexs
 Score 87: DB 10: Length 394: Pred: No. 1,46e-07: 1: Mismatches 0: Indels
 (2)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMILLED (AFR.1993) TO LIVE TI.
SUBMILLED (AFR.1993) TO LIVE FRUIT/SEQUENCE (TR.) directors:
FMBL, ALO22146: CAA.88.12.1
MENDEL, 29068: Arath.1068:29068.
PFAM: PROOFER, PROCEETS 1.
PRINTS: PROCESCT: AMBALLERGEN.
 Submitted (MAR-1938) to the FMBL/SenBack/DDBJ datubases
 Created)
Last sequence update)
Last annotation update)
 Last sequence update;
Last annotation update;
 SIĞNAL : 21 POTENTIAL.
CHAIN 22 375 CHAO1.
SEQUENCE 375 AA: 40258 MN: A0981492 CRC32:
 SEQUENCE 394 AA: 43299 MW; 8B9A93C9 CRC32;
 394 AA
 394 AA
 Arabidopsis thaliana (Mouse-ear cress).
 Created)
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 PRT;
 01-AU3-1998 (TrEMBLIE) 07.
01-AU3-1998 (TrEMBLIE) 07.
01-NOV-1999 (TREMBLIE) 12.
PECTATE LYASE LIKE PROTEIN.
FINZO.183.
 01-AUG-1998 (TEMBLIEL 07, 01-AUG-1998 (TEMBLIEL 07, 01-NOV-1999 (TEMBLIEL 12, PECTALE LYASE LIKE PROTEIN.
 82.18;
 cuery Match
Bost Local Similarity 100.08:
Matches 15: Conservative
 Glery Match 82.1%;
Hest Local Similarity 91.7%;
Matches 11; Consgrvative
 PRELIMINARY;
 232 KSMKVTVAFNOFGPN 246
 PRELIMINARY:
 LILL TILL FL
L KSMKVIVAFNUFGPN IS
 256 MKVTVAFNHFGP 267
 SEQUENCE FROM N.A.
 TISSUE-POLLEN
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 30.50
Arabidopsis thallana (Mouse-ear cress).
Bubrayota Viridhiplantae: Streptophyta: Embryophyta: Truchhophyta: euclidis Streptophyta: Embryophyta: Spermatophyta: Magnollophyta: euclidis yleddis: Oze euclidis II: Brassicales: Brassicales:
 MAYER &
 Arabidopsis thaliana (Mouse-var cross).

Eukaryota: Viridiplantae: Sire robbyta: Entryophyta: Trachemphyre
euphyllophytes: Spermatophyta: Magnoliophyta: eldicotyledins:
core eldicots: Rosidae: eurosiss II: Brassicales: Brassicaceae
Arabidopsis.
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 C1-NOV-1996 (TrEMBLre). C1, Created)
O1-NOV-1996 (TrEMBLre). O1, Last sequence update)
O1-NOV-1999 (TrEMBLre). 12, Last annotation update)
PECTATE LYASE (EC 4.2.2.2) (PECTATE TRANSELIMINASE) (FRAGMENT).
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 Desgth 3900
 Serve 87: DB 10: Legath 194.
Pr d. No. 1.46e-07:
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 SECONDE FROM N.A. BEVEN WAMBUTT BUT BANCHOFT IO, MEMES BOW
 EU ARABIDOPSIS SECUENCING PROJECT:
Submitted (APR-1998) to the EMBL/GenHank/PUHD databases.
EMBL, ACC22140: CAA19111:11: -.
MENDEL: 24747; Arath.1088:29747.
PFAM: PFGU544: pec_lyase: 1.
 Submitted (MAR-1998) to the EMBL/Genbank/DDBJ databases
 (TremStrel, C7, Created)
(TremStrel, C7, Last sequence update)
(TremStrel, 12, Last annotation update)
 390 AA; 43354 MW: EDF32FB4 CRC32:
 394 AA: 43476 MW: 95399178 CPC32.
 Mismatches
 398 AA
 347 AA
 FRI
 PRINTS: PRC0807; AMBALLERGEN
 Match 82.1%; Local Similarity 91.7%; tes 11; Conservative
 Query Match
Best Local Similarity 71.4%:
Matches 10: Conservative
 PRELIMINARY;
 PRELIMINARY;
 244 KIMRVTIAFNHFGP 257
 L KSMKVIVAFNQFGP 14
 256 MKVTVAFNHFGP 267
 RESULT
ID 04
AC 04
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DT 01
DT 01
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Eukaryota, Viridiplantae: Streptophyta, Embryophyta. Tracheophyta: euphylophytes; Spermatophyta; Magnollophyta; eudicotyiedous; core eudicots; Asteridae: eusterids II; Asterales; Asteraceac. Asteroideae Hellantheae: Zinnia.
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Strentophyra: Embryophyta: Trachuophyra: Eukaryota: Viridiplantae: Strentophyra: Embryophyta: Trachuophyra: ephyllophyra: Spermatchyta: Mugnollophyra: endicutyiedons: core eudicots: Kosidae: euros:ds ll. Hrassicales: Hrassicaceae; Arabidopsis:
 RCUNDLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON K.C. SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D., SOMERYILLE C.R., VENTER J.C.; SUBMERYILLE C.R., VENTER J.C.; SUBMITTEE (J.R., VENTER J.C.)
SUBMITTEE (J.R., VENTER J.C.)
SUBMITTEE (J.R., VENTER J.C.)
MAR-1998) to the EMBL/GenBank/DDBJ databases.
MENDEL: 285051 AAAC63500.1; MAGOSSOS.
PFAM: PF00544; pec_lyase: i.
 SEQUENCE FROM N.A.
MEDLINE: 98345940.
DOMINGO C., ROBERTS K., STALEY N.J., CONNERTON I., MCCANN M.C.
"A pectate lyase from 21nnia elegans is auxin inducible.";
Plant J. 13:77-28(1998).
EMBL: Y09541; CAA70735.1: -.
EMBL: Y09541; CAA70735.1: -.
PRAM: PFC0544: pec_lyase: 1.
PRINTS: PRO0807; AMBALLERGE."
Signal: Lyase.
 Score 78: DB 10: Length 40: Fr.3. No. 2.96e-05: Mismatches 1: Indeis
 Score 76; DB 10; Length 455
Pred. No. 9.30e-05;
2: Mismatches 2; Indels
 Created)
Last sequence update)
Last annotation update)
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Last annotation update)
 P TENTIAL,
PECTATE LYASE,
C4C07131 CRC32;
 EBA0B82D CRC32;
 459 AA.
 455 AA
 Created)
 PRT;
 SEQUENCE 455 AA; 51257 MW;
 SEQUENCE 401 AA; 44407 MW:
 PRINTS: PRO0807; AMBALLERGEN
 01-JAN-1998 (TrEMBL:el. 05, 01-JAN-1998 (TrEMBL:el. 05, 01-NOV-1999 (TrEMBL:el. 12, PECTATE LYASE PRECURSOR.
 y Match
Local Similarity 69.2%;
 01-AUG-1998 (TrEMBLrel. 07, 01-NOV-1999 (TrEMBLrel. 12,
 y Match
Local Similarity 69.2%:
hes 9; Conservative
 01-AUG-1998 (TrEMBLrel. 07,
 9; Conservative
 PRELIMINARY;
 PRELIMINARY:
 2C
401
 261 KNMQVTIAFNHFG 273
 PUTATIVE PECTATE LYASE
 309 KKMQITVAFNHFG 321
 1 KSMKVTVAFNOFG 13
 I KSMKVTVAFNGFG 13
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA:
 Zinnia elegans.
 Query Match
 Query Match
 LT 10
023665
023665;
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 Matches
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 Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-GLUC-4-ENURONOSYL GROUPS AT
 Gaps
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 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyra: Embryophyta: Tracheophyta: euhyliophytes: Spermitophyta: Mandiliophyta: eudicityledons: core eudicots: Rosidan: eurosids II: Brassinales: Brassicaneae; Arabidopsis.
 Eukaryoda: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytus: Spermatophyta: Magnollophyta: Lillopsida:
Zingiberales: Musaceac: Musa.
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 KULIKAUSKAS R., MCCCRMICK S.:
"Identification of the tobacco and Arabidopsis homologues of poller:expressed LATS9 gene of tomato.";
Plant Mol. Biol. 34:899-814(1997).
BEBL: U8362.; AA869761.1;
MENDEL: 25561; Arath;1088:25561.
PFAM: PF00544: pec_lyase: 1.
 Score 78: DB 10: Length 226;
Pred. No. 2.96e-05;
3: Mismatches 1: Indels
 Score 82: DB 10; Length 398;
Pred. No. 2.87e-06:
3: Mismatches 2: Indels
 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 01-JAN-1998 (TrEMBLIE): 05, Created)
01-JAN-1998 (TrEMBLIE): 05, Last sequence update)
01-NOV-1999 (TrEMBLIE): 12, Last annotation update)
PUTATIVE PECIATE LYASE (FRAGMENT).
 226 24 25103 MW; SFIC8DD2 CRC32;
 STRAIN-CV. DWARF CAVENDISH: TISSUE-RIPE FRUIT:
DOMINGUEZ-PIUGJANER E.:
 SEQUENCE FROM N.A.
STRAIN-CV, DWARF CAVENDISH: TISSUE-RIPE FRUIT:
DOMINGUEZ-PUIGJANER E.:
 398 AA; 43712 MW; ESE9B38A CRC32;
 AA.
 226 AA
 PRT;
 THEIR NON-REDUCING ENDS.
EMBL: V92943: CAA6549611: -
MENDEL: 9136: Musaci1089-9136.
PFAM: PF00544: pec_lyase: 1.
 Cuery Match 73.6%;
Best Local Similarity 69.2%;
Matches 9; Conservative
 Juery Match
Best Local Similarity 66.7%;
Matches 10: Conservative
 PRELIMINARY;
 258 KSMQVTIAFNHFGED 272
 PRELIMINARY:
 : KSMKVTVAFNQFGPN 15
 Musa acuminata (Banana)
 196 KNMQVIIAFNHFG 208
 1 KSMKVIVAFNOFG 13
 SEQUENCE FROM N.A. MEDLINE: 97422403.
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450 AA;
 431 AA;
 1 KSMKVTVAFNOFG
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 Nicctiana.
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 Saps
 Arabidopsis tialiana (Mouse-ear cress).
Eukaryota, Viilalplantae: Streptophyta: Embryophyta: Iracheophyta: euphyllophytes: Spermatophyta: Magnolicphyta: old:ookyledons: core eudhots: Hosidae: ellosids II: Brassicales: Brassicaceae
 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: etafycophyta: ephyticophytes: Spertophyta: Magnollophyta; evalcotylodors; core eudioots; Rosidae: eurosids II: Brassicales: Brassicaceae;
 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIM-CV. OTTHINGSAL
SERGARE B.I. VESTINATE V. S. THEIDMI M. YU G. FULL J.D. LIU S.
LI J.HOANG L. BUEHLER E. CONWAY A.E. CONWAY A.R. BEWAR K.,
KYM C. BUEHLER E. LI Y. SHINN P. SUN H., DEWAR K.,
ECKER J.R., FEDERSPIEL N.A. THEOLOGIS A.,
SUBMILLED (AUG-1997) to the EMBL/GenBank/DDBJ databases.
 the
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 SEQUENCE FROM N.A. MEDLINE: 974.22403.

MEDLINE: 974.22403.

MULTRAUGRAS N., MCCORNICK S.:
Identification of the tobacco and Arabidopsis homologues of the plant Mol. Blot. 2 the tobacco and Arabidopsis homologues of the plant Mol. Blot. 2 the tobacco and Arabidopsis homologues of the plant Mol. Blot. 2 the tobacco and Arabidopsis. PRBL: 0386.99. Arath/1088:2559.

PERML: PRO0544: pec__wase: 1.
 Length 459,
 Tagers
 THEOLOGIS A.;
Submitted (JUL-1997) to the EMPL/GenBank/DDBJ databases
 Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases DBBL. ACO02476; ARB80622.1; -. MENEL. 25798. Arath.1088;25798. PFAM: PF00544; pcc_lyase; 1.
 Subritted (AUG-1997) to the EMBL/GenBank/DDBJ databases
 Last sequence update)
01-JAN-1998 (IrEMBLrel. 05, Created)
01-JAN-1998 (IrEMBLrel. 05, Last sequence update)
01-NOV-1999 (IEMBLrel. 12, Last annotation update)
PUTATIVE PETTATE LYASE.
 Score 75, CB LC: 71.78, Score 75, CB LC: Let hest Local Similarity 69.28, Pred. No. 9.30e-05, Matches 9; Conservative 2; Mismatches 2;
 459 AA: 51420 MW: 41EB59D8 CRC32:
 431 AA.
 Created)
 023017,
01-JAN-1998 (TrEMBLrel. 05, Ct
01-JAN-1998 (TrEMBLrel. 05, La
01-M0-1999 (TrEMBLrel. 12, La
11G11.7 PROTEIN.
 PRINTS: PROCECT: AMBALLERGEN.
 PRINTS: PROC807: AMBALLERGEN
 PRELIMINARY:
 313 KKMQITVAFNHFG 325
 I KSMKVIVAFNCFG 13
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
THEOLOGIS A.:
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA:
 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
 PHECLOGIS A.:
 Arabidopsis
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3
 Medicago sativa (Alfalfa).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Iracheophyta:
euphyllophytes: Spermatophyta: Macrollophyta: ecdicotyledons:
core eudicots: Rosidae: eurosids I: Fabales: Fabareae: Papilionoldoac:
 STRAIN-SAMSUN;
ROGERS H.C., LONSDALE D.M.:
ROGERS H.C., LONSDALE D.M.:
SUDBLITEG (JUL-1991) to the EMBL/Gensank/DDEC databases.
SUDBLITEG (JUL-1991) to the ELMINATIVE CLEAVAGE OF PECURATE J. GIVE
1. CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECURATE J. GIVE
OLIGOGRACHERIDES WITH 4.DEDXY ALPHA D.G.UC.4.ENURGN.9YL GR-UFS AI
 8.35%
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 01-NOV-1996 (IrEMBLrel. 01. Dreated)
01-NOV-1996 (IrEMBLrel. 01. Last sequence update)
01-NOV-1999 (TEMBLrel. 01. Last annotation update)
PECTATE LYASE (EC. 4.2.2.2) (FRAZMENT).
Nicotiana tabadum (Common tobacco).
Ricotiana tabadum (Common tobacco).
Eukaryota: Viridiplantae; Stroprophyta: Embryophyta: Itacheophyta:
 euphyllophytes: Spermatophyta: Macholiophyta: eudicotyledons:
core eudicots: Asteridae; euasterids I; Solanales: Sulanareve.
 3
 Length 450:
 Length 26.9
 Score 75: DB 10: Length 430: Pred. No. 1.64e-04: 4. Mismatches 1: Indexs
 WO.Y., QIU X., DU S., ERICKS.N L.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: C41472: AAA86241.1:
MENDEL: 9042; Medsa:1088:9042.
 01-NOV-1996 (TrEMBLrel. 01, Greated)
1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PECTATE LYASE HOMOLOG.
 69.8%; Score 74; DB 16;
 50155 MW: B35FCF9E CRC32;
869EC285 CRC 42;
 24806A CRD32.
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E
-MW 07772
 263 AA: 29449 MK;
 59.88; 5
 PFAM; PFC0544; pec_lyase; 1. PRINTS; PR00867; AMBALLERGEN.
 Local Similarity 51.5%;
nes 8; Conservative
 Query Match
Hest Local Similarity 61.5%:
Matches 8: Conservative
 PRELIMINARY:
 PRELIMINARY;
 136 KEMKITLAYNEEG 148
 289 KAMQVTIAYNHFG 301
 8
 1 KSMKVIVAFNUFG 14
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SEQUENCE FROM N.A.
STRAINSON GOLDSCUP: TISSUE-SHOOT:
STRAINSON GOLDSCUP: TISSUE-SHOOT:
MEDILINE: 94083584
TURCICH M.P., BAMILTON D.A., MASCARENHAS J.P.;
ISOLATION and characterization of pollen-specific maize genes with sequence horology to ragweed albergens and pectate lyases.";
Plant Mol. 33.1061-1065(1993).
OLIGOSACCHARIDES WITH 4-DECXY-ALPHA-D-GLUC-4-ENURONOSYL GROUPS AT THER NON-REDCCING ENDS.
EMBL: L20140: AAA1476 1: ...
RENDEL: 1165: Zeama:12086:1165.
RENDEL: 1165: Zeama:12086:1165.
PRINTS: PROC841: PROCLYBERGEN.
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 "Cloning, molecular characterization and expression pattern of a strawberry Tipening-specific CDNA with sequence homology to pectate lyase from higher plants."
Plant Mol. Biol. 34:867-877(1997).
EMBL. 06350; AAB31208-1; -
PRENEL: 26059; Frax; 1089:26559.
PFAM: PF00544; pec_lyase; 2.
 Gaps
 Saps
 Eukaryota, Viridiplantae, Streptophyta, Erbryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnollophyta; Liliopsida, Poales, Poaceae, Zea,
 Fragaria ananassa (Strawberry).
Eukaryota: Viridiplandes: Streptophyta: Embryophyta: Tracheophyta:
euphyilophytes: Spermatchytya: Magnoliophyta: eudicotyledons:
core eudicots: Rosidae: eurosids I: Rosales: Rosaceae: Fragaria.
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 MEDLINE: 97435972.
MEDINA-ESCOBAR N., CARDENAS J., MOYANO E., CABALLERO J.L.,
MUNOZ-BLANCO J.;
 Cuery Match 67.9%; Score 72; DB 10; Length 438; Rest Lonal Similarity 81.8%; Pred. No. 8 82e-04; Matches 9; Conservative 1; Mismatches 1; Indels
Pred. No. 2.88e-04;
2: Mismatches 2: Indels
 04.3862:
01-NOV-1996 (TrEMBLTel. 0). Created)
01-NOV-1996 (TrEMBLTel. 0). Last sequence update)
01-NOV-1999 (TrEMBLTel. 12, Last annotation update)
POLLEN SPECIFIC PECIFIE LYASE HCMOLOGUE (EU 4.2.2.2)
(PECIATE TRANSELIMINASE).
 LT 15 PRELIMINARY PRT: 405 AA. 024416 C24416 (C24416) (D.5AN-1998 (TEMHILE). 05, Created) (D.5AN-1998 (TEMHILE). 05, Last sequence update) (D.1NOV-1999 (TEMBILE). 12, Last annotation update) PECTATE LYASE.
 SEQUENCE 438 AA: 49138 MW; 10585369 C: 132:
 PRI; 438 AA
Best Local Similarity 69.2%;
Matches 9, Conservative
 PRELIMINARY
 309 KIMCITVAFNHFG 321
 1 KSMKVTVAFNCFG 13
 300 MQVTVAFNHFG 310
 3 MKVIVAFNUFG 13
 SEQUENCE FROM N.A. SIRAIN-CHANDLER;
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11.77
 Length 405.
 Ouery Match 67.0%: Score 71; DB 10; Length 40% Best Local Similarity 61.5%; Prod. No. 1.53e-03; Matches 8; Conservative Mismatches 2; Indels
45744 MW: 289944A0 CRC32;
 Search completed: Mon Jun 19 16:09:37 2000 Job time : 12 secs.
 309 KOMQVTIAYNHFG 321
 1 KSMKVTVAFNQFG 13
405 AA;
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Release 3.1A John F. Collins, Biccomputing Research Unit. Copyriait (c) 1993-1998 University of Edinburgh. U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, ising Smith-Waterman algorithm Mon Jun 19 16:12:28 2000: MasPar time 3.59 Seconds 210.858 Million ceil updates/sec MPsrch\_pp Rut. on:

508-09-142-524A-10 (1.32) from USO9142524A.pep 227 Tabular output not generated.

1 BEYLILSARDVLAVVSKRRMKVIVAFNQFGPN 32 Description: Perfect Score: Sequence:

188963 segs, 23686106 residues PAM 150 Gap 11 Searched:

Scoring table:

Minimum Match 0% Elsting first 45 summaries Post-processing:

a-geneseq35 l:genesegp Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.257

Variance 92,032

Mean 23.654;

Statistics

## SUMMARIES

| Result<br>No. | Score      | Query | Length                                | æ.<br>C | 10      | Description              | Pred. Nc. |
|---------------|------------|-------|---------------------------------------|---------|---------|--------------------------|-----------|
|               | <b>. .</b> | 50.2  | · · · · · · · · · · · · · · · · · · · | :       | R67.486 | M. Tebrae Oroms Investor | 8.776-03  |
| 7             | 103        | 45.4  | 7.02                                  |         | R22364  | S structural pr          | 0         |
| ~)            | es<br>es   | 43.2  | 5.1                                   | -       | 3       | ese cedar pol,           | 576       |
| 7             | 19<br>19   | 43.2  | V)                                    | -       | W57755  | Residues 211-225 of Cr   | 5.5       |
| u 1           | 9.9        |       | 1.7                                   | -       | 8       | Sudi allergen protein    | .57e      |
| Ø             | 9.8        |       | 20                                    | -       | $\sim$  | Ξ                        | .53       |
| 7             | es<br>es   | 43.2  | 20                                    | -       | ~       | I Japanes                | .57e      |
| æ             | 86         |       | 20                                    |         | S       | I pollen allerg          | .57e      |
| σ             | 86         |       | 26                                    | ٠,      | S       | I pollen                 | . 57      |
| 10            | 9.6        | 43.2  | 26                                    |         | 2       | I poilen                 | 2.57e     |
| 11            | 85         |       | 26                                    | -       | 2       | I pollen a               | 2.57      |
| 12            | 86<br>6    |       | 28                                    | r- 1    | S       | I pollen                 |           |
| 13            | 86         | 43.2  | 28                                    | . 1     | R45589  | I pollen a               | 2.57      |
| 14            | 9.5        |       | 28                                    | ٠ ،     | R45593  | pollen a                 | 2.57      |
| 15            | 86         | 43.2  | 30                                    | . 4     | 845588  | I pollen                 | 2.57e     |
| 16            | 9.8        |       | 30                                    |         | 468     | 1 epitope p              | .57e      |
| 17            | 9.8        | 43.2  | 30                                    | ٠,      | 55      | I pollen                 | 2.57e-01  |
| 18            | 86         |       | 36                                    | -       | 155     | I pollen                 | 5         |
| 19            | 9.8        |       | 353                                   |         | 53      | anese cedar              | .57e      |
| 20            | <b>8</b> 5 |       | 353                                   | -       | 10      | Cedar pollen allergen    |           |
| 21            | 86         |       | 354                                   | -       | W42121  | res                      | 57        |
| 22            | 86         | 43.2  | 354                                   | _       | m       | aris cot                 | 5         |
| 23            | ос<br>Э    |       | 367                                   | -       | R45577  |                          | 2.578-01  |

| 2.57e-01               | 2.57e-01 | 2.57e-01               | 2.57e-01              | 2.57e-01               | 4 776-01              | 4 77e-61              | 4 776-61 | 5.850-01       | 8.836-01              | 1 336-00 | 00+>86·7              | 2.986-00    | 646-00    | 4 456-00 | 6 63e-00   | 6.530-00 | 6.63e+00 | 6.53e-00 | 1.20e+01 | 1.20e-01               | 3.170.01              |
|------------------------|----------|------------------------|-----------------------|------------------------|-----------------------|-----------------------|----------|----------------|-----------------------|----------|-----------------------|-------------|-----------|----------|------------|----------|----------|----------|----------|------------------------|-----------------------|
| Cry j I pollen allerae | Ory 1 t. | Cry j I Japanese Cedar | Japanese cedar pollen | Chamaecyparis obtusa t | Multi-epitope peptide | Multi-epitope peptide |          |                | Sug: allergen profein |          | Sug: allergen protes: | allerger    | i I Japan | . al.    | the used t |          |          | allergen | :        | S. cerevisiae Picl pro | Buman thymus receptor |
| R45541                 | R31937   | R82490                 | R60165                | W64:45                 | W27369                | W27370                | W2-:71   | R4 378         | W8 358                | ¥6 796   |                       | W80351      | R92178    | W80352   | ¥01795     | W80356   | W80357   | W80353   | RC5700   | R53732                 | W70526                |
| ٦                      | . 4      | -1                     | ٠.                    | ٠,                     |                       | 4                     |          |                |                       | ٠,       |                       | r: <b>4</b> | ٠,        | ٠,       | ٠.         | . 1      | ٠,       | ٠,       |          | , ,                    | ٠,                    |
| 374                    | 374      | 374                    | 374                   | 375                    | 9<br>9<br>9           | 135                   | 134      | 370            | 81                    |          | 47                    | ٠ <u>٠</u>  | 22        | 1.7      | 11         | 47       | 47       | 47       | 56       | 869                    | 1021                  |
| ~                      | a        | ~                      | ~                     | 7                      | σ'n                   | ď                     | S        | •              | S                     | S        | ď                     | dr.         | ٦,        | Ç        | ~4         | _        | ٦.       | _        | ထ        | σn                     | Ç)                    |
| 43                     | 43.      | 43.                    | 43                    | 43.                    | 4.                    | 41.                   | 41.      | . <del>4</del> | <b>₽</b>              | 39.      | 37.                   | 37.         | 37.       | 37.      | 36.        | 36.      | 36.      | 36.      | 34.      | 34.                    | 32.                   |
| 85                     | 86       | 85                     | 85                    | 86                     | 9.5                   | 95                    | 95       | <b>3</b> 6     | 7                     | Ö        | y)                    | ω           | S         | ٠,       | 7          | 7        | 21       | 2        | Q,       | עו                     | 7.4                   |
| 24                     | 25       | 26                     | 27                    | 28                     | 29                    | 3.0                   | 31       | 32             | e<br>8                | 34       | 35                    | 36          | 37        | رب<br>30 | 39         | 4 0      | . *      | 42       | 43       | 4                      | 45                    |

## AL GNMENTS

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0
EESULI 1 Record of the protein; 9. AA. British Standard; Protein; 9. AA. British Standard; Protein; 9. AA. British Standard; Protein; 12-JUN-1995 (first entry)

E. M. Leprae GroEs-like protein.

M. GroEs-limunogen; Vaccine; di gnostic; heat shock protein; HSP; Mycobacterium leprae.

M. Wooldoor, Helicobacter; fells.

M. Wooldoor, British Br
 Gaps
 Disclosure: Fig. 78(1-11): 16kpp: English.
The sequence of the Heliocharter pylori heat shock protein B (given in 1867373) was compared to that of other GroES-like proteins from Legionella pre-mophis (R67387). Escherichia coli (R67389). Clostidium perfittingens (M5789). Mycobacterium legiane of homology were identified.
Sequence 93 AA:
 .;
0
 Length 93;
 0: Indels
 Ouery Match 50.2%; Schre 114; DB 1: 3
Best Local Similarity 100.0%; Pred. No. 8.77e-63;
Matches 17; Conservative 0; Mismatches 0;
 .r. 2
R22364 standard; Protein; 102 AA.
R22364;
 29-JUL-1992 (first entry)
GroES structural protein.
Heat shock protein; groEs gene.
Strepromyces albus.
 77 EEYLILSARDVLAVVSK 93
 1 EEYLIJSARDVLAVVSK 17
 19-MAR-1992
 RESULT
 RESULT
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 ö
 Japanese cedar pollen aliergen Cry) I derived T-cell epitope peptide.
Japanese cedar: pollen aliergen; Cryj I: T-cell epitope: peptides:
prevention: treatment: cryptomeria pollenosis.
 New cryptomeria pollen altergen Treell epitope peptide tused for prevention, treatment and investigation of Japaness cedat pollencsis claim is page 2: 8pp: Japanesse.

775388 is the Japaness ecdar pollen allergen Cryj I, from which the recell opitope peptides R89289-R89295 were terived. The peptides can be used for the prevention and treatmen of cryptomeria pollencis, and also for the investigation of pollenosis.
 Gaps
 Dairiki K. Kino K. Kume A. Sone T. WPI: 98-2975;7/26. WPI: 98-2976;7/26. Septidos derived from Japanese cedar pollen antigens are inaumoriherape-tic agents - useful for allergy treatment and typing HLA class II molecules in allergy suiterers.
 Recombinant DNA conta. hear inducible promoter and heterologous gene also vectors, transformed cells and new heat shock proteins of Streptococcus albus. Disclosure: Fia 5, 50pp. French. The sequence: Fia 5, 50pp. French. structural gene a trait of the GroES protein which is encoded by the structural gene arofes. Sec also 022477-022486.
 Fesdouss 211-25 of Cry j l.
Resdouss 211-255 of Cry j l.
Gry j l. Bancese cedar polien antigen: allergy: immunotherapy:
HLA Class II molecule.
Cryptomeria japonica.
 0
 Length 102;
 Score 103: DB 1: Length 102
Pred. No. 9.04e-02;
 1. taskely
 Length 15:
 Score 98. (3.1) La
Prod. No. 2.57e-01:
1. Mismannes 1.
 A.
 20-001-1993; 262626.
20-001-1993; 3P-262626.
(MEIP.) MEIJI MILK PROD CO LTD.
WPI; 95-203834/27.
 12-NOV-1997; J04129.
13-NOV-1996; JP-302053.
(MEIP.) MELJI MILK PROD CC LTD.
 .r
R89293 standard: peptide: 15
R89293:
 Gwery Match
best Local Similarity 86.7%:
Matches 13: Proservative
 Guery Match 45.4%;
Best Local Similarity 76.5%;
Matches 13; Conservative
 (tirst entry)
 86 ESYLVLSARDVLAIIEK 102
03-SEP-1991; F0C701.
10-SEP-1990; FR-C11186.
(INSP.) INST PASTEUR.
Macodier P. Guglielmi G:
WPI: 92-114-858/14.
NSDB: C22483.
 1 EEYLILSARCVLAVSK 17
 1 KSMKVIVAFNORGPN 15
 : TITT, TITT;
18 RRMKVIVAFNOFGPN 32
 Cryptomeria japonica.
J07118295-A.
 12-MAR-1996
 22-MAY-1998
 09-MAY-1995
 UND PROKENTAL CALL
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Claim 12; Page 28; 50pp; Japanese.

This sequence represents residues 211.225 of the Cry j l protein, and is a peptide of the invention. The peptides are derived from Japanese cedar pollen antigens, and are used as immunotherapeutic agents in the treatment of allergy. The peptides can be used for identification and typing of the particular HLA class II mollecules in an allergy sufferer, and also for peptide immunotherapy of an allergy. Using these peptides the immunotherapy of an allergy using these peptides of the individual patient, allowing more effective treatment of an allergy including those paties is for whom treatment with a convectional immunotherapeutic agent is ineliective.
 W80339-58 represent epitopes for cells, derived from the suminalience proteins Cryll (M8038-44, M80350-53 and W80356-58) and Cryl2 (W80345-49) and M80354-55). The peptides are useful for the treatment of sugirpollinosis, an altergin reaction of the body to pollen.
 ..
o
 ö
 Threal epitope peptide 24 from Japanese cypress pollen antipen Chaol. Japanese cypress pollen, antigen; Threal epitope: Chaol; Chaol; diagnosis; aliengy; spring tree pollen disease; pollinosis.
 9.7
 Threell epitope peptide portion of Japanese cypress polien antigens Chaol and Chaol - used for diagnosis and treatment of spring tree
 11-JAN-1999 (first entry)
Sugiallergen protein Cry52 derived epitope for 7 cells.
T cell epitope, sugiallergen proteins Cry51: Gry52: treatirent:
sugi-politinosis, allergic reaction: pollen.
 ં
 Score 98: UB 1; Length 15:
Pred. No. 2.57e-01:
1; Mismatches 1; Indels
 used for the treatment
 (HAYB) HAYASHIBARA SEIBUTSU KACAKU.
(SANY) SANKYO CO LTD.
WPI; 98-577037/49.
A linked I cell epitope peptide - us
 7; Page 18: 21pp: Japanese.
 17 AA
 W42144 standard: peptide: 20 AA W42144:
 Loral Similarity 85 78 es 130 Communication
 Match 43.2%;
Local Similarity 86.7%;
les 13: Conservative
 င္ပ
 16-JUN-1998 (first entry)
 .T
W80349 standard: peptide:
 18-DEC-1997.
12-JUN-1997; JO2031.
14-JUN-1996; JP-153527.
(MELP) MEJJI JILK PROD CC
Dairiki K. Kino K:
WPI: 98-052242/C5.
 2 KSMKVIVAFNOFGPN 15
 1 KSMKVTVAFNQFGPN 15
 22-DEC-1997; 353448.
24-DEC-1996; JP-343441.
 diagnosis; allergy; ;
Chamaeyparis obtusa.
 17 AA:
 sugi-pollincsis
 pollen disease
 W09747648-A1.
 Synthetic.
J10259198-A.
 29-SEP-1998
 Query Match
 Sequence
 Seguence
 Query Match
 W80349;
 Claim
 Matches
 Matches
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01-SEP-1992; US-938990.
(IMMU-) IMMULOGIC PHARM CORP.
 15-JAN-1993; UOC139.
10-JUL-1992; WO-1056
01-SEP-1992; US-9389
 26 AA
 Seguence
 allergy
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 Shaked 2:
Shaked 2:
Shaked 2:
Shaked 2:
WPI: 95-366391/47.

Modified Cryptomeria japonica (7ry j) I poptide(s) - useful for
treating allergy to japanese cedar polien allergen or
immuncologically cross reactive allergens
immuncologically cross reactive allergens
immuncologically cross reactive allergens
is bischourer Figure 2: 60pp; English.
Showed peptides of cry j I have been modified as part of a
preformulation scheme to develop an optimised drug product for
therapeulic irreatment of humans suffering from allergy to Japanese
cedar pollen allergen or an allergen witch is immuncologically cross
creactive with Japanese cedar pollen allergen; Such codified peptides
possess certain characteristics which render them inticularly
modified and inmodified, are diven in 182491-18255. This peptide
fragment corresponds to amino acids 21:-250 of the allergen mature
 ..
0
Claim 1: Page 27-28: 71pp: Japanese. The pricope peptide from Japanese cypress police antigen Cheoi. The present invention describes peptides which correspond to the Trcell epitope sites on Japanese cypress police antigens Cheoi and Cheoi. The present invention of as a reagent for the diagnosis of allergy to Japanese cypress pollen, and as an antigen in the Treatment and prevention of spring tree pollen disease in which the pollinosis invelves reactivity to Japanese cypress pollen.
 Saps
 R82512 standard; Protein: 20 AA.
R82512.
15-April996 (first entry)
Cry j I Japanese Cedar pollen allergen; modified; drug production: allergy; Crytpomeria japonica.
Crytpomeria japonica.
W09527786-A1.
 Gaps
 0
 ..
 R45563;
13-JUL-1994 (first entry)
Cry J Doilen allergen poptide CJI-22.
Japanese cedar: detection; allergy: treatment; diadnosis;
I cell epitope; sensitivity.
 Score 98: UR 1: Length 20:
Pred. No. 2.570-61:
1: Mismatches 1: Indels
 1: Indels
 Score 98: OB 1: Length 20: Pred. No. 2.57e-01; 1: Mismatches 1: Indels
 Evans S, Franzen HM, Kuo M, Powers SP;
 R45563 standard; Protein: 20 AA
 (IMMU-) IMMULOGIC PHARM CORP.
 47.28:
 query Match
Hest Local Similarity 96.7%;
Matches 13; Conservative
 Conservative
 1 KSMKVIVAFNOFGPN 15
 1 KSMKVTVAFNQFGPN 15
 18 RRMKVTVAFNOFGPN 32
 06-APR-1995; UC4249.
08-APR-1994; US-226248.
06-DEC-1994; US-350225.
 20-JAN-1994,
15-JAN-1993, UCC139,
10-JUL-1992, WO-305561
 Cryptomeria japonica
 Local Similarity
 20 AA:
 WO9401560-A.
 19-0CT-1995
 protein.
Sequence
 Query Match
 Matches
 RESULT
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 8998888888
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ä
 Ö
 claim 1: Fig 13: 137pp: Enclish.
The sequence is that of an isolated peptide of the Japanese redar.
The sequence is that of an isolated peptide of the peptide. CJI-22 can be used for the treatment and diagnosis of altergies associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allerges bequence. 20 As.
 diadrose
 The sequence is that of an isolated poptide of the Japanese celar pollen allergen Cry j I. The p-ptide, CJI-43.10, can be used for the treatment and diagnosis of allerges associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergess.
 Antigens derived from Japanese rodar poller allergen Cry) 1 contain at least two T cell epitope(s), used to treat or diagnose
 .
ن
 13-JUL-1994 (first entry)
Cry 1 pollen alkergen peptide CJI-43.10.
Japanese cedar; detection; allergy; treatment, diagnosis:
T cell epitope; sensitivity.
Cryptomeria japonica.
 Cry j I pollen allergen peptide CJI-43.12.

Cry j I pollen allergen peptide CJI-43.12.

Japanese cedar; detection; allergy; treatment; diagnosis; I cell epitope; sensitivity.

Cryptomeria japonica.

W09401560-A.
 Antigens d rived from Japanese cedar polien allergen Cry
 ò
 1: Indeis
 i: Indeis
 Score 98; 58.1; Leigth 25;
Pred No. 2.57e+61;
 Gengih 26
 contain at least two T cell spitope(s), used to treat allergy
Claim 76; Fig 18; 137pp; Engl. A.
 (IMMU-) IMMULOGIC PHARM CORF.
Bond JF. Garman RD, Griffith IJ. Kuc M. Pollock J.
WPI; 94-03 066/04.
Bond JF, Garman RD, Griffith IJ, Kuo M, Pollock J:
WPI: 94-035056/04.
 Score 98: DE 1: D
Pred. No 2:57e-01:
1: Mismatches 1
 1; Mismatches
 R45594 standard: Protein: 26 AA.
R45594:
 R45592 standard; Protein: 26 AA
R45592;
 Query Match
Best Local Similarity 86,7%:
Matches 13; Conservative
 Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
 1 KSMKVTVAFNOFGPN 15
 18 RRMKVIVAFNOFGPN 32
 1 KSMKVTVAFNOFGPN 15
 20-JAN-1994,
15-JAN-1993; 000139,
10-JUL-1992; WO-U05661,
01-SEP-1992; US-938990.
 WO-105661.
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Sedmence
 Query Match
 a)
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 Gaps
 Gars
 Contain and the control of the Capanese cedar allersy claim 76: Fig 19: 137pp; English.

The sequence is that of an isolated peptide of the Capanese cedar polich aliergen fry j L. The peptide, COI-43.12, can be used for polich attentions of allergies associated with Japanese cedar polich. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens.

Socience 26 AA:
 alleryy Claim 76: Fig 18: 137pp: English.
Claim 76: Fig 18: 137pp: English.
Claim 76: State of an isolated peptide of the Japanese cedar pollon allergin Gry 7: The peptide, CJI-43:9, can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollon. It has enhanced therapeutic properties but reduced side effects, compared to naturally occurring allergies.
 Antiques derived from Japanese cedar pollen allerges {\rm Cry}\ j . contain at least two T cell epitope(s), used to treat or diagnose
 Antigons derived from Japanese codar pollon allergen Cry) : contain at least two T rell epitope(s), ised to irest or diagnose
 .
O
 R45590 standard; Protein; 28 AA.
R45590.
R3-1094 (first entry)
Cry 1 polien allergen peptide CCI-43.8.
Japanese cedar; detection; allergy; treatment; diagnosis:
T cell epitope; sensitivity.
 [3-JJL-1994] (instentry)
Cry j I police allereen peptide CJI-43.9.
Japanese cedari detection: allergy: treatment: diadosis;
 Score 98: DB 1: Length 26: Pred. No. 2.57e-01: 1: Mismatches 1: Indels
 Score 98 LB 1/ Legith 26/
Pred. No. 2.57e-61:
1: Mismatches 1: Intels
 15-JAN-1993: UGU139.
10-JUL-1992: WD-065661.
21-SEP-1992: US-918990.
MMJ-) IMMMIGGIC PHARM CORP.
Bond JP, Garman RD, Grittith IJ, Kuo M. Pollock JP.
WPI: 94-033064/04.
(IMMU-) IMMULGGIC PHARM CORP.
Bond JF, Garman RD, Griffith IJ, Kuo M, Pollock J;
WPI: 94-035065/04.
 R45591 standard: Protein: 26 AA
R45591:
 20-JAN-1994.
15-JAN-1993: UC0139.
10-JUL-1992: WJ-J05661.
GL-SEP-1992: US-938990.
(IMMC-) IMMULGIC PHARM COMP.
 T cell epitope: sensitivity.
Cryptomeria japonica.
 chery Match
hest Local Similarity 86.7%;
Matches 13: Conservative
 43.28.
Best Local Similarity 86.78.
Matches 33, Conservative
 1 KSMKVTVAFNQFGPN 15
 1 KSMKVIVAFNOFGPN 15
 18 REMKVIVAFNOFOFN 32
 Cryptomeria japonica.
W09401560-A.
 Segmence
 a)
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5
 districtions of the sequence is that of an isolated peptide of the Japanese cedar. The sequence is that of an isolated peptide of the Japanese cedar. The sequence Cry J. The populae, CJI-45 6, can be used for pollen allerane Cry J. The populae, CJI-45 6, can be used for the treatment and diagnosis of alleranes associated with Japanese cedar poller. It has enhanced therapeutic properties but reduced cade effects compared to naturally occurring alleranes. Sequence 28 AA:
 (IMMC.) IMMINGGEO PROME COMP.

WORD 54 COSTONE NO. STATISTED ID. KTO M. FOLLOCK J.:

WARP 94 COSTONE OF CONTRACT OF THE CONTRACT OF J.:

Antiqens derived from Japanese redar pollon alletden Cry J.:

contain at least two J cell. Itope(8), used to treat or diagnose.
 allergy Claim 75: Fig 18: 137pp; End. ...
The sequence is that of an isolated perfilds of the Japanese reduring an allergen Cry j I. The pertide, CJI-43.7, can be used for the treatment and diagnosis of allergues associated with Japanese cedar pollen. It has enhanced therapeutic properties but redured side effects compared to naturally occurring allergens.
Bond JF, Garman RD, Griffith IJ, Kuc M, Pollock J: WPD1: 94-035066/04. Antigens derived from Japanese cedar pollen allergen Cry J : Contain at least two T cell opitope(s), used to treat or diameses
 allergy: treatment: diagnosis.
 Shore 96. [FR]: Lebalb 28:
Pred; No. 2 57e 51.
11. Mishalphes [1: Indexs
 13-JUL-1994 (first entry)
Cry J i pollen allergen peptide DJ-43.11.
Japanese cedar; detection; alle: y: treatment; diagnosis;
T cell epitope; sensitivity.
 Length 28:
 20-JAN-1994.
15-ZNN-1993: U00139.
15-ZNN-1993: U00105661.
01-SEP-1992: US-938990.
(IMMU-) IMMULOGIC PHARM CORP.
Bond JF, Garman RD, Griffith IJ, Kuo M, Pollock J;
 Score 38; DB 1; Lo
Pred. No. 2:57e-91;
1; Mishatches 1;
 Cry 1 pollen allergen peptide CJI-41,7,
Japanese cedar, detection: allergy: treat
I ceil epitope; sensitivity.
 A A
 AA.
 T 13
R45589 standard; Protein; 28
R45589;
 R45593 standard; Protein: 28
R45593;
 Opery Match
Best Local Socilarity 96.7%:
Matches 13: Conservative
 Query Match
Best Local Similarity 86.7%:
Matches 13: Conservative
 (3-JUL-1994 (first entry)
 1 KSMKVTVAFNOFGPN 15
 1 KSMKVIVAFNQFGPN 15
 REMENTATION 32
 20-JAN-1994.
15-JAN-1993; U00135.
10-JUL-1992; WO-U05661.
01-SEP-1992; US-938990
 Cryptomeria japonica.
WC9401560-A.
 Cryptomeria japonica.
WC9401560-A.
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 Subs
 Gaps
 allergy Claim 76: Fig 18: 137pp; English. Claim 76: Fig 18: 137pp; English. Claim 76: Fig 18: that of an isolated peptide of the Japanese cedar The sequence of Y; I The peptide, Cur-43.6, can be used for the treatment and diagnosis of allergies associated with Japanese cedar poller. It has enhanced therapeutic properties but reduced side offects contared to naturally occurring allergens. Sequence 35 AA:
WPI: 94-035066/34.

Antiquess derived from Japanese cedar pollen allergen Cry 1 : contain at least two T cell epitope(s), used to treat or diagnose allery
allery
claim 76: Fig 18: 137pp; English.
The sequence is that of an isolated peptide of the Japanese cedar pollen allergen Cry 1. The peptide, CJI-43.11, can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen. It, has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens.
 15-JAN-1994.

15-JAN-1993: UO0139.

10-JU-1992: WS-908661.

01-SEP-1992: US-938890.

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(IMMU-) IMMUDDGIC PHARM CORP.

(IMMU-) IMMUDDGIC PHARM CORP.

(IMMU-) IMMUDDGIC PHARM CORP.

(Antiques derived from Japanese cedar pollen allergen Cry 1 I -
 0
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 R45598 standard; Protein; 36 AA.
R45593 standard; Protein; 36 AA.
R45587 [13-00]
R45587 [13-00]
Cry 2 [100] alleraen peptide CJI-43.5.
Cry 3 [100] alleraen peptide CJI-43.5.
Total epitope; sensitivity.
 Score 98: DB 1: Length 28: Pred. No. 2.57e-01: In Mismatches 1: Indels
 1; Indels
 Score 98: 08:1: Length 30:
Pred. No. 2.57e-01;
1: Mismutches 1: Indels
 Query Match
Best Local Similarity 95.7%:
Matches 13; Conservative
 Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
 1 KSMKVTVAFNQFGPN 15
 1 KSMKVIVAFNOFGPN 15
 : [1] : [1]|-:
18 RRMKVIVAFNOFGPN 32
 18 RRMKVTVAFNOFGPN 32
 Cryptomeria japonica
WO9401560-A.
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Search completed: Mon Jun 19 16:12:39 2000 Job time : 11 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search. using Smith-Waterman algorithm

Tue Jun 20 13:36:17 2000: MasPar time 2.72 Seconds 169:949 Million cell updates/sec kun 00:

>US-09-142-524A-10 (1-32) from GSO9142524A.pep 227 Tabular output not generated.

1 EEYLILSARDVLAVVSKRRMKVTVAFNOFGPN 32 fitte: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

145341 segs, 14437480 residues Searched:

Fost-processing:

a-issued 1:5A\_CCMB 2:5B\_CCMB 3:6\_CGMB 4:PC1\_CCMB 5:backfiles1 Minimum Match 0% Listing first 45 summaries

Catabase:

scale 0.252 Mean 22.159: Variance 87.947; Statistics:

Pred. No. is the number of results predic 'd by chance to have a score greater than or equal to the score——the result being printed, and is derived by analysis of the total since distribution.

SUMMARIES

|   | Pre 1, 80,     |                                       | 2.4        | o.   | 8.8        | .57e-     |       | δ.    | δ.         |                        | 'n  |            |     | 6.30e |     |     |            |     | cati 5.   | sati 6.<br>Itio 6. | 6.30<br>6.30<br>7.60<br>7.60        | 14004<br>2004<br>2006<br>3006                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|---|----------------|---------------------------------------|------------|------|------------|-----------|-------|-------|------------|------------------------|-----|------------|-----|-------|-----|-----|------------|-----|-----------|--------------------|-------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|   | Description    | Sequence 36, Applica:                 | : 1        | ( 4  | (+)        | 4, Applic | 2,    | 23,   | 23,        | Sequence 79, Applicati | 27, | 15,        | 16, |       | 'n  | 4   | 29         |     | 10. Appli | 10. Appli          | 10. Appli<br>7. Applic<br>2. Applic | 10. Application Ap | 7, Application App | 10, Application Ap |
|   | 1:             | • • • • • • • • • • • • • • • • • • • | US-08-347- | -    | JS-08-467- | 9-80-     | 8-80- | 1-60- | 08-08-685- | -07                    | 80  | US-08-838- | 80  | 85    | 80- | 80- | US-08-570- |     | -08       | 80.                | -08-33<br>-08-47<br>-08-61          | 80.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 80.000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 800000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | Lenath Ds      | :                                     |            | 558  |            | 5         |       |       |            |                        |     |            |     |       |     |     | 687        |     | 704       | 704                | 704<br>287<br>876                   | 704<br>287<br>876<br>94                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 704<br>287<br>875<br>94<br>97                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3284<br>1828<br>1878<br>1876<br>946<br>1878<br>1888<br>1888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| æ | Query<br>Match |                                       | 31.7       | 31.3 |            |           | 30.8  |       |            |                        |     |            |     |       |     |     |            |     |           |                    |                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|   | Score          | 114                                   | 7.2        | 7.1  | 70         | 70        | 3.C   | 28    | 99         | <b>6</b> 8             | 68  | 68         | 68  | 67    | 63  | 67  | 67         | 4   |           | 9                  | 653                                 | ው<br>ው<br>ው<br>ው<br>ው                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ህ ነነ ነነ<br>ው ው ው ው                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Ე Ი Ი Ი Დ Ქ :<br>Დ Დ Დ Დ Დ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|   | Result<br>No.  |                                       | 7          | ٣    | 4          | 'n        | Φ     | 7     | œυ         | S                      | 10  | 11         | 12  | 13    | 7.4 | 5.  | 16         | 1.1 |           | ao<br>r-t          | 19                                  | 2 1 1 8<br>2 2 3 5 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 188<br>200<br>210                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 198<br>200<br>22                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

| ٠.          | ٠.          |            | 4           | . 10e-     | 1.106+02    | 106+   | 106-   | .1Se-       | . 15e-      | 1.33e+02  | 336-       | 1,386-02    | 1.330-02   |             | 1.33e-02   | 336-        | 336.           | 1.336-02   | 33e-02      | ٠           | 1.336-02    |
|-------------|-------------|------------|-------------|------------|-------------|--------|--------|-------------|-------------|-----------|------------|-------------|------------|-------------|------------|-------------|----------------|------------|-------------|-------------|-------------|
| Ö           | Applicatio  | Applicatio | ė           | Applicatio | Applicates  | 10     | Ö      | Applica:    | Appli       | . Applica | Applicatio | atı         | Applicatio | Applicatio  | Applicatio | Applicatio  | Applicatio     | Applicatio | Applicatio  |             | •           |
| Sequence 2, | Seguence 6, |            | Seguence 9, |            | Sednerce 9, |        |        | Sequence 5, | Sequence 12 | 3         |            | Segmence 2, |            | Segmence 1. |            | Segmence 9, | Sequence 5.    |            | Sedmence 4. | Sequence 2, | Seguence 14 |
| -08-82      | 08 - 83     | 99-10      | 1-0895      | 08-02      | 99-10-      | -08-36 | -08-58 | 00-60-      | -99         | -:8-21    | -0.895     | 38-35       | 38-16      | US-08-219-  | 38-21      | 38-21       | 08-23          | 26-60      | ė           | 09-27       | 77-80       |
| ~           | 7           | - 1        | 7           | 7          | ~1          | 7      | ~      | 7           | ~           |           | 4          | 7           | _          | -           | -          | -           | 1              | -          | _           | _           | -           |
| 1052        | 291         | 359        | 501         | 501        | 501         | 501    | 501    | 616         | 686         | 24 C      | 797        | 797         | 973        | 1012        | 1012       | 1012        | 1012           | 1012       | 1012        | 1012        | 1012        |
| œ.          | 'n          | m          | m.          | œ.         | m.          | m      | m.     | m.          | œ.          | ۲.        | ۲.         | ۲.          | ۲.         | 27.8        | ۲۰         | ٠.          | ۲.             | ۲.         | 7           | ۲.          | ۲.          |
| 65          | 9           | 64         | <b>64</b>   | 64         | 64          | 64     | 64     | 24          | 64          | 63        | 63         | 63          | 63         | 63          | 63         | 63          | 63             | 63         | 63          | 63          | 63          |
| 24          | 25          | 56         | 27          | 28         | 58          | 30     | 3:     | 32          | 33          | 34        | 35         | 36          | 37         | 38          | 33         | 0.4         | , <del>,</del> | 42         | 43          | 4 4         | 4           |

# 93 AA. P.R.1 STANDARD:

ALIGNMENTS

Sequence 36, Application US/08467822

Sequence 35, Application US/09467822 Patent No. 5843460 GENERAL INFORMATION:

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateutin Nelease #1.0, Version #1.36
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-00N-1995
CLASSIFICATION: 435 COUNTRY: USA 21P: 20005-3315 

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US (8/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION

```
TYPE: AMINO ACID
STRANDEDBESS: Single
TOPCLOGY: licear
MOLECULE TYPE: protein
HYPCTHETICAL: NO
 [SIEPHUNE: 212-799-48-
|SIEFAX: 212-75] --943
|INF-PMATION FUR SEG II- N-
 SEQUENCE CHARACTERISTICS LENGTH: 558
 TISSUE TYPE:
CELL TYPE: fibroblast
CELL LINE: NIH-313
 COUNTRY: USA
21P: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
 STRAIN:
INDEVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
 NEW YORK
: USA
 ORIGINAL SOURCE:
ORGANISM: mouse
 NAME/KEY: RelB
 NEW YORK
 LT 3
PCT-US93-03027-2
 ORGANELLE:
FEATURE:
 LOCATION:
 XXXXX
 RESULT
ID PC
 Sequence 2, Application US/08347594A
Patent No. 584936
GENERAL INFORMATION
APPLICANT GARTINGE TO THE SECTION OF HUMAN VON
TILLE OF INVENTION: CLONING AND PRODUCTION OF HUMAN VON
TILLE OF INVENTION: MILLEBRAND FACTOR GPID SINDING DOMAIN POLYPEPTIDES AND
TILLE OF INVENTION: MILLEBRAND FACTOR GPID SINDING DOMAIN POLYPEPTIDES AND
TILLE OF INVENTION: MILLEBRAND FACTOR GPID SINDING DOMAIN POLYPEPTIDES AND
TILLE OF INVENTION: MILLEBRAND FACTOR GPID SINDING DOMAIN POLYPEPTIDES AND
TILLE OF INVENTION: MILLEBRAND FACTOR GPID SINDING DOMAIN POLYPEPTIDES
ACCURRED TO THE SECTION OF THE AMERICANS
CITY: New York
GOUNTRY: USA
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 Gaps
 Ġ
 Cuery Match 50.2%; Score 114: DB 2; Length 93; Hest Local Similarity 100.3%; Pred: No. 4.56e-33; Matches 17: Conservative 0: Mismatches 0; Indels
 NAME: Meyers, Kenneth J. REGISTERILW NUMBER: 25,146
RETERNIZACOCKET NUMBER: 25,146
RETERNIZACOCKET NUMBER: 03495.0137-2000
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acids
 MOLECULE TYPE: protein
SECUENCE 2050 AA: 225692 MW; 21477294 CN:
 PRT;
 TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 93 AA: LOOOZ MW: 4803C CN:
 Sequence 2, Application US/08347594A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
LENGTH: 2050 amino acids
 STANDARD;
 SS: Single
linear
 77 EEYLILSARUVLAVVSK 93
 1 EEYLILSAROVLAVSK 17
 namino acid
Lusk: linear
 linear
 STRANDEDNESS:
 RESULT 2
10 US-08-347-594A-2
 SEQUENCE
 xxxxxx
 855488514888883
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Sequence 1, Application PC/TUS93 #827

SERREAL INFORMATION:
APPLICANT: LEDNARD, WARREN: TOLEDAND,
APPLICANT: MICHEL
TITLE OF INVENTION: CONTROL AND/OR
TITLE OF INVENTION: PREVENTION OF BINDING OF NF- H/PEL/10-MSAL
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
 0
Query Match 31.7%: Score 72: DB 2: Lengtl. 2050; Best Local Similarity 34.6%: Pred. No. 2.43e-01; Matches 9; Conservative 8: Mismatches 9; Indels
 MEDIUM TYPE: FLORPY DISK
COMPUTER: BW PC CORPATIBLE
COMPATING
SUFTAME: WORDENFECT 5.)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U.9/C.NUZ?
PLING DATE: 199304c;
PRIOR APPLICATION CATA:
APPLICATION NUMBER: PCT/U.9/C.NUZ?
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PS/2/8(2.187)
FILING DATE: OS-APR-1992
ATORNEY/AGNT INFORMATION:
NAME: DOSCHING ANTH
PEGISTRATION NUMBER: P-36,434
PEGISTRATION NUMBER: P-36,434
PEGISTRATION NUMBER: LOAD-401,171
PEGISTRATION NUMBER: LOAD-401,17
 ..
3.
 Sequence 2, Application PC/TUS9303727
 198 YILLLGKALSVVWDRHLSISVVLKU 223
 3 YLILSAROVLAVSKRRKKVIVAFNG 28
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Scips
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دے
 Sequence 4, Application US738519554
Patent No. 5821353
GENERAL INFORMATION:
APPLICANT CHREBET Gary L.
APPLICANT CHREBET Gary L.
APPLICANT CLEMAS, Joseph
APPLICANT FOOR FOREST
APPLICANT RAIN, John fel.
APPLICANT NORTH, John fel.
APPLICANT NORTH JOHN SYNTHASE SHADHIS
NUMBER OF SEQUENCES:
ADDRESSED JOSEPH A. COPPOLA - MERCK & CO., INC.
STREET 120 CORP.
APPLICANT NORTH AVENUE - P.O. BOX 2000
 Score 70: DB 2: Length 94: Pred. No. 3.57e+Cl: 3: Mismatches 3: Indels
 OUESATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 01-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 1895 AA
 03495.0137-02000
 US 08/432,697
 PRI;
 MOLECULE TYPE: protein
ENCE 94 AA: 10343 MW: 45288 CN:
 APPLICATION NUMBER: US 08/432, FILING DATE: 02-MAY-1995 CLASSIFICATION: 435 ATTOREY AGENI INFORMATION NAME: Meyers. Kenneth J. REGISTATION NUMBER: 25.146 REFERENCE/DOCKET NUMBER: 03495 TELECOMMUNICATION INFORMATION: TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
 Sequence 4. Application US/08619554
 COMPUTER: IBM Compatibl
 LENGTH: 94 amino acids
 STANDARD;
 Diskette
 Match 30.8%; Local Similarity 57.1%; es 8; Conservative
 single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 PRIOR APPLICATION DATA:
 TYPE: amino acid
STR/NDEDNESS: sir
 TOPULOGY: linear
 80 EYMILRESDILAVI 93
 2 EYLILSARDVLAVV 15
 USA
 RAHWAY
 COUNTRY: US
ZIP: 07065
 S
 US-08-619-554-4
 SEQUENCE
 Query Match
 XXXXXX
 Matches
 RESULT
 ò
 GENERAL INFORMATION:

APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Schard L.
APPLICANT: Ferrero, Richard L.
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TILLE OF INVENTION: HELICOBACTER INTECTION, POLYPEPTIDES FOR USE IN THE
TILLE OF INVENTION: DOLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finney Henderson, Farabow, Garrett &
ADDRESSEE: Finney
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 contains region of high similarity with proteins of Rel tamily.
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 CUCKTRY. USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIJON TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN PC-DOS/MS-DOS
SOFFWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447.177
FILING DATE: 19-MAY:1995
CLASSIFICATION: 435
CLASSIFICATION: 435
 Juary Match 31.3%: Score 71; DB 4; Length 558; gest Local Similarity 42.3%: Pred. No. 2.95e+01; datches 11; Conservative 7; Mismatches 9; Indels
IDENTIFICATION METHOD: contains region
IDENTIFICATION METHOD: of high similarity with p
IDENTIFICATION METHOD: Rel lamily.
CTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Ryseck, R.-P.: Bull, P.:
AUTHORS: Takaminy M.: Bours, V.: Siebenlist,
AUTHORS: U.: Dobrzatski, P.: Bravo, R.
IIILE: RelB, a new Rel family
IIILE: Lanscription activator that can
IIILE: interact with p50·NF··B.
JOGERAL: Mol. Cell: Biol.
 94 AA
 558 AA; 60304 MW; 1645898 CN;
 . I.R.C.
 Sequence 38, Application US/08467822 Patent No. 5843460
 FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NC:
 Sequence 38, Application US/08467822
 400 LSSSDPHGIESKRKKKRPVFLDHFLP 425
 6 LSARDVLAVVSKRRKKVTVAFNQFGP 31
 STANDARD;
 CITY: Washington
STATE: D.C.
 ISSUE:
PAGES: 674-684
DATE: FEB-1992
DOCUMENT NUMBER:
 RESULT 4
ID US-08-467-822-38
 SECUENCE
 XXXXXX
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MOLECULE TYPE: protein SEQUENCE 2813 AA; 309523
 SEQUENCE
 xxxxxx
 RESULT
ID US
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 APPLICANT VENERAL PARTICK C
APPLICANT VIZDASIYAN GUTKAN, VIEWS
APPLICANT SCHALL WILLIAM D
APPLICANT SCHALL WILLIAM D
APPLICANT SCHALL WILLEBRAND
TITLE OF INVENTION DNA ENCODING CANINE VON WILLEBRAND
TITLE OF INVENTION FATTOR AND METHODS OF OSE
NUMBER OF SECTIONS: 11
CORRESPONDENCE ADDRESS: 11
CORRESPONDENCE ADDRESS: Dickey & PIFICE, PLLC.
 / Match 30.8%, Score 70, DB 2; Length 1895; Local Similarity 37.5%, Pred. No. 3.57e-01; es. 9; Conservative 6; Mismatches 9; Indels
 COMPUTER: Figging disk
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COFFRAING SYSTEM: PC-DCS/MS-DCS
SCHWARE: Patentin National System #1.25
CURRENT PEPLICATION DATA:
APPLICATION NUMBER: US/08/896,449A
FILING DATE: 18 JUL-1997
ATTORNEY ANTHE
 2813 AA
 ATTORREY/AGENT INFORMATION:
NAME: Smith Deann F.
REEPENCE/DOCKET NUMBER: 2115-001226
:LECCOMMUNICATION INFORMATION:
TELEFRAN: 248-641-1600
 MCLEGULE TYPE: protein
SEQUENCE 1895 AA: 216988 MW: 18982348 CN:
 NAME: COPPOLA, COSEPH A
REGISTRATION NUMBER: 38,413
REGISTRATION NUMBER: 19104P1
TELECOMMUNICATION INFORMATION:
TELEFONE: 732-594-6734
TELEFEAS: 732-594-4720
 P.3.1
 Sequence 2, Application US/08896449A Patent No. 6040143 GENERAL INFORMATION:
 Sequence 2, Application US/09896449A
 ADDRESSEE: Harness, Dickey & STREET: 5445 Corporate Drive city: 1109 True to Corporate Drive city 1109 True to Country: USA
 TELEFAX: 248-641-0270
TELEX: 287637
:NFURNATION FINE SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
EDNSTH: 2813 arrino acids
TYPE: arrino acids
 658 FULLSLADPIMILSTISMRCIGEY 681
 3 YIILSAREVLAVVSKREMKVTVAF 26
 INFORMATION FOR SEQ 10 NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 1895 amino acids
 ATTORNEY/AGENT INFORMATION:
 STANDARD:
 SS: unknown
unknown
 TYPE: dmino acid
STRANDEDNESS: unl
 linear
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SEQUENCE 2. APPLICA

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 GENERAL INFORMATION:

APPLICANT: TOTAS, NICHOLAS

APPLICANT: FILIT. ANGTHE ANGTHE ANGTHEN

TITLE OF INVENTION: TYROSINE PHINSPRATASES

NUMBER OF SEQUENCES: 36

CORRESPONDERED ANDRESS:

ADDRESSEE: HAMILTON, BE YY, SMITH & REYNOLDS, P.C.

STREET: TWO MILITA DE:

CITY: Lexington

STATE: MA
 Length 2813:
 Length 254;
 :pde:
 4; Indels
 COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: FASTSEQ for Windows Version 2.05 CORRENT APPLICATION DATA: US/09/144.425 FILING DATE:
 Query Match
Best Local Similarity 29.6%; Prod. No. 3.57e-01;
Matches 8; Conservative 11; Mismatches 9;
 254 AA
 Score 58; DB 2; D6
Pred. No. 5.21e+01;
4: Mismatches 4.
: 40158915 CN;
 TOPOLOGY: linear MCLECULE TYPE: peptide 254 AA: 29034 MW; 364832 CN;
 2
 BEERKUEZOOKEL NIMBES. (26) 4. IEEECOMMUNICATON INFORMATION TELEPONEN 781 861-624.
 Sequence 23, Application US/09144925 Patent No. 5951979
 087485.992
 960 QYVILLEGKALSVVWDHRLSISVILKR 986
 Sequence 23, Application US/09144925
 8
3
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685
FILING DATE: 0419 25, 1996
ATTORNEY/AGENT THENSHMATTINA
NAME: 03443430 FOLTONIA
 2 EYLILSARDVLAVVSKRRMKVIVAHKL
 SEQUENCE CHARACTERISTICS:
LENGIH: 254 amino acids
TYPE: amino acid
 STANDARD:
 COUNTRY: USA
21P: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
 INFORMATION FOR SEQ ID NO:
 TELEFAX: 781-861-9540
 sinale
 Query Match
Best Local Similarity 46.7%;
 7: Conservative
 230 IRKORMKMVQTFTQF 244
 : |::|||: :| |::
15 VSKRRMKVTVAFNQF 29
 CLASSIFICATION:
 STRANDEDNESS:
 US-09-144-925-23
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RESULT
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 Gaps
 <u>.</u>.
 Match 30.0%; Score 68; DB 2; Length 254; Local Similarity 46.7%; Pred. No. 5.21e+01; Conservative 4; Mismatches 4; Indels
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Iwo Militia Drive
 SIREEI: Two Militia Drive
CITY: Lexington
SIATE: MA
COURTRY. UGA
ZIP: 02173
COMPUTER RADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows Version: 2.0b
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,932
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION 3475
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 Segrence 23. Application US/08685992
Patent No. 591218
GENERAL INFORMATION:
GENERAL INFORMATION:
MPPLICANT FILE, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING FROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEGUENCES: 36
CORRESPONDENCE ADDRESS:
 269 AA
 254 AA
 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32.227
REFERENCE/OOCKET NUMBER: CSHL96-03
TELECOMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-5540
 PRT:
 PRT:
 TOPOLGGY: Linear
MOLECULE TYPE: peptide
SEQUENCE 254 AA; 29334 MM; 364832 CN.
 Sequence 79, Application US/07857224B
 Sequence 79, Application US/07857224B
 Sequence 23, Application US/08685992
 INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
 STANDARD;
 FILING DATE: ATTORNEY/AGENT INFORMATION:
 SIANDARD;
 SIRANDEDNESS: single
 230 IRKORMKMVQTETQF 244
 TYPE: amino acid
 15 VSKRRMKVTVAFNOF 29
 US-07-857-224B-79
 RESULT 8
ID US-08-685-992-23
 Query Match
 xxxxxx
 XXXXX
 RESULT
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ZUP: (note: this an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc.; iskette, 1.4 Mb storage
COMPUTER: Apple MacInc.; iskette, 1.4 Mb storage
COMPUTER: 0375754
APPLICATION DATA: User: 1.0
CLASSIFICATION NUMBER: User: 1.0
CLASSIFICATION DATA: no. 6
FELEPHOME: (International) 41 i 262 2437
TELEPHOME: (International) 41 i 262 2437
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Pred "ling Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Buller
 Sequence 27, Application U./08701191A
Patent No. 5942428
GENERAL INFORMATION:
APPLICANT: Moosa Mohamma ., Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
AITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
IITLE OF INVENTION: OF NCN-INSULIN RECEPTOR TYROSINE KINASE
 --
 Query Match
Best Local Similarity 44.4% in 35. No. 5 25er01;
Matches 8: Conservative Makenions 3, Indexs
 304 AA
 FEATURE: Protein kinase, Table 8 column 90 PUBLICATION INFORMATION: ACTHORS:
 PRT;
 ACTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TILLE: THE protein kinase family.
JOURNAL: Science
 43458 CN:
 Seguence 27, Application US/08701191A
 STREET: Hadlaubstrasse 151 CITY: 2 unich
 STANDARD.
 MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
 269 AA: 30804 MW:
 133 LAARNIL-VAEGRKMKIS 149
 COUNTRY: Switzerland
 6 LSARDVLAVVSKRRMKVT 23
 amino acid
 linear
 ORGANISM: human
 PAGES: 42-52
DATE: 1988
 US-08-7C1-191A-27
 TOPOLOGY:
 SECUENCE
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CLONE:
SEQUENCE 33
 Query Match
 Matches
ò
 Sequence 15, Application US/08938957A
Parent No. 5998137
GENERAL INFORMATION:
APPLICANT Residual Martin L.
APPLICANT Breithan, Martin L.
APPLICANT Duront, Daniel J.
APPLICANT SECURICES 32
CORRESPONDED ADRESS:
ADDRESSED BEFERIN & Parr
STREET 40 King Street West
CITT TOTATIO
STATE: Ontatio
COUNTRY Canada
ZIP: MSH 372
 query Match 30.0%: Score 68: DB 2: Length 304: Fest Local Similarity (4.4%: Pred. No. 5.2) -01: Matches 8: Conservative 6: Mismatches 3: Indeis
 CORRESPONDENCE AUGUMENS.

ADDRESSEE: John E. John E. John Street.
STREET: Galifor at Galifornia COUNTY. Los Angeles
STATE: Galifornia COUNTY. Los Angeles
STATE: Galifornia COUNTY. U.S.A.
ZIP: GCOLI. 2066
COUNTY. U.S.A.
ZIP: SCOLI. 2066
COUNTY AND COUNTY. INCOMPATION COUNTY AND COUNTY. INCOMPATION CATA. INCOMPATION CATA. INCOMPATION CATA. APPLICATION CATA. INCOMPATION. INCO
 TOPOLOGY: Linear
MCLECULE TYPE: protein
JENCE 304 AA: 34656 MW: 480234 CN:
 Sequence 15. Application US/08838957A
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
 165 LAARNIL-VAESRKMKIS 181
 6 LSARDVLAVVSKRRMKVT 23
 T 11
US-08-838-457A-15
 SECUENCE
 XXXXXX
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Sequence 5, Application US/00119101
Patent No. 552330
GENERAL INFORMATION:
APPLICANT Travis, James
APPLICANT: Potempa, Jan
APPLICANT: Barr, Philip J.
APPLICANT: Ravloff, Nature
IITLE OF INVENTION: Porphyromonas gingivalis Arginine-specific proteinase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
 Gaps
 Gaps
 7
 .:
 Length 737:
 Length 368:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disconduting Computer; Tam FG confails to OPERATING SYSTEM: PCPE, MSS-DUS SOFTWARE: Patentin Release #1.0, Version #1.25 CORRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/119.36;
FILING DATE: 10-SEP-1993
CLASSIFICATION: 424
ATTORNER/AGENT INFORMATION:
 Query Match 29.5%; Score 67; DB 1; Length 737; Best Local Similarity 52.0%; Pred. No. 6.30e+01; Matches 13; Conservative : Mismatches 9; Indels
 10: Mismatches 10: Indels
 737 AA
 737 AA.
 29.5%; Score 67: DB 2: L
Local Similarity 32.3%; Pred. No. 6.30e+01;
ies 10; Conservative 13: Mismatches 10
 ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 261
 283 EELLEKTVKNCLALADERKLK-SIAFPSIGS 312
 MOLECULE TYPE: protein
SEQUENCE 737 AA: 81332 MW; 1874143 CN;
 PRT;
 LIBRARY: GenBank
CLONE: 205276
SEQUENCE 368 AA: 39086 MW: 716242 CN;
 PHT
 Sequence 5, Application US/08119361
 87 ILS-RS-LAVSDIREMKVEVVSSKF 109
 REGISTRATION NOMBER: 4478
REFERENCE/COCKEL N'MBER: 2.
TELECCHMONINATION INFORMATION
TELEPHONE: 3634497-808.
 LENGTH: 737 amino acids
TYPE: amino acid
TOPOLOGY: linear
 STANDARD:
 STANDARD
 Ferber, Donna M
 TELEFAX: 303-499-8089
INFORMATION FOR SEC ID NC:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acid
 303-664-808
 linear
 SIREET: 5370 MS
CITY: Boulder
STATE: CO
 JSA
 RESULT 15
ID US-08-336-308A-4
 US-08-119-361-5
 COUNTRY:
 Query Match
 xxxxx
 Matches
 ð
 / Match 30.0%: Score 68: DB 1; Length 316: Local Similarity 44.4%: Pred. No. 5.2!e-01: es 8: Conservative 6; Mismatch: 3: Indels
 PACHOL NO. 598.221
GENERAL INCRMATION:
APPLICANT: HILLMAN JOHNIEL L.
TITLE OF INVENTION: EIN
KUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE PHARMACCULICALS, INC.
SIREET: 3174 Portor Drive
CITY: Palo Alto
 COUNTY: USA
ZIN: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: BM COMPATIBLE
COMPUTER: BM COMPATIBLE
COMPUTER: DISS SOFTWARE: PASSISEC IN WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,824,878
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08,824,878
FILING DATE: FILED HERWITH
APPLICATION NUMBER: 36,749
RECESTRATION NUMBER: 415-655-0556
TELEPHONE: 415-655-0556
REFERENCE/DOCKET NUMBER: 3153-111
TELECOMMUNICATION INFORMATION:
TELEPANE: (416) 364-731
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH 316 amino acids
TYPE: amino acids
 316 AA: 35696 WW: 526817 CN:
 - E
 Sequence 3, Application US/08824878 Patent No. 5981221
 Sequence 3. Application US/08824878
 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 LENGTH: 368 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 STANDARD;
 152 LAARNIL-VAEGRKMKIS 168
 6 LSARDVLAVVSKRRMKVT 23
 TOPOLOGY: Tinear
MOLECULE TYPE: CONA
IMMEDIATE SOURCE:
CLONE: Ret
 USA
 RESULT 13
ID US-08-824-878-3
 COUNTRY
 SEQUENCE
 wery Match
 xxxxxx
 Matches
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CUMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER:
COMPUTE
 Usery Match 29.5%; Score 57; DB 3; Length 737; Best Local Similarity 52.0%; Pred. No. 6.30e+61; Matches 13; Conservative 1; Mismatches 9; Indels
 ADERESSEE: Greenlee, Winner and Suilivan, P.C. STREET: 5970 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Oclorado
AUDINEY: US
AUDINEY: US
AUDINAY: US
 Sequence 4. Application US/083363C8A
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Gaps ..

Search completed: Tue Jun 20 13:36:23 2000 Job time : 6 secs.

<u>و</u>. Š US-09-142-524A-10.rap

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp - protein - protein database search, using Smith-Waterman algorithm

Mon Jun i9 16:26:34 2000; MasPar time 17:22 Seconds 187.279 Million cell updates/sec R ::: on:

Tabular output not generated.

>US-09-142-524A-10 (1-32) from US09142524A.pep 2 EEYLILSARDVLAVVSKRRMKVIVAFNOFGPN 32

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

721208 seqs, 100765575 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-pending 1:eCT 2:06 3:050 4:07 5:080 6:081 7:092 8:083 9:084A 10:084B 11:085 12:086 13:087 14:068 15:089 16:090 17:091 18:092 19:093 20:094 21:095 22:NEWP 23:NEWD60 24:NEWU8 25:NEWU9

Mean 26.635; Variance 90.120; scale 0.295 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| ered.<br>No.          | 1.68e-02   | 1.68e-02   | 1.39e-01   | 2.21e-01   | 2.21e-01     | 2.21e-01   | 2.21e-01   | 2.21e-01   | 2.21e-01   | 2.21e-01   | 2.21e-C1   | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|                       | Applicati  | Applicati  | Applicat   | Appl       |            |              | Applicat   | Applicat   |            |            |            | Applicat   |
| :<br>::               |            | 36,        | 'n         | 236,       | 236.       | 236,       | 236,       | 222,       | 222,       | 222,       | 222,       | 222.       | 228.       | 229.         | 229.       | 228.       | 228.       | 229.       | 228,       | 229.       |
| Description           | Sequence   | Seguence   | Sequence   | Sequence   | Seguence   | Sequence   | Sequence   | Seguence     | Seguence   | Seguence   | Seguence   | Seguence   | Sequence   | Sequence   |
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| <u> </u>              | 10         | 6          | 0,1        | œ          | 10         | J C        | 10         | 10         |            |            |            | <u>ှ</u>   |            |              |            |            |            |            |            | 10         |
| Guery<br>Match Dength | 6.5        | 65         | 13         | 13         | 19         | 5          | i,-i       | 2.9        | 29         | 29         | 59         | 29         | 26         | 26           | 26         | 56         | 25         | 26         | 25         | 26         |
| Cuery<br>Match        | 50.2       | 50.2       | 46.3       | 46.3       | 46.3       | 46.3       | 46.3       | 45.3       | 46.3       | 45.3       | 46.3       | 46.3       | 45.4       | 45.4         | 45.4       | 45.4       | 45.4       | 45.4       | 45.4       | 45.4       |
| Score                 | 114        | 114        | 105        | 105        | 105        | 105        | 105        | :05        | 105        | 105        | 105        | 105        | 103        | 103          | 103        | 103        | 103        | 103        | 103        | 103        |
| Result<br>No.         |            | 2          | ~          | 4          | <b>t</b> n | S          | 7          | œ          | o,         | 10         | 11         | 12         | 13         | <del>1</del> | 15         | 9.1        | L          | 00<br>r:1  | 61         | 20         |

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APPLICANT
GIFFER, ITHIN 5.:
APPLICANT
BORG, JULIAN F.:
APPLICANT
GARMA, RICHARD S.:
APPLICANT
ROO, ABLICANT
YEARD, SIU-mei H.:
APPLICANT
YEARD, SIU-mei H.:
APPLICANT
RALEY, MARK A.:
APPLICANT
POWER, SIU-mei H.:
APPLICANT
POWER, SIU-mei H.:
APPLICANT
TILLE OF INVENTION: Albergenic Proteins And Peptides From TITLE OF INVENTION: Japanere Cedar Polle:
NUMBER OF SEQUENCES: 261
CORRESSONDENCE ADDRESS:
ADDRESSEE: Immulogic Ph.:marculical Corporation, Inc.
STREET: 616 Lincoln S:
CITTE NATH AM
 ä
 Score 114, UB 9, Length 93;
Prv3, No. 1,68e-62;
Mismatches 0; Indels
 . Version #1.25
 NAME: Darlene A. Vanstone
REGISTRATION UNMBER: 35,729
REFERENCE/DOCKEI NUM. 4: 025.6 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
 19 AA
 FILING DATE:
CLASSFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6: 994
APPLICATION NUMBER: 08/256,248
FILING DATE: SP11 6: 994
APPLICATION NUMBER: 07/338,990
FILING DATE: September 1: 1992
APPLICATION NUMBER: 07/338,990
FILING DATE: September 1: 1992
APPLICATION NUMBER: DIT/US93/00139
FILING DATE: January 15: 1993
ATTORNEY/AGENI INFORMATION:
 I Ha
 15 18-15/3-1/5
 e 236. Application US/3846894U
ENERAL INFORMATION:
APPLICANT: Grif-
 : Floppy cisk
IBM PC conjuitble
YSTEM: PC:D S/MS:10 S
 COMPUTER: Tam PC conjustible OPERATING SYSTEM: PC D S/MS-H S SOFTWARES: Outcome Restaure F. CURRENT APPLICATION NUMBER: Syce/Arm.D. APPLICATION NUMBER: Syce/Arm.D.
 Sequence 236, Application US/08468943
 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 93 AA; 10002 MW: 48036 CN:
 IELEPHONE: (617) 466-6000
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
 STANDARD
TYPE: arino acid
STRANDEDNESS: single
TOPOLOGY: linear
 COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
 Ouery Match
Best Local Similarity 160.08;
Matches 17: Conservative
 77 EEYLILSARDVLAVVSK 93
 | FEYLLESARDVLAVSK 17
 USA
 US-08-468-94C-236
 ZIP: 02154
 COUNTRY:
 Sequence 236.
 GENERAL
 XXXXX
 RESULT
 Sequence 16, Application US/08432697
GENERAL INFORMATION:
APPLICANT Labigne, Agnes
APPLICANT Saucroban, Sebastien
APPLICANT Saucroban, Sebastien
APPLICANT Formero, Richard L.
APPLICANT: Friberge, Jean-Michel
IIILE OF INVENTION: LAWONGENIC COMPOSITIONS AGAINST
IIILE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
IIILE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS!
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 Score 114: DB 10, Longth 93: Pred, No. 1.68e-02: 0: Mismatches 0: Indels
 Danner Benderson, Farabow, Sarrett & Danner (1900 I Stroet, N.W.)
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Pateniin Release *1.0, Version *1.30
CURRENT APPLICATION DATA:
 RESISTRATION NUMBER: 25,146
REFERENCE/COCKET NUMBER: 03495,0137-00000
TULECOMNUNICATION INFORMATION:
TELEPHONE: (202),408-400
INFORMATION FOR SEQID NO: 36:
SECUENCE CHARACTERISTICS:
SECUENCE CHARACTERISTICS:
LENGIH: 93 amino acids
 NAME: Moyers, Kenneth J. ACJSTRAILON NUMBER: 25,146
 REJESTRAILON NUMBER: 25,146
 REPERENCE-ZOCKET NUMBER: 03495,0137-02000
 IELEPHONE: (202) 408-4400
 IELEPHONE: (202) 408-4400
 INFORMATION FUR SEQ ID NO: 36: SEGUENCE CHARACTERISTICS:
 93 AA
 APPLICATION NUMBER: US/08/432,597
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
 587
 STRANDEDNESS: SIGALE
STRANDEDNOSS: SIGALE
TOPOLOGY: Treat
MCLECULE TYPE: TOTALE
SEQUENCE: 93 AA: 10002 MW; 48030 CN;
 Sequence 35, Application US/08432697
 ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 STANCARD:
 LENGIH: 93 amino acids
TYPE: amino acid
 whery Match
Best Local Similarity 100.0%;
Matches 17: Conservative
 77 EEYLILSARDVLAVVSK 93
 CITY: Washington
STATE: P.C.
 20005-3315
 ASC:
 ADDRESSEE: STREET:
 US-06-432-697-46
 ADDRESSER
 COUNTRY
 XXXXXX
 RESULT
ID US
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19 AA
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 Sequence 236, Application US/08467006
 TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 19 AA: 2181 MM: 2056 CN:
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 19 AA; 2181 MM; 2058 CN;
 FILING DATE: December 6: 19
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remiliard
REGISTRATION NUMBER: 38.872
 STANDARD
 19 amino acids
 Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
 2 KKSMKVTVAFNÇFGPN 17
 TYPE: amino acid
TOPOLOGY: linear
 USA
 US-08-467-006-236
 COUNTRY:
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 Gaps
 APPLICANT Griffeth, Irwin J.;
APPLICANT Griffeth, Joanne.
APPLICANT Bond, Julian F.;
APPLICANT Bond, Julian F.;
APPLICANT Garman, Richard D.;
APPLICANT Woo, Mark A.;
APPLICANT Yeung, Slu-mei H.;
APPLICANT FENSY, Mark A.;
APPLICANT Exiev.
APPLICANT Stagen. Steven P.
ITILE CF INVENTION: Allergenic Proteins And Peptides From TITLE CF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CCRRESPONDENCE ADDRESS:
 ö
 ADDRESSEE: Immulcqic Pharmaceutical Corporation, Inc. SIREGT: 610 Lincoln St CITY: Waitham STATE: MA CUNTRY: USA ZIP: 0.2154 COMPUTER READABLE FORM:
 Score 105; DB 10; Length 19;
Pred. No. 1.83e-01;
1; Mismatches 1; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILDLE
COMPUTER: IBM PC COMPAILDLE
COMPUTER: IBM PC COMPAILDLE
COMPAINS SYSTEM: DC DC.X/MS.OCS
SOFTWARE: Faterill Release *1.5. Version *1.25
CURRNY APPLICATION DAIA
APPLICATION NUMBER: US/28/350.25
FILING APPLICATION A14
PROGRAFICATION NUMBER: 08/226.248
FILING DATE: April 8.1994
APPLICATION NUMBER: 07/938.99
FILING DATE: April 8.1994
APPLICATION NUMBER: DOI/938.99
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Datlene A. Vanstone
RECISTRATION NUMBER: 02.6.6 US (IMI-028CP2)
IELECOMMUNICATION INFORMATION:
NAME: GLING TOWN NUMBER: 03.00
FELEFACE (617) 466-604
INFERMATION POR SED ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
TYPE: arming acids
 24 A.A.
 PRT
 Sequence 236, Application US/08350225
GENERAL INFORMATION:
TYPE: amino control of the total of t
 Sequence 236, Application US/08350225
 STANDARD:
 Ouery Match
Rest Local Similarity 87.5%:
Matches 14; Conservative
 2 KKSMKVIVAFNQFGPN 17
 12 KRRMKVIVAFNOFGPN 32
 IOPOLOGY: linear
 JE 4
US-08-350-225-236
 SEQUENCE
 Query Match
 xxxxx
```

```
0
 APPLICANT: Griffeth, Irwin J.;
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Johnse.
APPLICANT: Bond, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Woung, Siu-me H.;
APPLICANT: Wenng, Siu-me H.;
APPLICANT: Exley, Mark A.
APPLICANT: Exley, Mark A.
APPLICANT: Dowers, Steven P.
ITLE OF INVENTION: Allequate Proteins And Peptides From IILE OF INVENTION: Allequate Pollen
CORRESONDENCE ADDRESS:
ADDRESSE: Immulogic F.armacestical Corporation, Inc.
SIRRET: 610 Lincoln St.
CITY: Waitham
SITAL: MA
 Saps
 Query Match 46.3%; Score 105; DB 10: Length 19: Best Local Similarity 87.5%; Pred. No. 1.39e-01;
 ZIP: JOSA
ZIP: JOSA
ZIP: JOSA
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPING SYSTEM: PC-D:S/MS-DOS
SOURCENT REPELLENT RELEASE #1 3. Version #1.25
CUSRENT APPLICATION NUMBER: US/WE/4+%, JOSE
FILING DATE: JOSE 6. 1495
CLASSIFICATION: 4.24
PRICE APPLICATION NATA:
APPLICATION NOMBER: US/350, 2.25
 REFERENCE/DOCKET NUMBER: 025.6 USD5 (IMI-028CPD6)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACIERISTICS:
Score 105: DB 8; Length 19;
Prod. No. 1.39e-01;
I: Mismatches 1; Indels
```

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APPLICAN:
 SECUENCE
 XXXXXX
 RESULT
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Gaps
 Gaps
 APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Retchard D.:
APPLICANT: Wound Weithchard D.:
APPLICANT: Weing, Sintmel H.:
APPLICANT: Weing, Sintmel H.:
APPLICANT: Weing, Mark A.:
APP
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ö
 COMPUTER FRANCE FORM:

MEDICM TYPE: Floppy disk
COMBALLER FRANCE COMPATIBLE
OPERATING SYSTEM: DC-OOGNES-CGS
SOFTWARE: Patentin Release #1.0, Ve 410n #1.25
CURRAIN APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION 142
FILING SATE:
APPLICATION 142
FRIDE APPLICATION 142
FILING SATE:
CLASSIFICATION 142
FRIDE APPLICATION 142
FILING SATE:
ANDRES: 39.45
ATTOREN/ACTION 100 PROPER: 39.45
ATTOREN/ACTION 100 PROPER: 30.25
RESCHAMELIAN 100 PROPER: 30.25
RESCHAMELIAN 100 PROPER: 30.25
RESCHAMELIAN 100 PROPER: 30.25
RESCHAMELIAN 100 PROPERIENCE: CAST 7400
TELEFRENCE: (617) 227 7400
TELEFRENCE: (617) 227 7400
TELEFRENCE: (617) 227 7400
TELEFRENCE: (617) 227 7400
TELEFRENCE: CAST SEQ 1D NO: 236: SEQUENCE: CAST SEQUEN
 Score 105; DB 10; Length 19;
Pred. No. 1.39e-01;
i: Mismatches 1; Indeis
Indels
 ADDRESSEE: Immuloque Pharmaceutical Corporation, STREET: 610 Lincoln St
 19 AA
Mismatches
 Application US/08467023
 Sequence 235. Application US/08457023
 Griffeth, Irwin J.:
Pollock, Joanne:
 TYPE: Internal
19 AA; 2181 MW; 2058 CN;
 STANDARD
 TOPOLOGY: linear
MCLECULE TYPE: peptide
FRAGMENT TYPE: internal
 Query Match
Bost Local Similarity 87.5%;
Matches 14; Conservative
Conservative
 2 KKSMKVTVAFNGFGPN 17
 1: (1::111).
17 KRRKVTVAFNÇEGPN 32
 amino acid
 Waltham
 U.S.A
 US-08-467-023-236
 COUNTRY
 APPLICANT
 STATE
14;
 SEQUENCE
Matches
 RESULT
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Sales
 APPLICANT COLOUR JULIAN F. APPLICANT GARDAL H.CHART D. APPLICANT GARDAL H.CHART D. APPLICANT GARDAL H.CHART D. APPLICANT FUND MEI-CHART APPLICANT FUNDY SITTURE OF STATE MATERIAL BRANCH P. APPLICANT POWERS, STEWER P. DAMESS, STEWER P. DAMESS, STEWER P. STEWERS D. STOUGHESS: 26. CORRESPONDENCE ADDRESS: ADDRESSE: ImmuLogic Fharmacevitical Corporation, 17.1. STREET 610 Lincoln St. CITY: Waltham STRIE COLUMN. MA
 Length 193
 Score 105: DB 10: Length 19
Pred. No. 1.59e-Cl:
I: Mismatches I: Indels
 NAME: Jane F. Remillard REGISTRATION NUMBERS RESIDENCE CHARACTERISTICS.
 SOFTWARE: Patentin Release #1.5 Version #1.25 SOFTWARE: Patentin Release #1.5 Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457.697
FILLING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
APPLICATION: 424
APPLICATION: UNMBER: 08/350,225
 19 AA.
 29 AA
 PRT;
 ..
ix.
0,
 MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DNS
 equence 236. Application US/U8467697
GENERAL INFORMATION:
 Sequence 235, Application US/00067697
 Griffeth, Irwin J.;
Pollock, Joanne:
Bond, Julian F.;
Garman, Richard D:
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 19 AA; 2181 MM: 2058 CN;
 FILING DATE: December 6
ATTORNEY/AGENI INFORMATION
 STANDARD
 STANDARD
 : 19 amino acids arino acids
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 Query Match 46.3%;
Best Local Similarity 87.5%;
Matches 14; Conservative
 2 KKSMKVTVAFNCFGPN 17
 17 KRRMKVTVAFNCFGPN 32
 inear
 RESULT 8
ID US-08-468-940-222
US-08-467-697-236
 TOPCLOGY:
 XXXXXX
 axex
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2 KKSMKVIVAFNOFGPN 17 1: ::!!!!::!!!!! US-09-142-524A-10.rap

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 Gaps
 APPLICANT GRIFFETH, Irwin J.:
APPLICANT GRIFFETH, Irwin J.:
APPLICANT GROOD, Julian F.;
APPLICANT GROOD, Julian F.;
APPLICANT GROOD, Siu-me! F.;
APPLICANT Kuo, Mei-Chang:
APPLICANT FEAUGR. Siu-me! H.;
APPLICANT Extey, Mark A.;
APPLICANT Extey, Mark A.;
APPLICANT FOWERS, Steven P.
IIILE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Alpanese Cedar Pollen
NUMBER OF SEQUENCES: 26;
CORRESPONDENCE ADDRESS:
 CORRESPONDE ADDRESS:
CORRESPONDE ADDRESS:
ADDRESSEE: Immulogic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoin St
STREET: 620 Lincoin St
STAIE: MA
CONTRY: USA
CONTRY: USA
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compa
 .;
0
 Score 105: DB 10: Length 29: Pred. No. 1.39e-01; Mismatches 1: Indeis
 NAME: Dariene A. Vassione
RESISSRATION NUMBER: 35,729
RESISSRATION NUMBER: 025.6 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-600
TELEFRAX: (617) 466-600
SINDERALICN FOR SEQ ID NC: 222
SINDERNCE CHARACTERISTICS:
 Sequence 222. Application US/08468940
 Sequence 222. Application US/38468940
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 29 AA: 3313 MM: 4103 CN;
 : 29 amino acids
amino acid
 Owery Match 46.3%;
Best Local Similarity 87.5%;
Matches 14; Conservative
 1 KKSMKVIVAFNOFGPN 16
 linear
 GENERAL INFORMATION:
APPLICANT: Griffe
 ropology:
 LENGTH:
 SEQUENCE
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29 A.A.

PRT;

STANDARD:

US-08-350-225-222

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 Gaps
 APPLICANT: Bond, Julian F.:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard E.:
APPLICANT: Garman, Richard E.:
APPLICANT: Yeung, Sluthmel H.:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Powers Steven F.:
IITLE OF INVENTION: Alietgenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Poilen
NUMBER OF SEQUENCES: 26.
CORRESPONDENCE ADDRESS: 26.
CORRESPOND
 ;
0
 MEDIUM TYPE: Floppy diak
COMPUTER: IBM PC COMPA:Ib.e
COMPUTER: IBM PC COMPA:Ib.e
COMPUTER: IBM PC COMPA:Ib.e
COMPATING SYSTEM: PC-D-S/MS-DOS
SOFTWARE: Patentin Release #1.C, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: 08/28/550,225
FILING DATE: December 6, 1994
CLASSIFICATION DATA:
RPPLICATION NUMBER: 08/226,248
FILING DATE: April 8, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US91/C0139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
 Score 105: DB 8: Length 29:
Pred. No. 1.39e-01;
l: Mismatches 1: Indels
 NAME: Darlene A. Vanst no
REGISTRATION UNMBER: 15,729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
 29 AA.
 PRT;
 Sequence 222. Application US/08350225
Sequence 222, Application US/08350225
 MOLECULE TYPE: peptide
FRACMENT TYPE: internal
JENCE 29 AA: 3313 MW: 4103 CN;
 Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
 TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ. 13 N. 278
SEQUENCE CHARACIERISTION
 STANDARD;
 29 amino actis
 2.P: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
 Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
 1 KKSMKVTVAFNOFGPN 16
 linear
 GENERAL INFORMATION APPLICANT: Griff
 USA
 US-08-467-023-222
 TOPCLOGY:
 COUNTRY:
 LENGIH:
 SECUENCE
 xxxxx
 RESULT ID US XX AX XX XX XX XX XX XX XX XX
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58.7
 Sequence 222, Application US, 9457697
GENERAL INFORMATION:
APPLICANT: GLIffeth, Irwin J.;
APPLICANT: POLIOCK, Joanne,
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D:
APPLICANT: Garman, Richard D:
APPLICANT: Kuo, Mei-Chang;
 Sequence 222, Application US/08467697
 TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: intercal SEQUENCE 29 AA; 3313 MW: 4104 CN.
 MEDICM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 STANDARD;
 ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
 Match
Local Similarity 87.58;
es 14; Conservative
 : 29 amino ac
amino acid
 1 KKSMKVIVAENDEGEN 18
 : II INI II
IP KERMKVIVAHNOFGPN 52
 Waltham
 SP
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 STATE: M
 Query Match
Best Local S
 Matches
Gaps
 ö
 CORRESPONDENCE ADDRESS: ADDRESS: Inc. Corporation, Inc. STREET: Cl. Lincoln St. CITY: Waitham
 PRIOR APPLICATION 174
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING CATE: December 6, 1994
ALIGRNEY/ADDENT LYECKMATION:
NAME: Jace 5, Remillard
REGISTRATION NUMBER: 38-972
REFERENCE/POOKET NUMBER: 025.6 USD2 (IMI-028GPD2)
TELEPHONE: (6.7) 227-7400
TELEPHONE: (6.7) 227-7400
TELEPHONE: (6.7) 227-5941
INFORMATION FOR SED ID NO: 222:
SEQUENCE CHARACTERISTICS:
 Score 1.5, DB 10; Lendth 29;
Pred, No. 1.39e-01;
1: Mismatches 1: Indels
 COMPUTER REACCIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tappy disk
COMPUTER: Tam Pec Compatible
DEFMAING SYSTEM: PC DCS/MS·DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/UB/467.023
FILLING PATE: June 6, 1995
CLASSIFICATION: 424
 Sequence 222. Application US/08467006
GENERAL INFORMATION:
APPLICANT: GLIffeth, Irwin C.:
APPLICANT: Pollock, Joanne:
 Sequence 222, Application US/08467023 GENERAL INFORMATION:
 Sequence 222, Application US/08467006
Sequence 222, Application US/08457023
 T IYPE: loternal
29 AA; 3315 MW; 4103 UN:
 STANDARD:
 29 amine acids
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
 Query Match
Best Local Similarity 97,5%:
Matches 14: Conservative
 1 KKSMKVTVAFNOFGPN 16
 17 KRRMKVIVAFNOEGPN 32
 TOPOLOGY: News
 USA
 US-08-467-006-222
 ď
X
 02154
 STATE: MR
 LENGTH:
 SEQUENCE
 XXXXXX
 RESULT
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ö
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Hei-Chang:
APPLICANT: Kuo, Siu-mei H.;
APPLICANT: Brauer. Andrew.
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Worfs, Steven P.
ITLE CF INVENTION: Aleraenic Proteins And Peptides From TILLE CF INVENTION: Japanese Cedar Polien
NUMBER OF SEQUENCES: 251
CORRESPONDENCE ADDRESS:
 ADDRESSEE: ImmuLogic Pharmacentical Corporation, ind
STREET: 610 Lincoln St
 Score 195: DB 10: Length 29:
Pred. No. 1.89e-01;
. Mismatches 1: Indels
 REFERENCE/JOCKET NUMBER: 38,872
REFERENCE/JOCKET NUMBER: 0.25.6 USU5 (1M1-0.28GFD5)
TELECOMMUTCATION INFORMATION
TELEPHONE: (617) 2.27-74.00
INFORMATION FOR SEQ ID NO: 2.22:
SEQUENCE CHRARCIERISTICS:
LENGTH: 29 amilt
 OPERATING SYSTEM: DECOMPARTING SYSTEM: DESCRIPTION 11.25
SOFTWARE: Patentin Release 11.0, Version 11.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,006
FILLING DATE: Usue 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/05/52/25
FILLING DATE: December: 6, 1994
ATTORNEY/AGENT INFORMATION:
 24 AA
 Garman, Richard D.
Kuo, Mei-Chang,
Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
 RESULT 12
XX
AC XXXXX
DY
XX
XX
XX
XX
C
Sequence 222, Applix
XX
C
Sequence 222, Applic
C
Seq
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Gaps
 APPLICANT Griffeth, Irwin 5.:
APPLICANT Griffeth, Joanne.
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard D.:
APPLICANT: Kuo, mai-Chang:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Exley, Mark A.:
APPLICANT: Exley, Mark A.:
APPLICANT: Dowers, Storen P.
TILLE OF INVENTION: A.ergenic Proteins And Peptides From ITLE OF INVENTION: A.panese Cedar Pollen.
NUMBER OF SEQUENCES: 261
APPLICANT: A.BARESS:
ARBARET A.BARET A.BARESS:
ARBARET A.BARESS:
ARBARET A.BARET A.BARESS:
ARBARET A.BARET A
 :
ت
 E: ImmuLogic Pharmaceutical Corporation, Inc.
610 Lincoln St
 Sire 103: DB 8: Length 26:
Pr d. No. 2.21e-01;
0. Mismatches 1: Indels
 CEREBIA APPLICATION DATE:

PELLING DATE: December 6, 1994
CLEASIFICATION: 424
CLEASIFICATION: 424
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/226,246
FILING DATE: APril 3, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/938,990
FILING DATE: January 15, 1993
ATORNEY/AGINI INFORMATION:
NAME: DATACHER A. VASECONE
REGISTATION NUMBER: 025.6 US (:MI-028CP2)
FLEEDHOWNICATION NUMBER: 025.6
TELECOMMUNICATION NUMBER: 026.6
TROOM SEQUENCE CHRARATERISTICS:
LENGTH: 26 malio acids
 MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC COMPA")Jie
CPERATING SYSTEM: PC"LO:/MS-FD3
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 26 AA
 3,
 Sequence 229, Application US/08*50228 GENERAL INFORMATION:
 Sequence 229, Application US/08350225
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 26 AA; 2956 MR: 3131 CN;
 STANDARD
 610 Lincol: St
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy :
 Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
 IYPE: amino acid
TOPOLOGY: linear
 1 RSMKVTVAFNQFGPN 15
 STREET: 610 Lir
CITY: Waltham
STATE: MA
 Waltham
 USA
 US-08-350-225-229
 02154
 ADDRESSEE:
 COUNTRY
 STREET:
CITY: WA
 xxxxxx
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 ö
 SdeS
 AFFLICANT: Griffeth, Irwin J.;
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne.
C APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D.;
APPLICANT: Kuo, Mark A.;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPL
APPLICANT: Powers, Steven P.
TILLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES:
CRRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
 Score 105: DB 10: Length 29;
Pred. No. 1.39e-61;
1: Mismatches 1: indels
 REFERENCE/DOCKET NUMBER: 025.6 USD4 (IMI-028CPD4)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7406
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
 SCETABLE PATENTIN SOLVESION #1.25
SCETABLE PATENTIN Release #1.0. Version #1.25
SCETABLE PATENTIN DATA:
APPLICATION NUMBER: US/09/467,697
FILING DATE: Use 6, 1995
CLASSIFICATION 1424
PRIOR APPLICATION DATE: 08/35C,225
FILING DATE: December 6, 1994
ATTON NUMBER: 08/35C,225
FILING DATE: December 6, 1994
ATTONEY/ASSIT: INFORMATION:
NAME: Jane E. Remiliard
REGIS:HATION NUMBER: 38.872
 26 AA
 D.Y.
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
 Sequence 228, Application US/08350225
 NT TYPE: internal
29 AA; 3313 MW; 4103 CN:
 STANDARD:
 MOLECULE TYPE: interior RAGMENT TYPE: interior
 Query Match
Bost Local Similarity 97.5%;
Matches 14: Conservative
 ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
 1 KKSMKVIVAFNQFGPN 16
 1: -1111 | -11111
17 KRRMKVIVAENČEGPN 32
 TYPE: amino acid
 STREET: 610 Lir
CITY: Waltham
STAIE: MA
 USA
 us-08-350-225-228
 COUNTRY
 SEQUENCE
 XXXXXX
 RESULT
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Search completed: Mon Jun 19 16:25:53 2000 Job time : 19 secs.
 888888888888888888888888888888888
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 Saps
 Sequence 229, Application US/08467023
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Griffeth, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Garman, Richard D;
APPLICANT: Yeung, Julian F.;
APPLICANT: Yeung, Alchang;
APPLICANT: Exiey, Mark A.;
APPLICANT: Exiey, Mark A.;
APPLICANT: Exiey, Mark A.;
APPLICANT: Exiey, Mark A.;
APPLICANT: Dowers, Steven P.
TITLE OF INVENTION: Allequenic Proteins And Peptides From UNUMBER OF SEQUENCES: 251
CORRESPONDENCE ADDRESS: 251
 ċ
 ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
 COMPUTER REALGABLE FORM:

COMPUTER REALGABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: DAY FOR COMPATIBLE
OPERATION NUMBER: PC-DOS/XS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,225
FILING CATE: December 6, 1994
CLASSIFICATION ADATA:
APPLICATION NUMBER: US/08/98,990
FILING CATE: September 1, 1992
APPLICATION NUMBER: PCTUUS93/00139
FILING CATE: September 1, 1993
ATTORNEY/AGENT INFORMATION:
NAMME: DATECRE A. DATA:
REFERENCE/COMMUNICATION NUMBER: US-09/98
FILING CATE: AND SECOND Score 103: D: 8: Length 26: Prod. No. 2.2.e-01: 0: Mismatches 1: Indels
 26 AA
 PRT;
 Sequence 229, Application US/08467023
 LENGTH: 26 amino acids
TYPE: unino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: interral
 STANDARD:
 Query Match
Pest Local Similarity 93.38;
Matches 14; Conservative
 1 RSMKVIVAFNQEGPN 15
 18 REMKVIVAENÇEGEN 32
 JT 15
US-08-467-023-229
 ž
STATE: M. TOBNIRY:
 COUNTRY:
 SEQUENCES
 XXXXXX
 RESULT
ID US
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Length 26:
ZIP: 02154
COMPUTER REAGABLE FORM:
MEDIUW IYEE: Floppy dis
COMPUTER: IBM PC compa* 16
COMPUTER: IBM PC compa* 16
COMPUTER: IBM PC compa* 16
CURRENI APELICATION DATA
CURRENI APPLICATION DATA
FILING DATE: US/68/467.023
REGISTRATION NUMBER: 08/15/226
ATTORNEY/AGENT INP/RMAI: 1944
ATTORNEY/AGENT INP/RMAI: 18
NAME: Jane E: Nemilland: 1944
NAME: Jane E: Nemilland: 18 - 72
REGISTRATION NUMBER: 34 - 72
REFERENCE/DOCKET NUMBER: 34 - 72
 :ndels
 3E - 72
B - (25.6 USLz (3M2-0280PU2)
B - M3
 Score 103; DB 10; L
Pred. No. 2.21e-01;
0; Mismatches 1;
 WT TYPE: Internal
26 AA: 2964 MW: 1681 CN:
 TELEFAX: (617) 227-594
INFORMATION FOR SEQ :D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
 TELECOMMUNICATION INFORMA TELEPHONE: (617) 227-7
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
 Query Match
Best Local Similarity 93:38:
Matches 14: Conservative
 1 RSMKVTVAFNCFGPN 15
 SEQUENCE
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Mon Jun 19 16:12:03 2000; MasPar time 6.47 Seconds 233.465 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-10 (1-32) from US09142524A.pep 227 : ESYLILSAROVLAVVSKRRMKVIVAFNGFGPN 32 Title: Description: Perfect Score: Sequence:

РАМ 150 Gap 11 Scoring table:

Post-processing:

142080 segs, 47172406 residues

Searched:

Minimum Match 0% Listing first 45 summaries

pir52 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Pred. No. is the number of results pred ted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 34,452; Variance 60,394; scale 0,570

Statistics:

## SUMMARIES

| 1 14 50.2 100 2 525180 heat shock protein gr 15 50.2 100 2 JH6556 10% T-cell antigen 15 50.2 100 2 JH6556 10% T-cell antigen 16 50.2 100 2 S72818 heat shock protein ch 16 50.3 102 2 S77565 heat shock protein ch 16 50.3 45.4 102 2 S77565 heat shock protein ch 16 50.3 45.4 102 2 S77565 heat shock protein ch 16 50.3 45.4 102 2 S77565 heat shock protein ch 16 50.3 34.3 34.4 2 JC2123 major allegen Cry 16 50.3 50.3 10.3 1 BVYCGS heat shock protein r 4 50.3 50.3 10.3 1 BVYCGS heat shock protein r 5 9 50.3 10.3 2 JC2123 major allegen Cry 17 50.3 50.3 10.3 1 BVYCGS heat shock protein r 5 9 50.3 10.3 2 JC2123 major allegen Cry 17 50.3 10.3 1 BVYCGS heat shock protein r 5 9 50.3 10.3 2 JC2123 major allegen Cry 17 50.3 10.3 1 JC2123 major allegen Cry 17 50.3 10.3 1 BVYCGS heat shock protein r 5 9 50.3 10.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 BVYCGS heat shock protein r 5 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 50.3 1 8 9 5 | ж<br>в<br>п<br>п<br>п<br>п<br>п<br>п | Score      | Query<br>Match | Leaat. | 8.3   | CI      | Description      | Pred No. |
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| 114 56.2 100 2 JH6556 100 T-cell artigen 114 56.2 100 1 BVMYBA chaperonin groes - My 1.14 50.2 100 1 BVMYBA chaperonin groes - My 1.15 102 2 837565 chaperonin groes - St 6.15 102 2 847325 chaperonin groes - St 6.15 103 2 A41325 chaperonin groes - St 6.15 103 2 A41325 chaperonin groes - St 6.15 103 2 A41325 chaperonin groes - St 6.15 103 2 BVCGS chaperonin groes - Sy 7.15 103 1 BVVCGS chaperonin groes - Sy 7.15 103 2 A3132 chaperonin groes - Sy 7.15 103 2 A3132 chaperonin groes - My 1.15 103 2 A3132 chaperonin groes - Cy 7.15 103 2 A31332 chape |                                      |            | 50.2           | 160    | . 7   | 525180  | shock protein    | 1.726-96 |
| 114 56.2 100 1 BVMYBA Chaperonin groes - My 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 7                                    | 114        |                | 100    | 7     | JHC556  | T-cell antider   | 7.2e     |
| 114 50.2 169 2 572818 heat shock protein ch 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | m                                    | 214        |                | 100    |       | BVMYBA  | n großs -        | 72e-     |
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| 98 43.2 374 2 JC2123 major allergen Crý j 1.8 8 38.8 242 2 E71621 ERCC1-116e excision r 4.8 8 38.8 242 2 E71621 ERCC1-116e excision r 4.8 13.2 103 1 BVYCGS chaperonin groes - Sy 7.8 103 1 BVYCGS chaperonin groes - Sy 7.8 103 2 103 2 11320 NADH dehydrogenase (u 7.9 34.8 100 1 BVMY7B chaperonin groes - My 1.7 8 34.4 103 2 T01830 Chaperonin groes - My 1.7 8 34.4 103 2 T06830 Chaperonin groes - My 1.7 8 34.4 103 2 T06830 Chaperonin groes - My 1.7 8 34.4 103 2 T06830 Chaperonin groes - Cy 1.7 8 34.4 372 5 10.8 34 4 4 230 2 E5931 NACH dehydrogenase (u 7.8 33.5 325 1 B40358 NADH dehydrogenase (u 2.7 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 33.5 325 1 BA0358 NADH dehydrogenase (u 2.7 5 34537 NADH dehydrogenase (u 2.7 5 34537 NADH dehydrogenase (u 2.7  | ۲-                                   | 86         |                | 374    | ~     | JC2124  | r ailergen Crv   | 1.00e-03 |
| 9         88         38.6         24.2         2         E71621         ERCC1-11ke excision r 4.           1         45.5         103.1         2         45.5         103.2         43721         Gpectate lyase (EC 4.2.1.           2         40.3         1         80.45721         Groes protein - Synec 7.         59.0         7           3         5.2         103.2         731320         NADH dehydrogenase (U. 7.         7           4         6.0         1         11938         NADH dehydrogenase (U. 7.         7           5         3.4         8         100.1         8WWYB         Chaperonin groes - My 1.           7         3         4.4         103.1         106830         Chaperonin groes - My 1.           7         3         4.4         103.1         1.53510         H+ transporting AIP s 1.           7         3         4.4         30.1         1.53510         H+ transporting AIP s 1.           7         3         4.4         30.2         2.53510         H+ transporting AIP s 1.           7         3         4.4         30.2         2.53510         Hebrid Groes AIP s 1.           7         3         4.5         3.4         3.5         1.40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 00                                   | 86         |                | 374    | 7     | JC2123  | or allergen      | 1.00e-03 |
| 1 10.0 84 37.0 455 2 T0C856 pectate lyase (EC 4.2 1.2 1.3 1 BVYCGS chaperonin gross - Sy 7.3 1 BVYTB chaperonin gross - My 1.3 1 BVWYTB chaperonin gross - My 1.3 1 BVWYTB chaperonin gross - My 1.3 1 BVWYTB chaperonin gross - Cy 1.3 1 BVMYTB chaperonin gross - Cy 1.3 1 BVMYTB chaperonin gross - Cy 1.3 1 BVMYTB chaperonin gross - Cy 1.3 1 BVMTB chaperoning chaperone - Cy 3.3 1 BVMTB chaperone - Cy 2.3 1 BVMTB c | 9                                    | 88         |                | 242    | 7     | E71621  | 21-like excision | 276-     |
| 80         35.2         103         1 BVYCGS         chaperonin groes - Sy 7.           8         35.2         103         2 A36721         groes protein - Synec 7.           4         60         35.2         328         2 T11938         NADH dehydrogenase (u 7.           5         79         34.8         100         1 BYMY7B         chaperonin groes - My 1.           7         78         34.4         103         2 T06830         chaperonin groes - My 1.           8         74         103         2 T06830         chaperonin groes - Cy 1.           9         34.4         230         2 F53610         H+-transporting AIP s 1.           9         76         33.5         96         2 S34937         heat shock protein hs 2.           1         76         33.5         325         1 BMWTU         NADH dehydrogenase (u 2.           1         76         33.5         325         1 DMWTU         NADH dehydrogenase (u 2.           7         6         33.5         325         1 DMWTU         NADH dehydrogenase (u 2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 10                                   | 84         |                | 455    | 7     | T00856  | lyase (EC 4      | 1.80e-01 |
| 2 80 35.2 103 2 A36721 groES protein - Synec 7. 85 2 35.2 310 2 T11320 NADH dehydrogenase (U 7. 9.3 4.8 100 1 BVMYTB Chaperonin groES - My 1. 9 34.8 100 1 BVMYTB Chaperonin groES - My 1. 78 34.4 120 1 A47257 1-phospharidylinosito 1. 9 34.4 230 1 F53610 H+-transporting ATP s 1. 9 34.4 310 2 C58931 NACH dehydrogenase (U 1. 76 33.5 325 1 B40358 NADH dehydrogenase (U 2. 76 33.5 325 1 DNWTU NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 NADH dehydrogenase (U 2. 76 33.5 325 1 S49576 N | -1                                   | 80         |                | 103    | -     | BVYCGS  | •                | 7.31e-   |
| 8 8 95.2 310 2 T11320 NADH dehydrogenase (u 7. 328.2 2 T11938 NADH dehydrogenase (u 7. 328.2 328.2 T11938 Chapperonin groeß - 7. 34.8 869 1 A47257 1-phosphatidylinostho 1. 78 34.4 103 2 T06830 Chapperonin groeß - Cy 1. 78 34.4 310 2 T06830 Chapperonin groeß - Cy 1. 78 34.4 310 2 T06830 NADH dehydrogenase (u 2. 5. 33.5 325 1 B40358 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 325 1 S49576 NADH dehydrogenase (u 2. 5. 33.5 33.5 33.5 33.5 33.5 33.5 33.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 12                                   | 80         |                | 103    | ~     | A36721  | protein -        | ۲.       |
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| 5         79         34.8         100         1         BVMY7B         Chaperonin grcES - My 1.           7         9         34.8         869         1         A47257         1-phosphatidylinosito 1.           7         9         34.8         869         1         2         2         2           8         34.4         230         1         F53610         H+-transporting AIP s 1.         2           9         76         34.4         330         2         58931         NADH dehydrograsse (u. 1.           0         76         33.5         325         1         840358         NADH dehydrogenase (u. 2.           1         76         33.5         325         1         A49576         NADH dehydrogenase (u. 2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 14                                   | 60         |                | 328    | 7     | T11938  | dehydrogenase    | 7.31e-01 |
| 6 79 34.8 869 1 A47257 1-phosphatidylinositó 1. 78 34.4 103 2 T06830 chaperolin grces - Cy 1. 9 74.4 310 1 F53610 H+transporting AIP s 1. 9 76 33.5 96 2 S34937 heat shock protein hs 2. 7 33.5 325 1 B40358 NADH dehydrogenase (u. 2. 7 33.5 325 1 DNWTCI NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 325 1 S49576 NADH dehydrogenase (u. 2. 7 33.5 33.5 33.5 33.5 33.5 33.5 33.5 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 15                                   | 7.9        |                | 100    | -     | BVMY 7B | groes -          | -        |
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| 6 33.5 325 1 S49576 NADH dehydrodenase (U. 2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 22                                   | 46         | 33.5           | 325    | ~     | DNWIC1  |                  | 2.846+00 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 23                                   |            | 33.5           | 325    | ٦     | 495     | ä                | 2.846+00 |

| NADH dehydrogenase (u. 1.846-00) heat shock protein Gr. 3.96e-00 hypotherical protein 3.96e-00 hypotherical protein 3.96e-00 heat shock protein 3.96e-00 heat shock protein 5.51e-00 ceil wall-associated 5.51e-00 heat shock protein 5.51e-00 heat shock protein 5.51e-00 heat shock protein 5.51e-00 heat shock protein 5.51e-00 hypotherical protein 5.51e-00 pectate lyase (E. 4.2 1.65e-01 how willebrand tactor 1.65e-01 NOW Willebrand tactor 1.65e-01                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ele<br>ES - Mycobacterium leprae<br>Tium ieprae<br>revision 03-Feb-1994 *text_chanse<br>e. S.: Osland, A.: Mike, T.L.: Hormans,<br>n. D.: Drijfhout, J.: Schoeningh. R.:<br>6.1995-2007<br>Wo groel genes: the second<br>groel gene is arranged in an operon<br>groel gene is arranged in an operon<br>the Library, November 1993<br>Osmid B229.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | uced protein<br>uced protein<br>rweight 10800 #checksum 7352<br>114: DB 2; Length 150;<br>No. 1.72e-06;<br>ismatches 0; Indels 0: Gaps 0; |
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#authors Shinnick, T.M.; Plikaytis, B.B.; Hyche, A.D.; van Landingham, R.M.; Waiker, L.L.
#journal Nucleic Acids Res. (1989) 17:1254
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#cross-references MJD:89160258
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 #authors Mehra, V.; Bloom, B.R.; Bajardi, A.C.; Grisso, C.L.; Stelli P.A.; Alland, D.; Convit, J.; Fan, X.; Bunter, S.W.; Frennan, P.J.; Rea, T.B.; Modlin, R.L.; Bunter, S.W.; ajournal, J. Exp. Med. (1992) 175-275-284
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 #authors Baird, P.N.; Hail, L.M.C.; Coates, A.R.M.
#journal J. Gen. M.:rrobiol. (1989) 135:931-939
#title Cloning and sequence analysis of the 10 KDa antigen gene of Mycobacterium tuberculosis.
#cross-references MulD:90095443
#accession A37166
 BUNYBA #type complete chapter.
Chaperonic großs - Mycobacterium tuberculosis
10K antigen: Bada immodia; CpnIC; heat shock protein 10K
(NspIO): immodiaentc protein BrG:a
#formal_name Mycobacterium tuberculosis
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16-521-1999 #scquence_revision 31-Dec-1990 #text_change
 10K Treell anticen - Mycobacterium leprae
*!ormal_name Mycobacterium leprae
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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 *accession SCI38.

**molecule_type DNA

**residues

**eross_reference EMBL:X12598: NID:q44551; PID:q581358

**EFFENCE
 nucleic acid sequence not shown
 ##rcsidues V.2-100 ##labcl BA2 ##cross-references GB:M25258; GB:X12598
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Rest Local Similarity 100.0%;
Matches 17; Conservative
 ##molecule_type DNA
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 TITLE
ALTERNATE_NAMES
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 ##Status
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 PRCANISM
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DATE
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Fauthors Cole, S.1.; Brosch, R.; Paikhill, J.; Garnier, I.; Thurcher, C.; Harris, D.; Gordon, S.V.; Englmeter, K.; Gas, S.; Barry, III, C.E.; Tekaia, F.; Haddoock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Conor, R.; Basham, D.; Brown, D.; Privell, T.; Gentles, S.; Hamilo, N.; Holroyd, S.; Frivell, T.; Gentles, S.; Hamilo, N.; Holroyd, S.; Hurshy, L.; Jagels, K.; Krogh, A.; Notean, J.; Monie, S.; Murphy, L.; Dilver, S.; Geborne, J.; Quail, M.A.; Rogers, J.; Rutter, S.; Seever, K.; Sajardom, M.A.; Rogers, J.; Rutter, S.; Seever, K.; Sajardom, M.A.; Rogers, J.; Rutter, S.; Seever, K.; Sajardom, M.A.; Rogers, J.; Barrell, B.G.; Siston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Siston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Libercolosis from the complete genome sequence.
##molecule_type DNA
##residues 1-160 ##!abel SH:
##cross-references EMBL:X13739: NID:q44571; PIDN:CAA32503.1: PIL:G581460
ENCE A47292
 **residues 1-100 **label KON
***residues EMBL:X60350; NID:044599; PIDN:CAA42908.]; PIL:USB1363
***note sequence extracted from NCB1 backbone (NCB1N:)_L450E;
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ATP; heat shock: molecular chaperone; stress induced protein
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 *product char ronin groES *status experimental *label
 sequence extracted from NOBI backbone (NOBIP:87128)
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 Proc. Natl. Acad. Sci. U.S.A. (1994) 90:26:39-24:2
Mycobacterium tuberculosis expresses two chaperminn
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 Score 114; DB 1; Length 100;
Pred. No. 1.72e-06;
0; Mismatches 0; Indels
 functional chaperonin includes 14 chains of
 #length 100 *molecular-weight 10804
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 84 EEYLILSARDVLAVVSK 100
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#domain signal sequence #status predicted #label SIS\
#product major allergen Cry] I (clone pCCI-15) #status
predicted *label MAI\
#binding_site carbohydrate (Asn) (covalent) #status
 JC2124 *type complete major allergen Cry j I precursor (clone pCC:-15) · Japanese
 **Recording to the state of the
 Mazodier, P., Gaglielmi, G.: Davies, J.: Thompson, T. J. Bacterioi, (1991) 173-7392-7386
Characterization of the groEL-like genes in Streptomycos
 #formal_name Cryptomeria japonica #common_name Japanese
14-Jal-1994 #scquence_revision 14-Jul-1994 #text_change
26-Aug-1999
 heat shock protein 18 - Streptomyces albus
heat shock protein groES homolog
*formal_name Streptomyces albus
17-Jul-1992 sequence_revision 17-Jul-1992 *text_change
12-Sep-1997
 Fauthors Sone, T.: Kon ma, N.: Shimizu, K.: Kusakabe, T.: Kauthors K.: Kino, K. Kille Biochem. Biochem. Biophys. Res. Commun. (1994) 199:t19-625 #title Cloning and sequencing of chNA coding for Cry : I. allergen of Japanese cedar Pollen.
 *Superfamily chaperonin groES *Robecks.m* *length 102 *molecular-weight 10955 *checks.m*
 predicted
#length 374 #molecular-weight 40702 #checksum
 Length 142
 S ore 98; DB 2; Length 374;
Pred. No. 1.00e-03;
1; Mismatches 1; Indels
 Score 103; DB 2; Le
Pred. No. 1.43e-04;
3; Mismatches 1;
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 glycoprotein: pollen
 *cross-references MUID:92041639
 Best Local Similarity 86.7%;
Matches 13; Constant
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 86 EEYLVLSARDVLAIIEK 132
 232 KSMKVTVAFNQFGPN 246
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**molecule_type mRNA
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 158, 191, 293, 354
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 submitted to the EMBL Data Library, Soptember 1993
Milecular characterization of two grobi genes in Streptomyces
Graficolor A3(2).
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 $72818 *type complete heat Shock protein chaptae heat Shock protein chp4 - Mycobacteri m leprae chaperonin . 10%; protein B1620_C3_227 *formal_name Mycobacterium leprae 19-mar-1997 *sequence_revision 25-Apr-1997 *text_change $72818
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 #type complete chapters coefficient and profit and streptomyces coefficient aronal chapter of complete formal name Streptomyces coefficient of Jan-1995 *sequence_revision 06-Jan-1999 *text_change 26-Aug-1999
 **rosidues 1-169 **'abel SMI
**cross-references EMEL:U00015; NID:g466931; PIDN:AAC43227.1;
PID:g466939
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Duchene, A.M.: Kieser, K.: Hopwood, D.: Thompson,
Mazodier, P.
 ;
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 Smith, D.R.: Robison, K
submitted to the EMBL Data Library, November 1993
 chpA superfamily chaperonin groES heat shock; molecular chaperone; stress-induced *iength 169 *molecular-weight 18097 *checksum
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PID:9809756
 *superfamily chaperonin groES heat shock: molecular chaperone; stress-induced *length i02 *molecular-weight 10946 *checksum
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 Mycobacterium leprae cosmid Bi620 S72818
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 Query Match
Best Local Similarity 100.0%:
 Query Match
Best Local Similarity 92.4%;
Matches 14; Conservative
 153 EEYLILSARDVLAVVSK 169
 86 EEYLVLSARDVLAIVEK 132
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 1 SEYLILSARDVLAVVSK 17
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 **residues 1-242 **!abel GAR
**cross-references GB:AE001377; GB:AE001362; NID:q3845111; PID:g3845112;
TIGR:PFB016GW
 #formal_name Cryptomeria japonica #common_name Japanese cedar
14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
26-Aug-1999
 #auchors Arador M.J. Tettelin, B./ Carucol D.C./ Cummings D.M., Arauthors Aravind L. Koolin E.V. Shallom S. Mason, T. Yu. K., Fully D. C., Pederson J. Shan, K. Jing, J. Aston, C., Lai, Z. Schautz, D.C.; Pettea, M.: Salzberg, S.: Zhou, L., Sutton, G.G.; Clayton, R.: White, O.; Smith, B.D.: Fraser, C.M. Adams, M.D.; Venter, J.C.; Hoffman, S.C. stille C.M. Adams, M.D.; Venter, J.C.; Hoffman, J.C.; Hoffman, S.C. stille C.M. Adams, M.D.; Venter, J.C.; Hoffman, J.C.; Ho
 22-53;58-81;219-232;236-258;299-307;346-372 ##label S02
the authors described carbohydrate binding site for
residue 279
major allergen Cry ; I precursor (clone pCCI-2-2) - Japanese
 ö
 #journal Biochem, Biophys, Res. Commun. (1994) 199:619-625
#title Cloning and sequencing of CDNA coding for Cry 1. a major allergen of Japanese cedar polich.
#Cross-references MUID:9418:234
 4 *binding_site carbohydrate (Asn) (covalent) *status
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*.ength 374 *molecular weight 40645 *checksum 2920
 Sdeb
 *checksum 9994
 Sone, T.: Komiyama, N.: Shimizu, K.: Kusakabe, T.:
K.: Kino, K.
 preliminary; nucleic acid sequence not shown;
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 Score 98: DB 2: Length 3:4:
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''.....rrees 1: Indels
 PFB0166w
#length 242 | #molecular-weight 28287
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alycoprotein: pollen
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 ##experimental_source poller
cession PC2065
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 6661-8EW-20
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**cross-references EMBL:X05925; NID:q48021; PIDN:CAA29361.1; PID:q48023
X functional chaperonin includes 14 chains of groEL and 7 of
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 synthase
 #100856 #type_complete
pectate_lyase (EC 4.2.2.2) 120F6.14 - Arabidopsis_trailann
#formal_name_Atabidopsis_thaliana #common_same_no.sev.vai
 Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.D.,
Brandon, R.C.; Sykos, S.M.; Kaul, S.; Mason, T.N.;
Kerlayage, A.R.; Adams, M.D.; Somerville, C.R.; Vorter,
 EVYGOS Figer megichio
chaperunia areks - Symethereneus spo (Sirain Hell 6-01)
heat shock protein lik (Mspig)
*formal_name Synchococcus sp.
30-Sep-1991 *sequence_revision 30-Sep-1991 *text_chance
16-Jul-1999 $
 Gatis
 :ence_revision 12-Feb-1999 *text_counce
 Fauthors Cozens, A.L.; Walker, J.E.
Fjournal J. Mol. B.ol. (1987) 194:359-383
Filtle The organization and Sequence of the genes for ATP systematics in the cyanobacterium Synechococcus 6301.
For an endosymbiotic origin of chloroplasts.
 1-455 ##label RCU
es EMBLIACO14/11: NID:q2947056: PIEN:AAC05/50.1.
PID:q2947 /
 .
ب
 *molecular-weight 51257 *checksur
 submitted to the 2.73. Data Library, March 1948 Arabidopsis thallatu chromosome II BAC 120FF 90
 Length 455:
 8: Mismatches 11: Indels
 Length 242
 mediates protein folding and renaturation
 Score 84, DB 2; Le Pred, No. 1.80e-01; 11: Mismatches 6
 cred No. 4.27e-02;
 translated from GB/SMH1/DDBJ
 *Superfamily pent to lysse LAIS9 carbon-daygen lysse *length 455 *molecular.weight 51
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 1 EEYLILSARDVLAVVSKRRMKV;VAFNÇFGPN 32
 **experimental_source cultiva Columbia
 294 DEVMLFGGTNK-DVIDKK-MQITVAFNHFG 321
 1 BEYLILSARDVLAVVSKRRKVINAFNOFS +0
 1-103 **label COZ
 66/2: 295/3: 375/3
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12-Feb-1999 #s
 37.0%;
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nes 11: Conservative
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 29-Sep-1999
TCC856
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T00856
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 ö
ATP: heat shock: molecular chaperone; stress-induced protein
 ö
 *authors Webb, R.: Reddy, K.J.; Sherman, L.A.

*journal J. Bacteriol. (1990) 172:5075-5086

*Litle Redulation and sequence of the Synechococcus sp. strain PCC 7942 groESL opercn. encoding a cyanobacterial chaperonin.

*cross-references MUD:90368561

*accession A36721
 *product chaperonin groES *status predicted *label MAT *length 103 *molecular-weight 1001 ...
 Turmel, M.; Lemieux, C.; Burger, G.; Lang, B.F.; Otis, C.; Plante, I.; Gray, M.W. Submitted to the EMBL Data Library, December 1998
The complete mitochondrial DNA sequences of Nephroselmis olivacea and Pedinomonas minor; two radically different
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 *
Pedinorocas minor mitochordrion (SGC3)
#formal_name mitochondrion Pedinomonas minor
15-011-1999 #sequence_revision 15-Jul-1999 #text_change
13-Aug-1999
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 A36721 *type complete gross sp. (strain PCC 7942) gross protein - Synechococcus sp. (strain PCC 7942) *formal_name Synechococcus sp. 12-Apr-1991 *sequence_revision :2-Apr-:991 *text_change_26-Aug-:999
 *Superfamily NADH dehydrogenase (ubiquinone) chain l
mitochondrion; NAD; oxidoreductase
*length 310 *molecular-weight 34938 *checksum 2458
 3
 *Superfamily chaperonin großs
*Length 103 *molecular-weigh: 10742 *checksum
 evolutionary patterns within the green algae
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 Score 80: DF 2: Length 103: Pred. No. 7.3le-Gi: 7: Mismatches 1: Indels
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Wolff, G.: Plante T.: Lang, B.F.: Kucck, J.: Burser, S. J. Mol. Bol. (2.) 237755-5-6 Complete Sequence of the nitochondrial DNA of the chlorophyte alga Protothera Wickerhamii, Gene content and accume
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 0
 BVMY7B *type mplete
chapercoin großs Mycutacterium bovis
heat shock protein, 19K (hepi8): immunogenic protein MPB57
*formal_name Mycubacterium bovis
11-Amr-1991 *sequence_revision 31-Mar-1991 *text_change
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 A69278
Fifis, T.; Costopculos, C.; Radford, A.J.; Bacic, A.; Kood,
 Ill938 *type complete
NACH dehydrogensew (dbigainone) (EC 1.6.5.1) chain ;
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 *Superfamily NACH dehydrogenase (ubiquinone) chaim imitochondrion: NAD: cxidoreductase alength 328 *molecular-weight 35437 *checksum 9332
 <u>:</u>
 ##residues 1.328 ##lare! WCL ##cross.references EMBL:002970: NID:g467843: PID:g467870: PID:g467870: ##experimental_source strain 263-11
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 Length 310:
 v Match 35.2%; Score 80; DB 2; Length 328 Local Similarity 33.3%; Pred. No. 7.31e-61; no. 7.31e-61; local Similarity 8; Mismatches 11; Indels Nes 10; Conservative 8; Mismatches 11; Indels
 8; Indels
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Pred. No. 7.31e-01;
Mismatches 8
 Infect. Immun. (1991) 59:800-807
 25 FLVLAERKVLASMQRRKGPNVVG11-1FQP 54
 3 YLILSARDVLAVVSKRR-MKV;VAFV;FGP 31
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxfo d Molecular Ltd

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protein - protein database search, using Smith-Waterman algorithm

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(1-32) from USO9142524A.pep 227 ot generated. debular cutput Description: Perfect Score: : Je :

1 EEYLILSARDVLAVVSKRRMKVTVAFNOFGPN 32 sednentes:

83857 seqs, 30454973 residues PAM 150 Gap 11 Searched:

Scoring table:

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swiss-prot38 Database

Statistics:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 35.264; Variance 53.818; scale 0.655

7.32e-01 1.05e+00 1.05e+00 1.54e+00 1.54e+00 Pred No 10 KD CHAPERCNIN (PROT 10 KD CHAPERCNIN (PROT 10 KD CHAPERCNIN (PROT 10 KD CHAPERONIN (PROT) Description SUMMARIES a Suery Match Length DP ഷക്ഷയയയയയയയയയയയയയയയയയയ (രേഖയസ്സസ്ക്കക്ക്ക്യയയയയയയയയ (യെക്ക്വ്വ്വ്യത്തക്ക്ക്സ്സ്സ്റ്റ്ര്ര്ദ് Score 

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| WPRA_BACSU<br>EPB5_HUMAN<br>CH10_THEBR<br>RELA_STRAT                                                                         | 9612_LYCES<br>PEL_LILLO<br>MFC_MYXXA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | VMF_BCMAN<br>CH10_LACLA<br>YH97_METTH                                                       | PSSK_HCKVC<br>NUIM_CHOCK<br>PES6_LYCES<br>RELB_MCUSE | YE22_YEAST<br>NIFV_FRAAL<br>HEM1_CHLVI                       | RELETHUMAN<br>GLSZ_YEAST<br>VWF_CANFA                                     |
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#### ALIGNMENTS

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Baird P.N., Hall L.M., Coates A.R.M.;
"A major actigen from Mycobacterium tubercolosis which is homolous to the heat shock proteins gross from E. coli and the httpA grown product of Coxiella burnet.";
Notleto Acids Res. 181904779047(1988).
 STRAIN*ERDMANN:
MEDLINE: 93219332.
KONG T.H., Coates AR.M., Butcher P.D., Hickman C.J., Shinnick T.M.:
Mycobacterium tuberculosis expresses two chaperonin-60 homologs.";
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 01-MAR-1989 (Rel. 10, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
16-CRAPERONIN (PROTEIN CPNIO) (PROTEIN GROES) (BUG-A HEAISELTK PROTEIN) (10 KD ANTIGEN)
MOPB OR GROES OR CRNIO CR RV3418C OR MTCY78.11.
Mycobacterium tubercuiosis
Bacteria: Firmicutes; Actinobacteria: Actinobacteridee: Actinomycetales: Corynebacte..oeau: Myrobacterideeae: Mycubalterium.
 "The M cobacterium tuberculosis BrG-a protein has homology with Escherichia coil GroES prote n.";
Nucleic Acids Res. 17:1254-1.54(1999),
 MEDLINE: 89160258.
Shinnick T.M., Plikaytis B.P., Hyche A.D., van Landingham R.M..
Walker L.L.:
 SIBAIN-HBTRV: MEDLINE: 98095443.
Baird P.N., Hall L.M.C., Coates A.K.M.
"Cloning and sequence analysis of the 10 kDa antiden gene of
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 56
 Mycobacterium tuberculosis.":
J. Gen. Microbiol. 135:931-939(1989).
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 89016584.
 SEQUENCE PROM N.A.
 STRAIN-ERDMANN:
1
CH10_MYCTU
PC9621;
01-M1
 STRAIN-H37RV
MEDLINE; 890
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Match
Local Similarity 100.0%;
les 17: Conservative
 83 EEYLILSARDVLAVVSK 99
 1 EEYLILSARDVLAVVSK 17
 Science 271:203-207(1996)
 SEQUENCE FROM N.A.
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 [6]
SEGUENCE OF 1-15.
MEDLINE, 92176646.
Barces P.E., Mohra V., Rivoire B., Fong S.J., Brennan P.J.,
Barces P.E., Mohra V., Rivoire B., Fong S.J., Brennan P.J.,
Voeqiline M.S., Minden P., Houghten R.A., B.Com B.R., Modiln R.L.,
Voeqiline M.S., Minden P., Houghten C. Mycobacterium tuberculosis.";
"Immunoreactivity of a 10-7480 antigen of Mycobacterium tuberculosis.";
"Immunol. 148:1835-1840(1992).
"Immunol. 148:1835-1840(1992)."
STRAIN-H37RV)

MCDLINE; 96395987.

MCDLINE; 96395987.

MCDLINE; 96395987.

MCDLINE; 11: Tekala F.,

Gordon S.V., Elgimeier K., Gas S., Barry C.E. III; Tekala F.,

BAGGOCK K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devilt K., Kelterli I., Genties S., Hamin N., Holroyd S.,

Hornsky T., Jauels K., Kroph A., McLean J., Moule S., Murphy L.,

Oliver S., Sebore J., Quali M.A., Rajandream M.A., Rogers J.,

Rutter S., Sepore S., Darrell B.G., Raylors S., Sqares R., Sulston J.E.,

Taylor K., Whitched S., Barrell B.G., Raylors S., Sqares R., Salston J.E.,

Tockithering the biology of Mycobacterium tuberculosis from the

Complete genome beginning Mycobacterium tuberculosis from the

Nature 393:637-544(1998).
 Gaps
 Actinomycetales: Corynebacterineae: Mycobacteriaceae: Mycobacterium
 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
10 kD CHAPERONIN (PROTEIN CPNIO) (PROTEIN GROES) (10 KD ANTIGEN).
MORD OR GROES OR CHPA OR B1620_C3_227 OR B229_C3_247.
 Ö
 Lendth 493
 Score 114: DB 1: Length 98:
Pred. No. 7:(7e-98:
0: Mismatches 0: Indels
 Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
 11- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY
 0 0 99 AAJ 17673 MW: 1001288750919AR7 CR0643
 99 AA
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-24. MEDLINE: 9.113469.
 PIR: 502727: WWNYBA.
PIR: A37166: A37166.
PIR: A47292. A47292.
PRINTS: PRO0297: CHAPERCNING_CPNIO:
PROSITE: PS0681: CHAPERCNING_CPNIO:
 79.8.T.;
 Chaperone: Anticen: Heat shock.
INIT_MET 0
 EMBL: X60.50; CAA42908.1;
EMBL: X12588: CAA3111.1;
EMBL: M35258: AA25340.1;
EMBL: X13759: CAA3203.1;
EMBL: Z77165: CAE01005.1;
 Match
Local Similarity 188.0%:
 17: Conservative
 83 SEYLILSARDVLAVVSK 99
 1 EEYLILSAROVLAVVSK 17
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 PFAM: PF00166:
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 ERRATUM.

Mande S.C., Mehra V., Bloom B.R., Hol W.G.J.:
Science 21:1655-1655(1996).
Science 21:1655-1655(1996).
I- FUNCTION: BINDS TO CPM60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES THE AIPASE ACTIVITY OF THE LATTER.
SUBJUIT: HEPPAMER OF 7 SUBUNITS ARRANGED IN A MINS.
--- SUBJUIT: BELONGS TO THE GROES CHAPERONIN FAMILY.
Mehra V.L., Bloom B.R., Bajardi A.C., Grisso A.C., Steling P.A., Alland D., Convit J., Fan X., Binter S.W., Brennen P.J., Rea T.B. Modlin R.L.:
"A major I cell antigen of Mycobacterium leptae is a 10-kD heat-shook cognate protein."
 MEDLINE: 96138402.
Mande S.C., Mehra V., Bloom B.F., Hol W.G.J.,
"Structire of the heat shock protein chaperonia-lu of Myrchacter:.m
leprae.":
 Sir
 CHIC_MYCAV STANDARD; PRI; 99 AA.
0850.17.
0850.17.
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last sequence update)
16-FEB-2000 (Rel. 39, Last annotation update)
11 CKD CHAPERONIN (PROTEIN CPNIS) (PROTEIN GROES) (10 KD ANTIGEN).
 "Mycobacteria contain two großt genes: the second Mycobanterium leprae großt gene is arranded in an operon with droßs.".
Mol. Microbiol. 6:1995-2007(1992).
 Hermans P W.K
 ..
ت
 MEDLINE: 92374850.
de Wit T.F.R., Bekelie S., Osland A., Miko I.L., Hermans P W
van Soolingen D., Drijthout J., Schweningh R., Janson A.A.M.
 Score 114; DB 1; Lengu...

No. 7.07e-08;
A No. 7.07e-08;
 Smith D.R., Robison K.; Submitted (MAR-1994) to the EMSL/GenBank/DNBJ databases
 99 AA; 10669 MW; 6028BB9833F7FDEB CRC64;
 PFAM: PF00166; cpnl0: 1.
Chaperone; Antigen; Heat shock: 3D-structure.
 EMBL, X59413: -; NOT_ANNOTATEL_CDS.
EMBL, 211665: -; NOT_ANNOTATEL_CDS.
EMBL, 300015: AAC4227.1; -; EMBL, 300015: AAC4227.1; -; EMBL, 3100015: AAC4227.1; -; EMBL, 3100015: AAC4227.1; -; EMBL, 3100015: JUSSE CONTROL SETTING TO THE SETTING TO THE SETTING THE S
 X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
 Exp. Med. 175:275-284(1992)
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SPECIES-S.COELICOLOR; STR.
 CH10_STRAL
Q00759:
 SECHENCE
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SPECIES-M.AVIJM: STRAIN-485 TYPE 21:

SPECIES-M.AVIJM: STRAIN-485 TYPE 21:

Creti R., Pietrobone R., Fattorini L., Orefici G.:

Sequence of the GroESL operon of Mycobacterium avium comprising the

Sequence of the GroESL operon of Mycobacterium avium comprising the

gene encoding the cpalo protein and a portion of the gene encoding the
 SECUENCE FROM N.A. SPEALN-A3(2) / J1501;
MEDLINE: 94299177.
DUCKERS A.M., Kleser H.M., Hopwood D.A., Thompson C.J., Mazodler P.;
"Characterization of two grobl genes in Streptomyces coelicolor
 paratuberculosis.")
Vet. Microbiol. 0:0-0(1999).
-i- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESS
THE ATPASE ACTIVITY OF THE LATTER (BY SIMILARITY).
-i- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A KING (BY
 Gaps
 SPECIES+M.PARATUBERCULOSIS, M.AVIUM. SIRAIN-AICC 19698, AICC 25291.
CObb A.J., Frothingham R.:
The Grobs antiquens of Mycobacterium avium and Mycobacterium
paratuparentosis ...
 Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
 GROES OR SC6G4.39.
Streptomyces coelicolor, and Streptomyces lividans.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
Actinomycetales: Streptomycineae: Streptomyces.
 0;
 Score 114: DB 1: Length 99:
Pred. No. 7.07e+08:
0: Mismatches C. Indels
 Mycobacterium avium, and Mycobacterium paratuberculosis.
 cpn60-1 proteis.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 ... SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY
 680A449740531002 CRC64;
 HESULT 4 TANDARD: PRT: 102 AA. AC. PR. 102 AA. AC. AC. PAGE 19. STANDARD: PRT: 102 AA. AC. PAGE 19. C. PROTEIN GROES).
 EMBL. AF079544: AACT1921.1:
EMBL. AF071829: AAD23277.1:
FRAL. AF071829: AAD23276.1;
FRAL. PFC0166: CPD10: 1
PRIN'S: PR00297: CHAPERONINO.
PROSITE: PS00801: CHAPERONINS_CPN10: 1.
CHAPETONE: ATL1960: Heat Shock.
INITAMES 99 AA: 10617 MW: 680A44974053
 BY SIM: LARITY
 Guery Match 50.2%;
Sest Local Similarity 100.0%;
Matches 17; Conservative
 83 EEYLLISARDVLAVVSK 99
 | EEXTILSARDVLAVVSK 10
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 ·.
 Mazodier P., Guglielmi G., Davies J., Thompson C.J.;
"Characterization of the groEL-like genes in Streptomyces albus.";
J. Bacteriol. 173:7382-7386(1991).
-:- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES
 Sapp
 Saunders D., Harris D., Parkhill J., Barrell B.G., Rajandrean M.A.
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 Actinomycetales: Streptomycineae: Streptomycetaceae: Streptomyces
 ë
 SEQUENCE FROM N.A.
SPECIES-S.LIVIDANS;
BOLINE: 99046461.
de Leon P., Marco S., Isiegas C., Marina A., Carrascosa J.L.
Mellado R.P.;
 Score 105: DB 1: Length 192:
:red. No. 4.32e-05:
 1: Indels
 THE ATPASE ACTIVITY OF THE LATTER.

SUBCULT: HEPTPAMER OF 7 SUBUNITS ARRANGED IN A RING (BY SIMILARITY).

SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 SUPCERTY (BY SIMILARITY).

-! SIMILARITY: BELONGS 7. HE GROES CHAPERONIN FAMILY.
 Streptomyces albus G.
Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
 102 AA: 10945 MW: 60F9FA68014AC800 CR064:
 01-APR-1993 (Rel. 25. Greated)
01-APR-1993 (Rel. 25. Great seq)
01-REB-1996 (Rel. 3) Lest seminatation update)
10 KB CHAPERONIN (PROTEIN CHALL) (PROTEIN CHALL)
 2: Mismatches
 102 AA
 EMBL: X75206; CAA53018.1; ---
EMBL; AL031317; CAA20417.1; --
EMBL; X95970; CAA65224.1; ---
PIR: S37565; S37565, S37565, PRINTS: PRO0297; CHAPERONIN. '
PROSITE; PS00681; CHAPERONIN. '
PROSITE; PS00681; CHAPERONIN. '
PROMI
 581 ·
!-A3(2);
 Ouery Match
Best Local Similarity 82.4%;
Matches 14; Conservative
 86 EEYLVLSARDVLAIVEK 102
 1111::11111 i:1 :
1 EEYLILSARDVLAVVSK 17
 STANDARD
 SEQUENCE FROM N.A. MEDLINE, 92041639.
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374 AA:
 MEDLINE; 96064154.
 SEQUENCE FROM N.A.
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 SECUENCE OF 1-23
 STRAIN=HB8;
 STRAIN-HB8
 Allergen:
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SUB_COTATA STANDARD: PRI: 374 AA.

SUB_COTATA
PUBS 32.

OI NOV-1990 (Rel. 16, Greated)
DI 10-NOV-1995 (Rel. 32, Last sequence update)
DI 10-NOV-1998 (Rel. 37, Last sequence update)
SUSI BASIC PROTEIN PRECERSOR (SBP) (MAJOR ALLERGEN CRY J 1) (CRY J 1).
SUSI BASIC PROTEIN PRECERSOR (SBP) (MAJOR ALLERGEN CRY J 1) (CRY J 1).
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SUSI BASIC PROTEIN PRECERSOR (SBP) (MAJOR ALLERGEN CRY J 1).
SUSING SUS
 **Antiquity of the olidosaccharide moiety of the Japanese cedar (Cryptomeria japonica) pollen allergeme, cry jl.*;

(Cryptomeria japonica) pollen allergem, cry jl.*;

(Int. Arch. Allergy Immunol. 105:198-202(1994).

(Int. Arch. Allergy Immunol. 105:108-202(1994).

(Int. Arch. Allergy Immunol. 105:108-202(1994).

(Int. Arch. Allergy Immunol. 105:108-202(1094).

(Int. Arch. Aller
 "N-terminal units acid sequence of a major alleraem of Japanese ordar
 Some T., Komiyama N., Shimizu K., Kusakabe T., Morikubo K., Kibo K., Clouing and sequencing of CDNA coding for Cry j I, a major allergen of Japanese cedar pollen."

Biochem. Biophys. Res. Commun. 199:619-628(1994).
 Gaps
 MEDLINE: 89031257.
Tabiai M., Addo S., Osu: M., Kurimoto M., Sakaqueh: M., Inouye S.
 .
;
 ARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1. I/AMB A 11/CRY J I SUBFAMILY.
 Lengt: 102;
 1; Indels
 Namba M., Kurose M., Torisco K., Fukuda S., Kurinoto M.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
 102 AA, 10987 MW: 5788F55954CFB283 CRC64;
 Score 103; DB 1; I
Pred. No. 1.05e-05;
3; Mismatches 1;
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
 or send an email to incense (isb-sib.ch).
 EMBL; M76657; AAA26752.1; -;
PRINTS: PR06297; CHAPERONINSO.
PROSITE; PS00681; CHAPERONINS_CPN10; 1.
 FEBS Lett. 254:329-332(1988).
 Guery Match
Fest Local Similarity 76,5%:
Matches 13, Conservative
 86 FEYLVLSARDVLAITEK 102
 faxodiaceae; Cryptomeria
 PROSITE, PSCO681; CHAPER
PFAM: PFSC166; cpn10: 1.
 SEQUENCE FROM N.A. TISSUE POLLEN
 CARBOHYDRATES.
MEDLINE; 95003748.
 MEDLINE: 94183234
 SEQUENCE OF 22-41
 SIMILARITY:
 ISSUE=POLLEN
 LISSUE-POLLEN
 pollen (Cry
 Chaperone.
 AMB A
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 MEDLINE: 92642183.

MEDLINE: 92642183.

Taguchi H., Konishi J., Ishii N., Yoshida M.;

"A chaperonin from a thermophilic bacterium, Thermus thermophil.s.

In that controls refoldings of several thermophilic enzymes.";

J. Biol. Chem. 266:22411-22418(1891).

I Biol. Chem. 266:22411.

I Biol. Chem. 26
 "Molecular cloping, expression, and characterization of chapteroxinof; and Coaperomic Linearias thermus the coaperoxinos are considered.
 Saps
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 Amada K., Yohda M., Odaka M. Endo I., Ishii N., Taquchi H.,
Yoshida M.;
 ophilus).
roup: Thermus group: Thermus
 Score 98: UB 1: Length 374: Pred. No. 9.54e-05: 1: Mismatches 1: Indels
 Erbeznik M., Joachimiak A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
 -! SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 PCTENTIAL.
74AB25950248F56F CRC64.
 SUGI BASIC PR. IEIN.
L > F (1N CRY J 18).
H > Y (1N CRY J 18).
S > 1 (1N CRY J 18).
L > S (1N CRY J 18).
C > H (1N CRY J 18).
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POTENTIAL.
POTENTIAL.
 CHIO_THETH STANDARD; PRT; 136 AA.
P45747; 0506017.
01-00V-1995 (Rel. 32. Created)
01-FEB-1996 (Rel. 33. Last selicated update)
01-NOV-1997 (Rel. 35. Last an itation update)
10 kD CHAPPRONIN (PROTEIN GPN.) (PROTEIN GROES).
 00544: pec_lyase: 1.
PR00807: AMBALLERGEN
:: Glycoprotein: Multigene family: Signal.
or send an email to license@isb-sib.ch).
 EMBL: D26544; BAA05542.1; -.
EMBL: D26545; BAAC5543.1; -.
EMBL: D34639; BAA7020.1; -.
PTA: 444773, A44773.
PFAM: PF00644; Pec_1yase: 1.
PRINTS: PR00807; AMBALLERGEN
 40645 MW.
 Bacteria: Thermus/Deinococcu
 aquaticus (subsp. th
 Query Match
Best Local Similarity 86.7%;
 Blochem. 118:347 354(1
 Conservative
 232 KSMKVTVAFNÇFGPN 246
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 Nucleic Acids Res. 17:6392-6392(1969).
-:- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES
THE ATPASE ACTIVITY OF THE LATTER.
-:- SCHUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING
(BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 synthase subunits
 Saps
 SIMILARITY TO CHAPERONINS.
MEDLINE: 89365672.
COOKSON M.J., Baird P.N., Hall L.M., Coates A.R.M.,
Identification of two unknows reading frames in Synerhococcus 5331
as homologues of the 1th and 65x antigen genes of Mycowacterius
tuberculosis and related heat shock genes in E. coll and Coxiella
 ..
 Score 86: DN 1: Length 100;
Pred. No. 1.60e-01;
3: Mismatches 1: Indels
 Cozens A.L., Walker J.E.;
The organization and sequence of the genes for AIP synt)
in the cyanobacterium Synechococcus 6301. Support for an
 19 R -> K (IN REF. 3).
83 86 DGEE -> APRRT (IN REF. 2).
100 AA: 10865 MW: 452F3DD9CCCBC0FA CRC64;
 103 AA; 10811 MW; FFEDIDESF515952F CRC64;
 Synechococcus sp. (strain PCC 5301).
Bacteria: Cyanobacteria: Chroococcales: Synechococcus.
 01-403-1988 (Rel. 08, Created)
01-803-1988 (Rel. 08, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
10 KD CHAPERRONIN (PROTEIN CPNIO) (PROTEIN GROES)
 103 AA
 endosymbiotic crigin of chloroplasts.";
J. Mol. Biol. 194:359-383(1987).
 EMBL: 045880; BAA08298.1; -.
EMBL: 029483; AAA83440.1; -.
PIR: B39313; B39313.
PRINTS; PR00297; CHAPERONING.
PROSITE: PS00683; CHAPERONINS_CPNIO; 1.
PFAM: PF00166; cpol0; 1.
 PIR: SIC836; BVYCGS.
PRINTS: PROD257; CHAPERCNINIG.
PROSITE: PSO3681: CHAPERONINS_CPNIG: 1.
PFAM: PF00166; cpn16: 1.
 PRT:
 EMBL: X05925: CAA29361.1: -.
 35.28;
73.38;
 Ouery Match
Best Local Similarity 73.3%;
These 11: Conservative
 STANDARD:
 85 EEYVILSERDLLAVL 99
 : EEVILLSARDVLAVV 15
 SEQUENCE FROM N.A
 873117.3
 CH10_SYNP6
P07889:
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 Webb R., Reddy K.J., Sherman L.A.;
"Regulation and Sequence of the Synechococcus sp. strain PCC 7942 großEL operan, encoding a cyanobacterial chaperonin.";
J. Bacterial, 172:5079-598(1990).
-i. FUNCTION: BINDS IO CPNEO, N THE PRESENCE OF MG-AIP AND SUFPRESSES
 01-APR-1990 (Rel. 14, Created)
01-ANG-1991 (Rel. 19, Last sequence update)
15-FEB-2000 (Rel. 19, Last annotation update)
10 KD CHAPERONIN (PROTEIN CPNIO) (PROTEIN GROES) (IMMUNOGENIC PROTEIN
 Actinomycetales: Corynebacterineae: Mycobacteriaceae; Mycobacterium
 Sans
 .;
 ö
 Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2)
Bacteria: Cyanobacteria: Chroococcales: Synechococcus.
 Scorpe No. 100 lt length live
Fred. No. 1 600-01;
7: Mismatches lt Indels
Score 80; DB 1; Length 103; Pred, No. 1.60e-01; 7; Mismatches 1; Indels
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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(BY SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY:
SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY:
 103 AA: 10742 MW, 893671958515952E CRC64.
 01-AUG-1991 (Rei. 19, Last sequence update)
01-FEB-1996 (Rei. 33, Last annotation update)
10 KD CHAPEKONIN (PROTEIN CPNI0) (PRUTEIN GROES).
 99 AA
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-20
 PIR: A36721; A36721;
PRINTS: PROCESTY; CHAPERONINIO.
PROSITE: PSCU661; CHAPERONINS_CPNIC: 1.
PFAM; PF00166; cpn10: 1.
 PRT:
 01-AUG-1991 (Rel. 19, Created)
 EMBL: M58751; AAA27313.1; -
 35.2%:
50.0%:
Query Match 35.2%;
Best Local Similarity 50.3%;
Matches 8; Conservative
 8: Conservative
 85 DDYVLLSEKDILAVVA 103
 88 DDYVLLSEKDILAVVA 103
 STANDARD;
 1 EEYLILSARDVLAVVS 16
 1 EEYLILSARDVLAVVS 16
 Mycobacterium bovis.
 query March
Best Local Similarity
 SEQUENCE FROM N.A
 90368561
 MOPB OR GROES.
 01-AUG-1991
 01-FEB-1996
 CH10_MYCBO
P15020;
 STRAIN-BCG;
 CH10_SYNP7
P22880;
 Chaperone.
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SEQUENCE FROM N.A.
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 MEDLINE: 93361018.
Flick J.S., Thorner J.W.;
"Genetic and biconemical characterization of a phosphatidylinositol-
"Spenitic phospholipase C in Saccharomyces cerevisiae.";
Mol. Cell. biol. 13:5861-5876(1993).
 SEQUENCE FROM N.A.
MEDINE: 93309469.
MEDINE: 93309469.
Payne W.E., Fitzgerald-Hayes M.;
Payne W.E., Fitzgerald-Hayes M.;
A mutation in Picl, a candidate phosphoinositide-specific
phospholipase C gene from Saccharomyces cerevisiae, causes aberrant
mitchic chromosome segregation.;
Moi. Cell. Biol. 13:4351-4364(1993).
 MEDLINE: 93189586.

YOKO-O I., Matsui V., Yaqisawa H., Nojima H., Ugo I., Toh-E A.;
"The putative phosphoinositide-specific phospholipase C gene, PLC1,
of the yeast Saccharomyes cerevisiae is important for cell growth.
Proc. Natl. Acad. Sci. U.S.A. 90:1864-1808(1993).
 Gaps
 Saccharomyces octevisiue (Buker's yeust).
Bukaryota: Pingi: Ascomynota: Saccharomycetes; Sachharomycetales;
Saccharomycetaceae: Saccharomyces.
 ö
 Yamaquchi R., Matsuo K., Yamazaki A., Nagai S., Terasaka K.,
 01-001-1993 (Rel. 27, Greated)
01-001-1993 (Rel. 27, Last Sequence update)
15-FEB-1200 (Rel. 39, Last annotation update)
15-PEB-1200 (Rel. 39, Last annotation update)
15-FEB-1200 (Rel. 39, Last annotation update)
16-0-014-113 (Rel. 1996) (Rel. 19
 2: Mismatches 0: Indels
 Score 79: 08 1: Length: 99:
Pred. No. 2.35e-01:
 99 AA: 10819 MW: 1DCDSE2199447AF7 CRC64;
 or send an email to license (isb-sib.ch)
 EMBL: X15970; CAA32149.1; -.
EMBL: X3589; AAA25365.1; -.
PIR: SQL784; BVYR-5
PRINTS; PROC297; CHAPERONINLO.
PROSITE: PSCU661; CHAPERONINS_CPN10: 1.
 PRT;
 PFAM: PF0166; cpn10; 1.
Chaperone: Activen: Heat shock.
 34.88;
 Guery Match
Rest local Similarity 84.5%.
Thosail Conservative
 STANDARD:
 83 EEYLILSARDVVG 95
 1 EEYLILSARDVLA 13
 SEQUENCE FROM N.A. MEDLINE: 93361018.
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 PLC1_YEAST
P32393;
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BY SIMILARITY.
T -> M (IN REF. 2).
A -> V (IN REF. 2).
A -> V (IN REF. 2).
A -> V (IN REF. 2).
MM: 13EE751259405E90 CRC64;
 Length 869
Delius H., Hebling U.;
Submitted (JUN-1996) to the EMIL/GenBank/DDBJ databases
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
10 KD CHAPERONIN (PROTEIN CPNIO) (PROTEIN GROES).
 Score 79: DB 1; L/
Pred: No. 2:35e-01;
 Mismatches
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 PERS A47557 A47257

PIR A48142; A48142

HSSP, P10688: 1D22

SGD: LG001448; PLC1.

PRINTS: PR00380; PHPHLIPASEC.

PROSITE: PS50004; C2_DOMAIN_2:

PROSITE: PS50004; C2_DOMAIN_2:

PROSITE: PS50009; PIPLC_X_DOMAIN: 1.

PRAM: PF00036; ef:add: 1.
 702 Y-VEKPKKELPVVTKAKM-IPLIYEHF 726
 3 YLILSARDVLAVVSKRRMKVTVAFNQF 29
 100547 MW:
 EMBL: D12738; BAAC2230.1; -. EMBL: L13036; AAA99927.1; -. EMBL: S63468; CAB32216.1; -. EMBL: Z73624; CAA98003.1; -. EMBL; Z73623; CAA98003.1; -.
 PF00387: PI-PLC-Y: 1.
PF00388: PI-PLC-X: 1.
 34.88;
29.68;
 Conservative
 STANDARD:
 Local Similarity
 869 AA:
 SEQUENCE FROM N.A.
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Matches
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 SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.

1. SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.

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 STRATN=LBSSS / PRINGSHEIM:
Stitewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,
Stitewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,
Submitted (CCT-1995) to the EMBL/GenBank/DDBJ databases.
-! FUCTION: SINDS TO CPN60 IN THE PRESENCE OF MC-AIP AND SUPPRESSES
-! FUCTION: BINDS TO CPN60 IN THE PRESENCE OF MC-AIP AND SUPPRESSES.
-! FUCTION: BINDS TO CPN60 IN THE PATER (BY SIMILARITY).
-! SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING
 SEQUENCE FROM N.A.
MEDLINE: 98094112.
Tanaka N. Hiyamat T. Nakamoto H.; Closhing, Characterization and functional analysis of groeSL operon Closhing, characterization and functional synchocous vulcanus.";
Biochim. Biophys. Acta 1243:335-348(1997).
I. FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-AIP AND SUPPRESSES THE ATPARE ACTIVITY OF THE LATTER.

OF SUBUNIT: HEPTAKER OF 7 SUBUNITS ARRANGED IN A RING (BY SIMILARITY).
 Gaps
 0
 Eukaryota: Glaucocystophyceae: Cyanophora-eae: Cyanophora
 Score 78: DB 1: Length 102: Pred, No. 3.44e-01: 7: Mismatches 1: Indels
 -!- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY
 BY SIMILARITY.
B7CC3617298BFF67 CRC64;
 Bacteria; Cyanobacteria; Chroococcales: Synechococcus
 01-NCV-1997 (Rel. 35, Created)
01-NCV-1997 (Rel. 35, Last sequence update)
01-NCV-1997 (Rel. 35, Last annotation update)
10 KD CHAPERONIN (PRUTEIN UPNIC) (PRUTEIN GROES)
 103 AA
 PRINTS: PRG0297; CHAPERONIN10.
PROSITE: PSG0681; CHAPERONINS_CPN10: 1.
PFAM: PF00156; cpn10: 1.
 PRI
 0 0 B'
102 AA: 10783 MW:
 EMBL: U30821: AAA81173.1; -
 Query Match
Best Local Similarity 50.0%:
Matches 8: Conservative
 87 EDYVLLSEKDILAIVG 102
 1 EEYLILSARDVLAVVS 16
 STANDARD;
 EMBL; D78139; BAA23816.
 Synechococcus vulcanus.
 GROES-A AND GROES-B.
 Cyanophera paradexa
 SEQUENCE FROM N.A.
 RESULT 13
1D CHIO_CYAPA
AC Q37761;
 Chaperone.
 SEQUENCE
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 -!- SIMIL RITY: BELONGS TO A FAMILY THAT GROUPS V-ATPASE SUBUNIT D. V-TYPE SODIUM ATPASE NIPD AND ARCHEAL ATPASE SUBUNIT D.
 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
12-DEC-1998 (Rel. 37, Last annotation update)
12 KD CHAPERONIN (PROTEIN CPNIO) (PROTEIN GROES) (HEAT SHOCK 10 KD
 Bacteria: Firmicutes: Bacillus/Clostridium group: Enterocorraceae:
 "Sequencing and characterization of the htp gene cluster for vacuolartype ma(*)-translocation appear of Enteroconcus himae.". biol. chem. 265:11037-11044(1994).
 ::
 Ö
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-1996 (Rel. 34, Last association update)
V-YPE CODIUM ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (NA(+):
TRANSLO ATING ATPASE SUBUNIT D.
 Takase K., Kakinuma S., Yamato I., Konishi K., Iqarashi K.
Kakinuma Y.;
 Query Match

34.4%; Score 78; DB 1; Length 236;
Best Local Similarity 40.0%; Pred. No. 3.44e-01;
Matches 12; Conservative 7; Mismatches 10; Indete
 Score 78; DB 1; Length 103; Pred, No. 3,44e-01;
 l: Indels
 950021384EE6EF03 CRC64:
 11240 MW; FF768479C0A90520 GRC64;
 Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
 96 AA
 Mismatches
 230 AA
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-14 STRAIN-ATCC 9790;
 78 DELLALPAENVSISVVEKNIMSVKVPLMNF 107
EMBL, U30821: AAA81293.1: -.
PRINTS: PROUS97: CHAPERONIN10.
PROSITE: PSOU681: CHAPERONINS_CPN10: 1.
PFAM: PF00166: cpn10: 1.
Chaperone: Cyanelle.
 PRT:
 PRI:
 Hydrolase: Hydrogen lon transport
SEQUENCE 230 AA: 27093 MW: 95
 EMBL: D17462: BAA04277.1; -
 Match 34.4%;
Local Similarity 50.0%;
es 8; Conservative
 EEYVLLSEKDILAIIA 103
 1 EEYLILSARDVLAVVS 16
 STANDARD;
 STANDARD
 Leptospira interrogans
 103 AA;
 Enterococcus hirae
 GROES OR HSP10.
 Enterococcus.
 LT 14
NTPO_ENTHR
P43435:
 STRAIN-ATCC
 CH10_LEPIN
P35472:
 SECUENCE
 Query Match
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SECUENCE FROM N.A.
SECUENCE FROM N.A.
STRAINES. 93123752.
A Ballard S.A. Segers R.P. Bieurisk-Piuym N.M., Fyl. J.A.M.,
Aballard S.A. Segers R.P. Bieurisk-Piuym N.M., Fyl. J.A.M.,
Adler B. M. Adler B. F. B. of the hisp (groe) operon of Leptospira interrogans serovar copenhagen.;
Mol. Microbiol. 81739-751(1993).
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SEROVAR LAI / HY.1;
STRAIN-SEROVAR LAI / HY.1;
SUBMITTED (NIV. 1997) to the EMBL/GenBack/DCBJ databases.
C. FYMITION SINUS TO CPN65 IN THE PRESENCE OF MG-ATP AND SUPPRESSES COPPRESSES CONTINITY OF THE LATTER.
C. SCHOUTH HEPFTAMER CF 7 SUBJUNITS ARRANGED IN A RING (BY SIMILARITY).
 Query Match 33.5%; Score 76; DB 1; Length 96; Best Local Similarity 62.5%; Pred. No. 7.32e-01; Matches 10; Conservative 2; Mismatches 4; Indels
 -:- INDUCTION: BY HEAT SHOCK.
-:- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 EMBL: L14682; AAA71991.1: -.
EMBL: AF02210: AAE86964.1; -.
PRINE: S3497: X65X$&6663X668
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPSICh\_pp

Mon Jun 19 16:11:24 2000; MasPar time 9.82 Seconds 225:834 Million cell updates/sec Run on:

not generated. Tabular output >CS-C9-142-524A-10 (1-32) from US09142524A.pep 227 1 BEYLILSARDVLAVVSKRRMKVTVAFNOFGPN 32 Description: Perfect Score: Sequence:

PAM 150 3ap 11 Scoring table:

Post-processing:

Searched:

225878 segs, 59334122 residues

Minimum Match 0% Listing first 45 summaries

sptremb112

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_manmal 7:sp\_mhc 8:sp\_organelle 5:sp\_bhage 10:sp\_plant 11::sp\_rodent 12:sp\_unclass:fied :3:sp\_vertebrate 14:sp\_virus

Mean 33.599; Variance 54.501: scale 0.616 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUVMARIES

|    |            |       |              |     | COMMARIEN |                         |           |
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| Sc | Score      | Match | Match Length | œ.  | OH.       | Description             | Pred. No. |
| :  |            | 50.2  | 001          | . 2 | 086017    | 10 KO CHAPERONIN (PROT  | 2.33e-07  |
|    | 65         | 43.2  | 367          | 10  | C0N260    | POLLEN MAJOR ALLERGEN   | 2.42e-04  |
|    | Ω/<br>Œ    | 43.2  | 9.45         | 10  | 096385    | CHAC1 PRECURSOR.        | 2.42e-04  |
|    | 43         | 42.7  | 459          | 10  | 023565    | PUTATIVE PECIATE LYASE  |           |
|    | 65         | 40.5  | 394          | 2   | 055457    | PECTATE LYASE LIKE PRO  | 2.90e-03  |
|    | 41         | 40.1  | 394          | 10  | 065456    | PECTATE LYASE LIKE PRO  | 4.35e-03  |
|    | 88         | 38.9  | 242          | S   | 095136    | ERCC1-LIKE EXCISION RE  | 1.45e-02  |
|    | 88         | 38.8  | 390          |     | 065388    |                         | 1.45e-02  |
|    | <b>.</b> 7 | 37.0  | 455          | 10  | 064510    | PUTATIVE PECTATE LYASE  | 7.52e-02  |
|    | 80         | 35.2  |              | ထ   | 092Y22    | NADH DEHYDROGENASE SUB  | 3.25e-01  |
|    | 80         | 35.2  |              | αŋ  | 037529    |                         | 3.25e-01  |
|    | 79         | 34.8  | 398          | 10  | 043783    | 77                      | 4.73e-01  |
|    | 78         | 34.4  | 330          | ထ   | 092203    | NADH-UBIQUINONE OXIDOR  | 6.88e-01  |
|    | 77         | 33.9  |              | 7   | 917X9Q    | PUTATIVE OXIDOREDUCTAS  | 9.96e-01  |
|    | 27         | 33.9  | 768          | 'n  | D6806d    | F55H12.1 PROTEIN.       | 9.96e-01  |
|    |            | 33.5  | 103          | 7   | 09x206    | 10 KD CHAPERONIN (PROI  | 1.44e+00  |
|    |            | 33.5  | 325          | 10  | 042576    | MITOCHONDRIAL NADH DEH  | 1.44e+00  |
|    | 75         |       | 325          | ω   | P92558    | NADH DEHYDROGENASE, SUB | 1.44e+00  |
|    | 16         | 33.5  | 331          | α   | 037565    | NADH DEHYDROGENASE (UB  | 1.446+00  |
|    | 7.         | 33.0  | 96           | 7   | 051384    | PYPOTHETICAL 11.4 KD P  | 2.07e+00  |
|    |            |       |              |     |           |                         |           |

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| AA LONG HYPOTHETICE E I POLYKETICE SYN FAMILY RECEPTOR E ES (FRAGMENT) H UBIOUNNE CALLO H UUR PECHETE LYASE TATUE CYTOCHROME P AT IVE CYTOCHROME P BIO.8 PROTEIN. A PROTEIN. A PROTEIN. A PROTEIN (FRAG BOOREDUCTASE. EN ESPECIFIC PECTA BOOREDUCTASE. BOOREDU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | GENCOPROTEIN PRECURSOR<br>RECEPTOR TYROSINE KINA |
| 0.058215<br>0.052315<br>0.052315<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304<br>0.052304                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | υ.<br>Σ. γ.                                      |
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| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 20                                               |
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#### ALIGNMENTS

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SECTIES W. N. A.

RR SECTIES W. N. A.

RA COBB ALJ. FRATUBERCULOR

RA COBB ALJ. FRATUBERCULOR

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RT The Groes antigens of Mycobacterium avium and Mycobacterium

RE FUNCTION: BINDS TO CPNG. N. THE PRESENCE OF MG-ATP AND SUPPRESS

C THE ATPASE ACTIVITY OF THE LATTER (BY SIMILARITY).

SIMILARITY)

C THE ATPASE ACTIVITY OF THE CROES CHAPERONIN FAMILY.

SIMILARITY AACTIGATION:

C THE ATPASE AND SUPPRESS

C THE ATPASE COPILO:

SEMBL: AFOTIGATE:

DR REMEL: AFOTIGATE:

DR PROSITE: PSOC681: CHAPERONINS_CPN10: 1.

DR PRINTS: PRO0156: CHAPERONINIO.

KW Chaperone: Heat shock.

SEQUENCE: 100 AA: 10748 MW: 0C4954DA CRG32;
 SEQUENCE FROM N.A.
STRAIN-485 TYPE 21.
SEQUENCE FROM N.A.
STRAIN-485 TYPE 21.
Sequence of the GroESL operon of Mycobacterium avium comprising the gene encoding the cpn10 protein and a portion of the gene encoding the cpn10 protein and a portion of the gene encoding the symmitted (JOD-1998) to the EMRIANCEMARK/DUBJ details.
 Mycobacterium avium, and Myo nacterium paratuberculosis.
Bacteria: Firmicutes: Actinolucteria: Actinobacteridae;
Actinomycetales: Corynebact neae: Mycobacteriaceae: Mycobacterium.
 Ouery Match 50.2%; Score 114; DB 2; Length 106; Best Local Similarity 100.0%; Pred. No. 2.33e-07; Matches 17; Conservative 0; Mismatches 0; Indels
 update)
 01-NOV-1998 (TrEMBLTel. 08, Created)
01-NOV-1998 (TrEMBLTel. 08, Last sequence update)
01-NOV-1999 (TrEMBLTel. 12, Last annotation update
10 kD CHAPERONIN (PROTEIN C:N:0) (PROTEIN GROES).
GROES.
 100 AA
 PRI;
 PRELIMINARY;
RESULT 1
ID 086017
AC 086017:
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18 RRMKVIVAFNQFGPN 32
 Arabidopsis.
 Arabidopsis
 F1N20.190
 RESULT 5
ID 065457
AC 065457:
 RESULT 4
ID 023665
AC 023665:
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 SUZUKI M., KOMIYAMA N., ITOH M., ITCH H., SONE T., KUNG K., TAKAGI I.,
 *Purification, characterization and molecular closing of Cha o i. a major allegen of Chamaevyparis obtusa (Japanese cypress) pollen."; MMO1. Immunol. 33:451-466(1996).

EMBL: D45404; BAA08246.1: -.

MENDEL: 7625; Chaob,1088:7626.

PFAM: PF00544; pec_1ysse: 1.

PRINTS: PRC0807; AMBALLERGEN.
 PEOPLEMENTE FRUM N.A.
MIDOMS-MORIUTI F.M., GOLDBLUM R.M., KURGSKY A., WOOD T.G.,
MIDOMS-GOLDBLUI F.M., GOLDBLUM R.M., KURGSKY A., WOOD T.G.,
MACACALAR GLODING OF MOINTAIN CREAT (Juniperus ashel) pollen major
allorgen, Jun a.i.,
allorgen, Jun a.i.,
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases,
EMBL AT106662, AADD3609.1) ...
EMBL AT106662, AADD3609.1) ...
EMBL AT106642, Junas:1088:36544.
MENDEL: 365445, Junas:1088:36545.
SEQUENCE 36745, Junas:1088:36545.
 Gaps
 Gaps
 096385 PRELIMINARY, PRI, 37° AA.
096385.
096385.
01-FBB-1997 (TEMBLER). 02. Created)
01-FBB-1997 (TEMBLER). 12. Last sequence update)
01-NOV-1999 (TEMBLER). 12. Last annotation update)
03-NOV-1999 (TEMBLER). 12. Last annotation update)
03-NOV-1999 (TEMBLER). 12. Last sequence update)
03-NOV-1999 (TEMBLER). 13. Last sequence updat
 01-MAY 1999 (TrEMBirel, 10. Created)
01-MAY 1999 (TrEMBirel, 10. Last sequence update)
01-MAY 1999 (TrEMBirel, 10. Last sequence update)
01-MAY 1999 (TrEMBirel, 12. Last annotation update)
POLLEN MAGOR ALLERGEN 1-2.
Juniperus ashe: (Szark White cedar)
Juniperus ashe: (Szark White Cedar)
Eurayotus virialisplandae, Streptophyta, Embryophyta, Iracheophyta;
Euxodiaceae; Juniperus, Conlieropsida; Conlierales;
 ö
 <u>:</u>
 Length 367;
 Length 375
 Score 98: DB 10; Length 367
Pred. No. 2.42e-64:
1: Mismatches 1; indels
 Indels
 query Match 43.2%; Score 98; DB 10; Lei
Pest Local Similarity 86.7%; Pred. No. 2.42e-04;
Katches 13; Conservative 1; Mismatches 1;
 375 AA: 40258 MW: A0981492 CRC32:
 367 AA
 POTENTIAL.
 583
 CHAOl
 Match
Local Similarity 86.7%;
les 13; Conservative
84 EEYLILSAROVLAVVSK 100
 1 EFYLLUSAROVLAVVSK 17
 232 KSMKVTVAFNQFGPN 246
 232 KSMKVTVAFNQFGPN 246
 PRECIMINARY
 18 RRMKVIVAFNOFGPN 32
 375
 SEQUENCE FROM N.A
 IISSUE-POLLEN:
MEDLINE: 96265194.
 SEQUENCE
 wery Match
 CHTA N.
 Signal
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C92NCQ
 10N260
 Matches
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 5455
 Gaps
 Arabidopsis thallana (Monso un cross).
Staryopus Viribiplantae: S. githytia, Embry phytu, iranizophyta:
edphyllophytes: Sperratophytu, Monodi shytus eduliniye bris:
core eudicots: Rosidae: eurosius il Brussinales, Brussina-edg:
 Arabidopsis thallana (Mouse-or cress).
Estaryota: Virialplantae; Storitophyra: Erbryophyta: Trachedoptic.
Euphyllophytes: Spermatophyra: Magnoliophyra: eudicoryledons:
core eudicots; Rosidae: euro- is II; Hrassicales; Brassicalee
 MAYER K.
 SEQUENCE FROM N.A.
MEDLINE, 97422403.
MEDLINE, 97422403.
MEDLINE, 97422403.
MIGHALÉSCARAS R., MCCORMICK S.:
"Identification of the tobacco and Arabidopsis horoloques of the pollen-expressed LAT59 gene of tomato.":
Plant Mol. Bloz. 34.809-814(1997).
EMB.: U83619; ARAB697951; ---
MENDEL: 25559; Arath:1088:2559.
PFAN: PFO0544: pec_lyase: 1.
PFAN: PFO05407: AMBALLER:IN.
 .,
(3
 <u>.</u>;
 Ouery Match 40.5%; sucre 92; DB 10; Length 394; Best Local Similarity 70.6%; ired. No. 2.90e-03; Matches 12; Conservative 2: Mismatches 3; Indels
 Length, 459
 Indels
 SEQUENCE FROM N.A.
BEVAN M., WEDLER H., WAMBUIT R., BANCROFT I., MEWES H.W.
SCHUELLER C.;
 [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT:
Submitted (APR-1996) to the EMBL/GenBank/EDBJ databases.
EMBL: ALG22140; CAA18112.1; -.
EMBL: 29068; Arath:1088;29068.
 Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 05, Lust sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last ammotation update)
PUTATIVE PECTATE LYASE.
 01-AUG-1998 (TrEMBLrel. 07, C:eated)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, 1st annotation update)
PECIATE LYASE LIKE PROTEIN.
 Query Match
42.7%; Score 97; DB 10; Ler
Best Local Similarity 46.7%; Pred. No. 3.68e-04;
Matches 14; Conservative 9; Mismatches 5;
 SEQUENCE 394 AA; 43299 MW 8B9A93C9 CRC32;
 SEQUENCE 459 AA; 51420 MW; 41EB5958 CRC32;
 394 AA
 459 AA
 298 QEVMLFGARDE-HVIDKK-MQITVAFNHFG 325
 1 EEYLILSARDVLAVVSKRRMKVTVAFNGFG 30
 G.
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 251 VKDVKMKVTVAFNHFGP 267
 PRELIMINARY:
PRELIMINARY:
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US-09-142-524A-10.rspt

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P SEQUENCE FROM N.A.

C STRAIN-CV. COLUMBIA,

VSOSTSKALA V.S., OSBORNE B.I. SCHWARTZ J.R., IORIUMI M., YU G.,

A VYSOSTSKALA V.S., OSBORNE B.I. SCHWARTZ J.R., IORIUMI M., YU G.,

(A KWAN A., OJI O., LIU S., BUCHLER E., CONWAY A.B.,

CANNAY A.B.,

A SEWN H., DANYIS R.W., ECKER J.R., FEDERSPIEL N.A., THEOLYGIS A.

SUBMITTED (MAY-1968) to the EMBL/GenBank/DBJ databases

R MNDEL, 20204, ARALLIO88129024.

DR MYNDEL, 20204, ARALLIO88129024.

DR PRAM: PPRO0544; pec_lyses: 1.

DR PRINTS: PRO0807: AMBALLERGEN.

SO SEQUENCE 390 AA: 43354 MK; ECF32F54 CRC32.
 Eukaryota, Viridiplantae: Stroptopnyta: Embryophyta: Tracheophyta: euphyllophytes; Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae;
 Score 88; DB 10; Length 340
Pred. No. 1.45e-62;
4; Mismatches 3; Indels
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, ast sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
F12F1.22 PROTEIN
 Arabidopsis thaliana (Mouse-ear cress).
 1 EEYLILSARDVLAVVSKRRMKVTVAFNOFG 30
 PMT;
 Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
 241 VEDKIMRVTIAFNHFGP 257
 15 VSKRKMKVIVAENQEGP 31
 PRELIMINARY;
 PRELIMINARY:
 Arabidopsis.
 1.0F6 24
 Query Match
 064510
 RESULT 8
ID 065388
AC 065388;
 Lyase
 Matches
 RESULT
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 Gaps
 MEDINES 99021743.
MEDINES 99021743.
MEDINES 99021743.
GARDCEI D.J., CUMMINGS L.M., ARAVIND L.,
KOONIN E.V., SHALLOM S., MASON T., Y., FUJII C., PEDERSCN J.,
SHEN K., JINS J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,
SALTSERG S., ZHCU L., SUITON G.G., CLAYTON R., WHITE C., SMITH H.O.
FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.,
"Chiomosome 2 sequence of the human malaria parasite Plasmodium
falciparum."
 Gaps
 MAYER K.,
 Arabidopsis thailana (Mouse-ear cress).
Eukaryota viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnollophyta: eudicotyledons:
core eudloots: Rosidae: eurosids II; Brassicales; Brassicaceae:
 .;
0
 ;;
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
 Length 394;
 SEGUENCE FROM N.A.
BEVAN M., WEDLER H., WAMBUTI R., BANCROFT I., MEWES H.W.,
 Score 88; DB 5; Length 242;
Pred. No. 1.45e-02;
8; Mismatches 11; Indels
 ::de:s
 BEVAN M., WEDLER H., WAMBLIE A., CHITTELER C.:
SCHUELLER C.:
Submitted (MAR-1998) to the EMBI/GenBank/DDBJ databases.
 C96136 PRELIMINARY: PRT: 242 AA.
C96136 C06136 C1 EMBLER): 10. Created
01-MAY-1990 (TEMBLER): 10. Last sequence uposte)
01-MAY-1999 (TEMBLER): 10. Last sequence uposte)
01-MAY-1999 (TEMBLER): 10. Last annotation update)
08-EBCC1-LIKE EXCISION REPAIR PROIEIN.
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PECTATE LYASE LIKE PROTEIN.
 Ġ
 Score 91; DB 10; Pred. No. 4.35e-03: 2; Mismatches 0
 Science 282:1126-1132(1998).
EMBL: AE001377: AAC71822.1: -.
SEQUENCE 242 AA: 28287 MW; AE90AD3C CRC32:
 Lyase.
SEQUENCE 394 AA: 43476 MW; 95399178 CRC32;
 45 EQYLLISLRQKLNPVIKKIKRVRYKFNNIIPD 76
 1 EEYLILSARDVLAVVSKRRMKVTVAFNQFGPN 32
 Query Match
Best Local Similarity 40.6%;
Matches 13; Conservative
 46.1%;
Local Similarity 84.5%;
les 11; Consoruar:
:111:111:111:
15 VSKRRMKVIVAFNQFGP 31
 PRELIMINARY;
 255 KMKVTVAFNHFGP 267
 19 RXKVTVAFNOFGP 31
 Plasmodium falciparum
 SEQUENCE FROM N.A.
 Arabidopsis.
 falciparum
Science 28
 F1N20.180.
 Query Match
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Length 390

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 Albendopsis thattana (Morse not Trocs)
Eukafyota, Viridiplantae, Stref optignational incomophyta.
Eukafyota
Euphyliophytes: Spermatophyta; Magnellophyta; endicenyledens:
core eudicots: Rosidae; enrosids II; Brassicales; Brassicancee;
Arabidopsis.
 SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

STRAIN-EV. COLUMBIA;

SOURCE S.M. LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,

SYKES S.M., KAUL S.M. MASON J.M., KERLAVAGE A.R., ADAMS M.D.,

SOMERVILLE C.R., VENIER J.C.,

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, ROG02521, AAC05550.1;

MENDEL 28055, Arath,1088,28505,

PRAM: PF06544, pec_lysse; 1.
 5;
 Length 455;
 Indels
 C1-AUG-1998 (InEMBirel, G7, Created)
(1.AG-1998 (InEMBirel, G7, Last, sequence update)
(1.AVA-1999 (INEMBirel, 12, Last admotation update)
(0.AVA-1999 (INEMBirel, 12)
 Match 37.0%; Score 84; DB 10; Ls Local Similarity 36.7%; Pred. No. 7.02e-02; les 11; Conservative 11; Mismatches 6;
 SEQUENCE 455 AA; 51257 MW; EBA0B82D CRC32;
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455
 294 DEVMLFGGTNK-DVIDKK-MQITVAFNHFG 321
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 (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-UTEX 1P 1350.

TURMEL M., LEMIEUX G., BURGER G., LANS B F., CTIS G., PLANTE I.,
GRAY M W.,
The complete mitochondrial DNA sequences of Nephroseims olivacea and
Pedinomonas Finor: two radically different evolutionary patterns
within the green algae. ".
Submitted (EC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AR116775; AR019672.1: -.
SEQUENCE RELIGIORS MW: 27CECAGA CR012;
 Mitochondrion.
Eukaryota: Viridiplantae: Chlorophyta: Pedinophyceae: Pedinomonadales:
Pedinomonadaceae: Pedinomonas.
 Chicrellales;
 STRAIN-263-11
STRAIN-263-11
WEDLINE: 9418-059+
WEDLINE: 9418-059+
MCDLINE: 9418-059+
MCDLINE: 9418-059+
*Complete sequence of the mitochondrial DNA of the chlorophyte alua
Protothera wickethamil. Gene content and genome organization.";
Protothera Miol. 23775-86(1994).
 Gaps
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 MENDEL, 21568: Prowitinadi.21568.
PPRAM PROGLEGE: NADHGH. 1.
Ubiquinche: Gxidoreductasc: Mitochondrich: NAD: Transmerbrane SEQUENCE. 328 AA: 36437 MM: F1269845 CRC32;
 Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophycae,
Chlorellaceae, Protothera,
 udery Match
Best Local Similarity 33.3%: Pred. No. 3.25e-01:
Matches 10: Conservative 8: Mismatches 11: Indels
 Score 80, DB 8; Length 310;
Pred. No. 3.25e-01;
6; Mismatches 8; Indels
 01-NOV-1996 (TrEMBLrel, 01, Created)
01-NOV-1996 (TrEMBLrel, 01, Last sequence .pdate)
01-NOV-1999 (TrEMBLrel, 12, Last annotation update)
NACH DEHYDROGENASE (JBIQCINONE), SUBUNIT 1 (EC 1.6.5.3).
NACH NACH AND AND AND A
LT 10
02222 PRELIMINARY; PRT; 31C NA.
052722 01-MAY-1999 (TEMBLEG: 1C, Created)
01-MAY-1999 (TEMBLEG: 1C, Last sequence update)
01-MAY-1999 (TEMBLEG: 1C, Last annotation update)
NADH DEHYDR-GENASE SCHOKII 1 (EC 1.65.3);
 AA
 328
 25 FLVLAERKVLASMQRRKGPNVVGIYGIFQP 54
 3 YLILSARDVLAVVSKRR-MKVTVAFNOFGP 31
 3 YLISARSVLAVSKERMKVIVAF 26
 28 FLVLIERKVIAYICRPRCPVFVGF 51
 35.2%-
Local Similarity 41.7%:
Les 10: Conservative
 PRELIMINARY:
 Prototheca wickerhamii.
Mitochondrion.
 NAD1.
Pedinomonas minor.
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 RESCLT 12
1D 043783
AC 0437831
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 Saiss
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheuplyta
euphyllophytes, Spermatophyta, Magnollophyta, Lillopsida,
Zingiberales, Musaceae, Musa,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PECTATE LYASE (EC 4.2.2.2) (PECTATE TRANSELMINASE) (FRAGMFWT)
 Length 398
 3100015
 34.4%; Score 78; DB 8; Length 330; 33.3%; Pred. No. 6.88e-0; ative 8; Mismatches 11; Indels
 DOMINGUEZ-PIUGJANER E.;
Submitted (APR-1996) to the EMRL/GenHack/DDBJ databases.
 0:-MAY-1999 (TTEMBLE). 16, Created)
U-MAY-1999 (TTEMBLE). 16, Cast Seguence spdate)
0:-MOY-1999 (TTEMBLE). 12, Last anodation update)
NADH-UBIQUINONE CXIDORECKSTASE CHAIN 1 (EC 1.6.5.3).
 Eukaryota, Rhodojdiyta, Banarojogo an Oyanidi sohoo
 34.8%; Score 79; DB 10; Le
41.4%; Pred, No. 4.73e-01;
vative 8; Mismatches 7;
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SEQUENCE 398 AA: 45712 MW: E5E9B38A CKC32:
 CAVENDISH: TISSUE-RIPE FROIT:
 STRAIN-CV. DWARF CAVENDISH: TISSUE-RIPE FRUIT:
DOMINGUEZ-PIUGJANER E.:
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 246 MLLGHSDELT - SCKSMQVTIAFNHFGED 272
 26 YLILAERKIIGAIQKRKGPNVVGMFGLLQP 55
 4 LILSARDVLAVVSKRRMKVTVAFNQFGPN 32
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 Local Similarity 33,3%;
es 10; Conservative
 Query Match
Best Local Similarity 41.40.
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 PRELIMINARY,
 Cyanidioschyzon merolae.
 Musa acuminata (Banana)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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US-09-142-524A-10.rspt

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<u>:</u>
 MEDLINE: 94150718
MEDLINE: 94150718
MILSON R. AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CCNNELL M., COPSY T., COCPER J., COLLSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSY T., COCPER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSIEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHNRAN A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WALERSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome "; hol. Microbicl. 21:77-96(1996). "Mb.: A049863: CA842953.... SEQUENCE 301 AA: 32531 MA: E4145A89 CRC32;
 for
 Gaps
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia: Rhabditida;
Rhabditina; Rhabditoidea: Rhabditidae; Peloderinae; Caenorhabditis.
 SCSH1.28C.
Streptomyces coelicolor.
Bacteria: Pirmicutes: Acticobacteria: Actinobacteridae:
Actinomycetales: Streptomycheae: Streptomyces
 MEDLINE: 97.00.551.
REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
 :
ت
 Query Match 33.9%: Score 77: DB 2: Length 305: Best Local Similarity 41.9%: Pred. No. 9.96e-01: Matches 13: Conservative 5: Mismatches 13: Indels
 DOBSON K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
 STRAIN+A3(2):
JAMES K.D., PARKHILL J., BARRELL B.G., PAJANDREAM M.A.:
Submitted (MAY-1999) to the EMHL/GenBank/DDBJ databases.
 01-MAY-1997 (TrEMBLrel. C), Greated)
01-MAY-1997 (TrEMBLrel. C), Last sequence update)
01-MAY-1999 (TrEMBLrel. 12, Last annotation update)
FSSH12.1 PR(TLIN)
 Last sequence update)
Last annotation update)
 758 AA
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 127 EENLRQIIGROHLDVVYLRRMRQDSVAEHFGA 157
 1 REYLILSARDVLAVVSKRRMKVIVAFNOFGP 31
 Created)
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01-NOV-1999 (TEMBLEE) 12,
01-NOV-1999 (TEMBLEE) 12,
PUTATIVE OXIDOREDICASE.
 PRELIMINARY:
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 Caenorhabditis elegans.
 SEQUENCE FROM N.A.
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 SEQUENCE FROM N.A.
 F55H12.1
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G
 Length 768.
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11; Mismatches 5
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 Search completed: Mon Jun 19 16:11.45 2000
elegans.";
Nature 368:32-38(1994),
EMBL: Z81091; CAB03142.1; -.
PRAM: PF00209; SNF: 2,
PRINTS; PR00176; NANEUSMPORT,
SEQUENCE 768 AA: 85132 MW; D
 669 FLVIPGFAIAAVINTRRMNIPI 689
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 4.60 Seconds 118.427 Million cell updates/sec Mon Jun 19 16:14:13 2000; Run on:

Tabular output not generated.

.US-09-142-524A-11 (1-20) from US09142524A.pep 143 1 IFSKNLNIKLNMPLYIAGNK 20 Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

188963 seqs. 23686106 residues Searched

Minimum Match 0% Listing first 45 summaries Fost-processing:

1 : genesegp a-geneseq35

Variance 65 008; scal. 0,308 Milan 20, 352; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Pred. No.             | 3.71e-08               | 3.71e-58              | 3.71e-08 | 3.71e-08 | 3.71e-08               | '      | - 4      | 1.15e-04               |                        | 1.15e-04               | i.15e-04              | 1.15e-04              |                       | 1.1      | 7                      | 1.                     | 1.1                   | 2.26e+00               | 3.6                   | 7.446+00               | 1.19e+01               | 2.39e+01 | 2.39e+01               |
|-----------------------|------------------------|-----------------------|----------|----------|------------------------|--------|----------|------------------------|------------------------|------------------------|-----------------------|-----------------------|-----------------------|----------|------------------------|------------------------|-----------------------|------------------------|-----------------------|------------------------|------------------------|----------|------------------------|
| wescription.          | :-cell epitope peptide | Multi-epitope peptide |          | iss poil | Chamaecyparis obtusa p |        | Jun v I. | Cry j I Japanese Cedar | Cry j I pollen allerae | I-cell epitope peptide | Multi-ep.tope peptide | Japanese cedar pollen | Cedar pollen allergen | Cry j I. | Cry 3 I pollen allerge | Cry j I Japanese Cedar | Japanese cedar pollen | T-cell epitope peptide | Multi-epitope peptide | T-cell epitope peptide | S. pneumoniae hemolyti |          | Amb a 1/Antigen E enco |
| qI                    | W42130                 | W27372                | W04344   | W42121   | W04345                 | R45577 | R45578   | 249                    | R45549                 | W44682                 | W27371                | R75388                | 88.587                | R31937   | R45541                 | R52490                 | R60166                | W42131                 | W27370                | W42129                 | W38604                 | R07347   | RC7346                 |
| m i                   | 7                      | _                     | _        | _        | ٦                      |        | ~        | ~                      | -                      | -                      | -                     | -                     | 7                     | -        | -                      | ч                      | -                     | ч                      | - 1                   | e-1                    |                        |          | ~                      |
| Query<br>Match Length | 20                     |                       | LO.      | 5        | 375                    | w      | 1        | 20                     | 20                     | 30                     |                       | 353                   | 10                    | 374      | 374                    | -                      | 150                   | 23                     | 105                   | 23                     | 183                    | 383      | 383                    |
| Ouery<br>Match        | 160.0                  | 100.0                 | ٠.       |          | 100.0                  | 86.0   | 86.0     | 79.0                   | 79.0                   | 79.0                   | 79.0                  | 79.0                  | 0.64                  | 79.0     | 79.0                   |                        | φ.                    | 5: 7                   | 50.3                  | 48.3                   |                        | 8        | 44.8                   |
| Score                 | 143                    | E † 1                 |          | 543      | 143                    | :23    | 123      | 113                    | 5.13                   | 113                    | 113                   | 1:3                   | 113                   | 113      | 113                    | 113                    | 113                   | 4.                     | 7.2                   | <b>ტ</b>               | 67                     | 54       | 54                     |
| Result<br>No.         | 1                      | 7                     | m        | √*       | 'n                     | 9      | ۲۰       | в                      | 6                      | 10                     | 11                    | 12                    | 13                    | 14       | 15                     | 91                     | 17                    | 92                     | ۍ<br>د ۱              | 20                     | 21                     | 22       | 23                     |

|                                                                                                                                                                                                                                                                                                                                              | 3.78e-01<br>3.78e-01<br>3.78e-01<br>5.96e-01                                                                                  |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| DATE a 1D clo<br>pollen Arb a<br>Pollen Alerg<br>Anb al a alle<br>ri GHPO 450 pr<br>occoccus aucus<br>occoccus aucus<br>Antigen E enc<br>Antigen E enc<br>Anb a 1 Antig<br>allergen UVZ<br>Pollen Allera<br>Anb ail alle<br>Antigen E enc<br>Antigen E enc<br>allergen UVZ<br>Antigen E enc<br>allergen UVZ<br>Antigen E enc<br>allergen UVZ | Radweed Poller Allorge<br>Radweed poller Anb a :<br>Radweed poller UNC a :<br>Staphylococcus aureus<br>Ragweed Poller Amb a 1 |
|                                                                                                                                                                                                                                                                                                                                              | W 4 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                     |
| анаянананананана                                                                                                                                                                                                                                                                                                                             |                                                                                                                               |
|                                                                                                                                                                                                                                                                                                                                              | 2440<br>2742<br>375<br>310                                                                                                    |
| 00 00 00 00 i⊣ 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                           | 4440m                                                                                                                         |
| 44444MMMMMMMMMMM                                                                                                                                                                                                                                                                                                                             | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                         |
| \$\phi \phi \phi \phi \phi \phi \phi \phi                                                                                                                                                                                                                                                                                                    | 00000<br>00000                                                                                                                |
| 40000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                       | ল (N M বু U)<br>বৈ ব ব ব ব                                                                                                    |

#### ALIGNMENTS

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M42130 standard: peptide: 20 AA.
W42130 standard: peptide: 20 AA.
W42130 standard: peptide 10 from Japanese cypress pollen antiqen Chaol.
DT 16-JUN-1998 (first entry)
DE T-cell epitope peptide 10 from Japanese cypress pollens antiqen: T-cell epitope: Chaol: Chaol.
M40474648-A1.
SO Chamaeyparis obtusa.
WW9474648-A1.
DE DECC: 97.
WW9474648-A1.
DE DECC: 97.
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 RESULT
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Gaps ; ; cuery Match 100.0%; Score 143; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 3.71e-68; Matches 20; Conservative n. within

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1 IFSKNINIKLNMPLYIAGNK 20 1 IFSKNINIKLNMPLYIAGNK 20 පු ò RESULT 1D W2 AC W2 DT 24 DE MM KW M M KW T COS ST

LT 2
W2732:
W2732:
24-MaR-1998 (first entry)
Walti-repitope peptide used as immunotherapeutic agent \*4.
Wulti-repitope peptide used as immunotherapeutic agent; allergic disease:
T-cell epitope region; allergen: lymphocyte; immunoqlobulin E.
W09732600-A1.

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Sequence
 Jun s 1.
 Seguence
 W04345;
 Matches
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ID R
AC R
DT 1
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Peptide immuno:therapeutic agent to treat allergic diseases contains multi-epitope peptide containing I cell epitope regions contains multi-epitope peptide containing I cell epitope regions Caim 9; Page 32: Supply Japanese.

The present sequence represents a multi-epitope peptide which is used as new immunostherapeutic agent. It comprises I cell epitope regions from 2 or more different alleraens (preferably linked via arginine or lysine dimers) where the I cell epitope regions: have a positivity index alleraens (by a meausired in a patient group responding to the alleraen; and are not reactive with immunoglobulin E responding to the alleraen; and are not reactive with immunoglobulin E (gls) antibodivis from patients responding to the alleraen; and are not reactive with immunoglobulin be used to prevent and ireal a wide variety of alleragic diseases, e.g. by desensitisation, side effects, e.g. those mediated by 1gE, are reduced.
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 Saps
 Gaps
 by a encoding chamaecypinis obtasa pollon allergo. I cell prophiopics) of which are secul in development of preventative and treating agent for chiusa pollen pollinosis. Claim 2: Pages 16-11. 17pp. Japanese. The present sequence is the G. obtasa pollon allergen Cha o I, the fresht sequence is the G. obtasa pollon pollinosis. The I cell optiopes of which can be used in the development of a preventive and treating agent for G. obtasa pollon pollinosis. Or obtasa pollon (2.4 kg) was degreased with distribut their, and dried at room temp. Overnight. Cha o I was sept from it and purified. RNA was extracted from G. obtusa pollon, and mRNA and purified.
 Chamaecyparis obtusa polém allergen Cha o I (A).
Pollen allergem Cha o I. T-cell epitope: prevention: treatment:
 W42121 standard; protein: 354 AA.
W4212::
16-JUN-1998 (first entry)
Japanese cypress pollen actigen: Chaol.
Japanese cypress pollen; antigen: T-cell epitope: Chaol: Chao2;
 ö
 .;
0
 Length 354:
 query Match
Fest Local Similarity 106.0%: Prod. No. 3.71e-08;
Matches 20: Conservative 0: Mismatches 0: Indels
 Length 31:
 Match 100.0%; Score 143; DB J; Length 31; Local Similarity 100.0%; Pred. No. 3.71e-08; es 20; Conservative 0; Mismatches 0; Indels
 (MEIP.) METSI MILK PROD GO LID.
DAIRTRÍ K. IWAMA A. Kino K. Kume A. Sone T.
WPI: 97-470495/43.
 Chamaecyparis Obtusa.
0/8176/52-A.
0/8176/52-A.
21-DEC-1994; 3/8089.
(MEIP.) MEUL MIK PROD OD UTD.
WPI: 96-369225/37.
 W64344 standard: Protein: 354 AA
 1 IFSKNLN:KLNMPLY:AGNK 20
 1 IFSKNINIKLNMPLYIAGNK 20
 1 IFSKNINIKLNMPLYTAGNK 20
 28-NOV-1996 (first entry)
 71 ISSKNINIKINMPIKIAGNK
 10-MAR-1997; J36740.
10-MAR-1996; JP-680702.
 354 AA:
 CONA derived
 Seel tecsa-N
 Sednesuc
 Matches
 RESULT
 1 8 0 0 %
0 0 0 0 %
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Example 1: page 14-15: 71pp: Japanese.

Example 1: page 14-15: 71pp: Japanese cypress pollen antiach Chaol. The present sequence represents Japanese cypress pollen antidens to the 1 cell epitope sites on Japanese cypress pollen antidens Chaol and Chaol. The peptides can be used as a reagent for the diagnosis of allergy to Japanese cypress pollen, and as an antiden in the treatment and prevention of spring tree poller, disease in which the pollinosis
 Gaps
 Scips
 ONA encoding characterpairs obtuse price ablerges of their epitope(s) of which are usern in development of preventative and freating agent for C. obtuse pulses pollinesis.

Claim 8: Pages 11.2: 17pp: Jamanese.
The present sequence is the C. obtuse pollen allerges that of a preventive and treating agent for C. obtuse pollen pollinesis.
C. obtuse pollen (2.4 kg) was degreased with diethyl ether, and dried at room temp. overnight. Che of was sepd. from it and cDNA derived.
 Dairiki K. Kino K.
WHJ, 98-052242/05.
T-cell epitope peptide portion of Japanese cypress pollen uniquens
Chaol and Chao2 - used for diagnosis and treatment of spring tree
 rell epitope; prevention; treatment;
 ċ
spring tree pollen disease; pollinosis
 Length 375:
 Length 354
 Score 143: DB i: Lengt): 354 pred; No. 3.71e-08; 0: Mismatches 0: Indels
 0; Indels
 allerger Cha o I cDNA (B).
 Sore 143; DB 1; P. ed. No. 3.71e-08;
 Mismatches
 LI 6
R45577 standard: Protein: 367 AA.
R45577
 W04345 standard: Protein: 375 AA
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 09-JUL-1996.
21-DEC-1994. 335089.
21-DEC-1994. JP-335089.
(METP.) MEJJI MILK PRUD CO 1175.
WPI: 96-368225/37.
 92 IFSKNLNIKLNMPLYIAGNK 1:1
 20
 90
 Query Match 100.0%;
Best Local Similarity 109.0%;
Matches 20; Conservative
 Query Match
Best Local Similarity 100.0%:
 13-JUL 1994 (first entry)
 14-JUN-1996: JP-153527.
(MEIP.) MELJI MILK PROD CO
 28-NOV-1996 (first entry)
Chamaecyparis obtusa poll
Pollen allergen: Cha o I:
 1 IFSKNLNIKLNMPLYIAGNK
 71 IFSKNLNIKLNMPLYIAGNK
 1 IFSKNENIKENMPLYIAGNK
 Conservative
 pollinosis.
Chamaecyparis oblusa
JC8176192-A.
 diagnosis; allergy;
Chamaeyparis obtusa.
W09747648-Al.
 18-DEC-1997.
12-JUN-1997: J02031
 N-PSDB; T38519
 pollen disease
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 Disclosure: Fig 17, 137pp; English.
The sequence is that of Jun v Z, a homologue of the Japanese caer police allergen Cry J Z. Antigenic peptides derived from it can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen.
 Gaps
 Disciosure, Fig 16: 137pp, English.

The sequence is that of Jun s I, a homologue of the Japanese cadar pollen alterate Cry 7 I. Antigenic peptides derived from it can be used for the treatment and diagnosis of allergies associated with Japanese redar pollen.
 Antiques derived from Japanese cedar pollen allergen Cry j I contain at least two T cell epitope(s), used to treat or diagnose
 N-PSDB: Q55272.
Antiqens derived from Japanese cedar pollen allergen Cry j I -
contain at least two T cell epitope(s). used to treat or diagnose
 Japanese cedar; pollen aliergen; allergy; treatment; diagnosis;
T cell epitope; sensitivity; desection.
Juniperus virginiana,
Japanese cedar; pollen aliergen; aliergy; treatment; diagnosis; T celi epitope; sensitivity; detection.
Juniperus sabinoides.
 ;;
 query Match 86.0%; Score 123; DB 1; Length 370; Hest Local Similarity 75.0%; Pred. No. 8.16e-06; Matches 15; Conservative 4; Mismatches 1; Indels
 Length 367;
 Melch 86.0%: Score 123; DE 1: Length 367 Local Similarity 75.0%: Pred. No. 8.16e-06; es 25; Conservative 4: Mismatches 1; Indeis
 20-JAN-2994.
15-JAN-2994.
10-JUL-1692. WC-105661.
01-REP-1992. US-938990.
(IMMC-) IMMULOGIC PHARM CORP.
BOOD UF. GARTIOR RD. GYLLELTH IJ, KHO M. POLLOCK J:
WPI: 94-035065/C4.
 20-JAN-1994.
15-JAN-1992.
10-JUL 1992: WO-U0566.
01-SEP-1992: WS-988990.
1MMU-) IMMULGUE PHARM CCRP.
BOND JF. Garmen FS. Griffith IJ. Kuo M. Pollock J:
WPI, 94-035066/04.
 /note- "signal peptide"
22, 1373
 /notes "mature peptide"
 l. .21
/note= "signal peptide"
 /note= "mature peptide"
 Location/Qualifiers
 Location/Qualifiers
 R45578 standard; Protein: 376
 92 IPSQNMNIKIKMPLYVAGHK 111
 1 : FSKNINIKLNMPLYIAGNK 20
 R45578:
13-JUL-1994 (first entry)
 367
 370 AA;
 N-PSDB; 055273
 W09401560-A
 WO9401550-A.
 Seguence
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92 IFSQNMNIKLKMPLYVAGHK 111

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WPI: 95-36699.747.

Wodified Cryptomeria japonica (Cry)) I peptide(s) - useful for treating allergy to japanese cedar pollen allerges or treating allergy to japanese cedar pollen allerges or immunologically cross reactive allergens.

Siccoure: Figure 2: 60pp: English.

Siccoure: Figure 2: 60pp: English.

Novel peptides of cry) I have been modified as a part of a preformulation scheme to develop an optimised drug product for therapeutic treatment of humans suffering from allergy to Japanese cedar pollen allerges or a liergen which is immunologically cross reactive with Japanese cedar pollen allerges. Such modified pertides possess certain characteristics which render them particularly cross suitable for drug product formulation. Peptide fragments of 7ry 3 to modified and unmodified, are aiven in R82491-R82525. This peptide fragment corresponds to amics acids 71-90 of the allerges mature
 ..
0
 Claim 1: Fig 13; 137pp; English.
The sequence is that of an isolated peptide of the Japanese cedar for sequence is that of an isolated peptide, CJI-8, can allergen CTy j I (amino acids 71-90). The peptide, CJI-8, can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens. Sequence 20 AA;
 Cry] I Japanese Cedar pollen allergen peptide fragment (UII-8).
Cry j I; japanese cedar pollen allergen: modified: drug production:
allergy; Crytpomeria japonica.
VOSSZ7786-AI.
 Saps
 20-JAN 1994. .:
15-JAN 1993. COO,39.
10-JUL-1992; WO-VOS661.
01-SEP-1992; US-938990.
(IMMU-) IMMULOGIC PHARM CORP.
(IMMU-) IMMULOGIC PHARM CORP.
APPL: 94-0350660.
Antigens derived from Jag Rese cedar pollen allergen Cry i I contain at least two I cell epitope(s), used to treat or diagnose
 5
 R45549:
13-JUL-1994 (first entry)
Cry j I pollen allergen peptide CJI-8.
Japanese cedar: derection: allergy; treatment; diagnosis:
Jeal epitope: sensitivity.
 ore 113: DB 1: Length 20:
ed. No. 1.15e-04:
: Mismatches 2: Indels
 Franzen HM, Kto M. Powers SP;
 SC AA
 ď
 06-APR-1995; UC4249.
08-APR-1994: US-226248.
06-DEC-1994; US-350225.
(IMMU-) IMMULOGIC PHARM CORP.
Chen X, Evans S, Franzen HM, Shaked 2;
 T 8
882498 standard; Protein: 20
R82496:
15-APR-1996 (first entry)
 7
 79.08:
 Query Match
Best Local Similarity 75.0%:
Matches 15; Conservative
 1 IFSGNMNIKLKMPMYIAGYK
 R45549 Standard: Protein
 20 AA:
 Seguence
 protein.
 ailergy
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J07118295-A.
 Sequence
 peptide
 peptide
 peptide
 peptide
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 peptide
 Matches
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 MAR 1997.

10-MAR 1997.

10-MA
 Cyptomeria japonica.

1000700-0-A

1000700-A

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 Gaps
 Saps
 LT il standard: peptide: 134 AA.
K27371 standard: peptide: 134 AA.
K27371
24-MAR: 999 (first entry)
Multi-epitope peptide: seed as immunotherapeutic arent #3.
Multi-epitope peptide: imminotherapeutic agent: allergic disease: Toel! epitope region: allergen: lymphocyte: imminoglobulin E.
Synthetio.
K09732600-Ai.
 :
 ö
 Length 36:
 Length 20;
 2: Indels
 2; Indels
 W44682:
01-MAY-1998 (first entry)
T-cell epitope peptide #1 of suga polien antigen.
T-cell epitope: suga polien antigen: suga polinosis.
 Cuery Match
19.0%, Score 113, DB 1, I
Nest Local Similarity 75.0%, Pred. No. 1.15e-04;
Matches 15, Conservative 3, Mismatches 2;
 Score 113: DB 1;
Pred. No. 1.15e-04;
 Kismatches
 r 10
W44582 standard: peptide: 30 AA
 I IFSCHMUIKLKMPMYIAGYK 20
 1 IPSKNLNIKLNMPLYIAGNK 20
 TESCHMITKLKMPMYIAGYK 30
 L IFSKNENIKENMPLYIAGNK 20
Cuery Match
Rest Local Similarity 75.0%;
Matches 15; Conservative
 desensitisation. S
Sequence 134 AA;
 Synthetic.
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 09-MAY-1993.
20-007-1993; 262626.
20-007-1993; 262626.
MELL J DP-262626.
MELL J MICK PROD CO LTD.
WPI: 95-203834/27.
New cryptomeria polien aliernen T-ceil epitope peptide - used for prevention, treatment and investigation of Japanese cedar pollencsis prevention, treatment and investigation of Japanese cedar pollencis pisclosure: Figs 1-2; 8pp: Japanese.
R75388 is the Japanese cedar Follen allergen Cryj I, from which the F75388 is the prevent: - mad treatment of cryptomeria can be used for the prevent: - and treatment of cryptomeria
 Scho
 Gans
 Cryl 1. Cell epitope, peptides.
 R81587;
24-MAY-1996 (first entry)
Cedar pollen aliergen B.
Cedar pollen allergen; immunoglobulin E: IgE; 7-cell epitope;
antibody; pollinosis: ther.py; immunotherapy.
Cryptomeria japonica.
EP-70029-A2.
 ·.
 Length 35%.
 Length 134
 Match 29.0%: Score 11:1 DB 1: Lenath 35: Local Similarity 25:0%: Prod. No. 1.15e-04; see 15: Conservative 3: Mismatches 2: Indels
 2: Indels
 DB 1; L
 /notex Treell epitope peptide 326, 340
 epitope peptide"
 "T-cell epitope peptide"
 T-cell epitope peptide"
 335. ,346
/note= "T-rell epitope peptide"
 "I-cell epitope peptide
 ria politosis.
 Mismatches
 ire 113;
3. No. 1.
 (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
Hino K, Saito S, Taniguchi Y;
WPI; 96-140976/15.
 Location/Qualiters
 ď,
 R81587 standard; Protein; 353 AA.
 bl. 75
/note= T-cell (
91, 105
/note= T-cell e
106, 120
 R75388;
12-MAR-1996 (first entry)
Japanese cedar pollen allerg
Japanese cedar: pollen aller
prevention: treatment, crypt
Cryptomeria japonica.
 /note= "I-cell
 4)
(A)
(A)
 06
 5
 1 IFSKNINIKLNMPLYIAGNK 20
 340
/note= "I-r
Query Match
Best Local Similarity 75.0%;
Matches 15; Conservative
 78 IFSGNMNIKLKMPMYIAGYK
 T 12
R75388 standard: protein;
 ::60
 71 IFSGNMNIKLKMPMYIAGYK
 | IFSKNLNIKINMPLYIAGNK
 13-MAR-1996.
08-SEP-1995; 306295,
10-SEP-1994; JP-242137,
14-JUL-1995; JP-200221,
14-JUL-1995; JP-200221,
 /note= '212:
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S

cell epitope: sensitivity

Cryptomeria japonica.

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2.14AN-1993
2.14AN-1993
2.14AN-1993
2.14AN-1993
2.14AN-1993
2.14AN-1993
2.14AN-1993
2.15-101-1991: US-72934
2.15-101-1991: US-
 .;
Ö
New peptide(s) derived from cedar pollen allergens - activate allergen-specific T-cells, but not allergen-specific IgE antibodies, used for treating cedar pollinosis
Claim 5: Paperides 11-32: JSpp: English.
Synthetic peptides based on portions of cedar pollen allergens A (R81585) and B (R81587) were tested for their ability to activate cedar allergen-specific T-cells. but not allergen-specific IgE antibodies. 6 Peptides (R81580-R81585) were identified as T-cell epitices. These peptides, plus subsequences (R81573-79) essential for T-cell recognition, and homologues peptides (R81588-895) can be used as immunotherapeutic agents to treat or prevent cedar believes, avending side-effects such as anaphylaxis.
 Saps
 Gaps
 cedar pollen; allergen; antigen; allergy; B cell; T cell.
 ..
O
 79.0%: Score 113: 08 1: Lenath 374: 75.0%: Pred. No. 1.15e-04: Antive 3. Mismatches 2: Indels
 Query Match 79.0%; Score 113; DB 1; Lenath 353; Best Local Similarity 75.0%; Pred. No. 1.15e-04; Matches 15; Conservative 3; Mismatches 2; Indels
 R45541 standard: Protein: 874 AA.
18-5541;
13-JUL-1994 (first entry)
Cry 1 poilen allergen.
Japanise cedar: detection: allergy: troatment: diagnosis:
 1. .21
/note= "stanal peptide"
 "nature Cry j i"
 Location/wwwlifiers
 I (4
R31937 standard: Protein, 374 AA
 71 :FSGNMNIKLKMPMY:AGYK 90
 TESKNENIKENMPLYTAGNK 20
 03-JUN-1993 (first entry)
 1 :FSKNENIKLNMPCYTAGNK
 92 TENGNMNIKIKMPMYIAGYK
 Best Local Similarity 75.0%;
Matches 15; Conservative
 22. .374
 /note-
 Cryptomeria japonica.
 W09301213-A
 Japanese
 Seguence
 Query Match
 Cry j I.
 peptide
 protein
 R31937:
 RESULT
 74488086608863
74488086608863
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 98988
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Job time

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N-PSDB: 055271. Antigens derived from Japanese redar politen allergen Cry _{\rm S} : contain at least two T cell epitope(s). SPB to treat or discusse
 Discissure: Fig 4: 137pp: Enaissh.
The sequence is that of the Laganuse cedar police allocace.
Cry ji which contains at least two T cell epitopes. Peptide antigens derived from it can be used to: the treatment and diagnosis of allerques associated with Capanesse cedar pollen. The peptides have enhanced thoraperitie properties but reduced side effects_compared to naturally occurring allergers.
 Length 474
 2: Indels
 (IMMO.) IMMULOGIC PHARM CORP.
Bond JP, Garman RD, Griffith 13. Kuo M. Pollock J:
WPI: 94-635066/04.
 Match 79.0%: Score 113: DR 1: 1
Local Similarity 75.0%: Pred. No. 1.15e-04:
les 15: Conservative 3: Mismatches 2
 /note= "signal peptide"
22. .374
 /note= "mature peptide"
 Search completed: Mon Jun 19 16:14:18 2000
 Location/Qualitiers
 92 IESSKMNIKIKMPMYIAGYK 111
 1 IFSKNLNIKLNMPLYIAGNK 20
 20-JAN-1994,
15-JAN-1993, U00139,
10-JUL-1992, WO-UU5661,
01-SEP-1992, US-938990,
 W09401560-A
 Segrence
 Query Match
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Tue Jun 20 13:36:40 2000: MasPar time 2.38 Seconds 121.313 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

>US-09-142-524A-11 (1-20) from US09142524A.pep 143 I IFSKNINIKLMREVIAGNK 20 Title: Description: Perfect Score: Sequence:

PAM 150 Cap 15 Scoring table:

145341 segs, 14437480 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued i.5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCI\_COMB 5:backfiles; Dalabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STAMMARTES

Mean 18:944; Variance 62:364; scale 0:304

Statistics:

| Pred No.       | 1.13e+01  | 1.138-01   | 1.13e+01  | 1.80e+01   | 1.80e+01  | 1.80e+01   | 1.80e+01  | မ          | 1.80e+01   | 1.80e+01  | 1.80e+01   | 1.80e+01  | 3.59e+01  | 3.59e+01  |            | 5.66e+01  | . 65      | 7.09e+01            | 7.39e-01   | .87        | .87e+    | 70+         | 87e+       |
|----------------|-----------|------------|-----------|------------|-----------|------------|-----------|------------|------------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|---------------------|------------|------------|----------|-------------|------------|
|                | Applicati | Applicati  | Applicati | Applicati  | Applicati | Applicati  | Applicati | Applicati  | Applicati  | Applicati | Applicat:  | Applicati | Applicati | Applicati | Applicati  | Applicati | Applicati | Applicatio          | Applicatio | . Applicat | Κ.       | App. scatio | Applicatio |
| g :            | 9         | 78,        | 78,       | 72,        | 72,       | 72,        | 59,       | 59,        | 65         | 74.       | 74.        | 74,       | 76,       | 76,       | 76.        | 33,       | 33,       | Ä                   | - 4        | 180,       | 139      | Ś           | ,          |
| Description    | Seguence  | Sequence   | Seguence  | Sequence   | Seguence  | Sequence   | Sequence  | Sedneuce   | Seguence   | Sequence  | Sequence   | Sequence  | Seguence  | Sequence  | Seguence   | Sequence  | Sequence  | Seguence            | Sequence   | Sequence   | Sequence |             | Sequence   |
| CI             | ,         | JS-08-290- |           | US-08-175- |           | US-08-290- | -08-29    | us-08-580- | US-C8-175- | - 68 - 1  | US-08-550- | -08-2     | -08-1     | Ü         | US-08-580- | -08-78    | -68-1     | -960-60- <b>S</b> n | - 38 - 75  | - 08 - 2   | -82      | CS-08-455-  | PCT-JS96-1 |
| 8 J            | -         | П          | -         | ,-1        | _         | ~          | ٦         | ٦          | -4         | ۲,        | . 1        | - 1       | -4        | -         | ~          | N         | ~         | 7                   | 7          | 7          | ~        | 7           | •          |
| Lengtr         | 00        | 383        | က         | 387        | œ         | 387        | 391       | 391        | o,         | σ         | S          | o         | Q,        | 9         | 9          | 868       | S         | 2                   | 2          | 34         | S        | 382         | WY.        |
| opery<br>Match |           |            |           | 4.3        | 43.4      | 43.4       | 43.4      | 43.4       | 43.4       | 43.4      | 43.4       | 'n        | ä         |           | ä          | 39.9      | 6         | o,                  | Ġ          |            | œ        | مه          | α)         |
| Score          |           | 99         | 54        | 62         | 62        | 62         | 62        | 62         | 62         | 62        | 62         | 62        | 59        | 25        | 59         | 57        | 57        | 9 5                 | 56         | 55         | 52       | 55          | ι)<br>()   |
| Result<br>No.  | F 1       | 7          | 3         | 4          | 5         | 9          | 7         | œ          | Ċν         | 10        | 1.         | 12        | 13        | 14        | 13         | 16        | 17        | 18                  | 19         | 2C         | 2:       | 22          | 23         |

| 24 55 38.5 1055 2 US-08-659- Sequence 5, Applicatio 8.87e-01 25 57.8 2080 5 5.23423.4 atent No. 5223423 26 57.8 208 6 5.23423.4 atent No. 5223423 27 8 77.8 289 4 277.0592-0 Sequence 1. Applicatio 1.11e-02 28 54 37.8 291 2 US-08-865- Sequence 6. Applicatio 1.11e-02 30 54 37.8 525 2 US-08-749- Sequence 1.0 Applicatio 1.11e-02 31 54 37.8 525 2 US-08-749- Sequence 2. Applicatio 1.11e-02 32 37.1 442 5 53.0667-6 atent No. 5310.667 33 37.1 509 2 US-08-749- Sequence 51. Applicatio 1.38e-02 34 53 37.1 509 2 US-08-745- Sequence 51. Applicatio 1.38e-02 35 37.1 509 2 US-08-745- Sequence 2. Applicatio 1.38e-02 36 37.1 509 2 US-08-75- Sequence 2. Applicatio 1.38e-02 37 1 10 509 2 US-08-75- Sequence 2. Applicatio 1.38e-02 38 37.1 509 2 US-08-75- Sequence 2. Applicatio 1.38e-02 38 37.1 509 2 US-08-55- Sequence 2. Applicatio 1.38e-02 38 37.1 509 2 US-08-55- Sequence 2. Applicatio 1.38e-02 38 37.1 509 2 US-08-55- Sequence 2. Applicatio 1.38e-02 38 37.1 509 2 US-08-55- Sequence 5. Applicatio 1.72e-02 39 55 36.4 222 2 US-08-75- Sequence 5. Applicatio 1.72e-02 41 52 36.4 803 1 US-08-156- Sequence 5. Applicatio 1.72e-02 42 52 08-76- Sequence 5. Applicatio 1.72e-02 | ALIGNAENTS  U.T.:  U.S. 08-175-0694-78 STANDARD: PRT: 193 AA.  SEQUENCE 78. APPLICATION US/08175059A  SEQUENCE 78. APPLICATION: "S/08175059A  SEQUENCE 78. APPLICATION: "S/08175059A  PRECIS NO. 576/81  RAPPLICANT: Raper. David G  APPLICANT: Raper. David G  AD189-198  CURRESPONDENCE ADDRESS: COMPUTER READABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: David G  COMPUTER: David G  SOFTWARE: Parently Release 11.0, Version #1.25  COMPUTER: David G  COMPUTER: David G  APPLICATION NUMBER: US/08/115,069A  FILING DATE: March 17 1989  APPLICATION NUMBER: US/08/115,069A  FILING DATE: March 17 1989  ATTOMERY/AGENT INFORMATION: NUMBER: US/08/115,069A  ATTOMERY/AGENT INFORMATION: NUMBER: March 17 1989  ATTOMERY/AGENT INFORMATION: NUMBER: May C) 1993  ATTOMERY/AGENT INFORMATION: TELECOMMUTICATION NUMBER: INI-018DV  TELECOMMUTICATION NUMBER: 1 11.018DV  TELECOMMUTICATION NUMBER: 1 11.018DV  TELECOMMUTICATION NUMBER: 1 10.01752-04C  TELECOMPUTER: SEADIL DATE: May C) 1993  ATTOMERY/AGENT TOWNER: 1 10.01752-04C  TELECOMPUTER: MAY C) 1993  ATTOMERY/AGENT TOWNER: 1 10.01752-04C  TELECOMMUTICATION NUMBER: 1 10.01752-04C  TE |
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| ପରାରା ପର୍ବିକ କିଲ୍ଲ ଅନ୍ତର୍ବିକ କିଲ୍ଲ ଅନ୍ତର ଅନ୍<br>ଆଧାର                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

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Sequence 78, Application /08290448A
Patent No. 5688204
GENERAL INFORMATION:
APPLICANT: Rapers, Bruce
APPLICANT: Rapper, David G.
APPLICANT: Rathar, Thorner
APPLICANT: Rathar, Thorner
APPLICANT: Rathar, and G.
APPLICANT: Rough Mei-chang
ITILE OF INFORTHON: Alle Jenic Proteins From Ragwood and Uses
NUMBER OF SUCUROES: 93
CORRESPONDENCE ADORESS:
 CUITY: Boston
CUITY: Boston
CUITY: Boston
COUNTRY: CSA
Z.P. 02109-1875
COMPUTER READABLE FORM
MEDIUM TYPE: FORM
OPERATING SYSTEM: PCCNOS/MS-DCS
SOFWARE: Patentin Release #1.9, Version #1.25
CUBRENT APPLICATION DATA
PPELICATION NUMBER: US/E6/290-44RA
FILING DATE: Margin 15, 1944
PRIOR APPLICATION DATA:
FILING DATE: Margin 15, 1944
APPLICATION NUMBER: US/C7/25, 96;
FILING DATE: Margin 15, 1940
APPLICATION NUMBER: US/C7/25, 96;
FILING DATE: Margin 15, 1940
APPLICATION NUMBER: US/C7/25, 96;
FILING DATE: Margin 15, 1940
APPLICATION NUMBER: US/C7/25, 96;
FILING DATE: Margin 15, 1940
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FILING DATE: Margin 15, 1940
APPLICATION NUMBER: US/C7/25, 96;
FILING DATE: Margin 15, 1940
APPLICATION NUMBER: US/C7/25, 96;
FILING DATE: MARGIN 16, 1940
FILING DATE: MARGIN 16, 1940
FILING DATE: WARGIN 16, 19
 Query Match

Query Match

Best Local Similarity 35.0%; Pred. No. 1.13e-01;

Matches 7: Conservative 6: Mismatches 7; Indels
 387 AA
 ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
 ٦.
٢.
 PRT:
 MOLECULE TYPE: protein
JENCE 383 AA: 41852 MW: 738971 CN;
 Sequence 78, Application 74708293448A
 : 383 amino acids
amino acid
 STANDARD;
 110 IFERDMVIRLDRELAINNDK 129
 SECUENCE CHARACTERISTICS
 linear
 RESULT 4
ID US-08-175-C69A-72
XX
AC XXXXXX
XX
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XX
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 US-08-290-448A-78
 TOPOLOGY:
 LENGIH:
 SECUENCE
 XXXXXX
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 Gaps
 Gaps
 APPLICANT: Roders, Bruce
APPLICANT: Rapper, David 3.
APPLICANT: Rainar, Thorun
APPLICANT: Walner, David 3.
APPLICANT: Walner, David 3.
APPLICANT: Walner, Marchang
TITLE OF INVENTION: Allerarcic Proteins From Ragweed and Uses
NUMBER OF SAQUENCES:
ADDRESSE: LAHIVE 4 COCKFIELD
STREEL: 60 State Street, suite 510
STREE: Massachusetts
 .;
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:
 Match tonal Similarity 35.0%; Pred. No. 1.13er01; Const Similarity 35.0%; Pred. No. 1.13er01; Pred. No. 1.13er01; Pred. Similarity 6: Mismatches 7; Indels
 Query Match 44.8%: Score 64: DB 1: Length 383; Best Local Similarity 35.0%: Pred. No. 1.13e+01; Matches 7: Conservative 5: Mismatches 7: Indeis
 UMEDIUM NIAMAGE FURDED DISK
COMPUTER I IBM PC COCCRAIDS COMPUTER I IBM PC COCCRAIDS COCCRAINS COCCANAINS COCCRAINS COCCRAINS COCCRAINS COCCANAINS COCCA
 383 AA
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1841
 MOLECULE TYPE: protein
JENCE 383 AA: 41852 MW: 738971 CN:
LENGTH: 383 amino acids
TYPE: arino acid
TOPOLOGY. linear
MOLECULE TYPE: protein
SEQUENCE 383 AA: 41652 MW: 738971 CN;
 Sequence 78, Application US/08290448A Patent No. 5676954
GENERAL INFORMATION:
 Sequence 78. Application US/08290448A
 TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 78; SEQUENCE CHARACTERISTICS: LENGTH: 363 amino acids
 STANDARD
 : 363 amino acids
amino acid
GY: linear
 110 IFERDMVIRLDRELAINNOK 129
 110 IFERDMVIRLORELAINNUK 129
 21P: 02109-1875
COMPUTER REGARDE FORM:
MEDIUM TYPE: FLOWER
COMPUTER
 1 TESKNINTKLNMPLYIAGNK 20
 US-08-290-448A-78
 TOPOLOGY:
 XXXXXX
 Matches
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SEQUENCE
 XXXXXX
 RESULT
 5
C
 ô
 APPLICANT: Rogers, Bruce
APPLICANT: Riapper, David G.
APPLICANT: Rafnar, Thorun
APPLICANT: Ruo, Mel-chang
TILE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD. LLP
STREET: 60 State Street
CITY: BOSSON
STATE: WALL
 Sequence 72, Application US/C8290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: ROPErs, Bruce
APPLICANT: Rapers, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Rafnar, Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
 ::
O
 Query Match
43.44; Score 62; DB 1; Length 397;
Best Local Similarity 25.0%; Pred. No. 1.80c-01;
Matches 5; Conservative 10: Mismatches 5; Indels
 CITY: Beston
CITY: Beston
COMUTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Florepy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Florepy disk
COMPUTER SYSTEM: PC DOS/WS-DOS
SOFTWARE: PARENTING SYSTEM: PC DOS/WS-DOS
SOFTWARE: PARENTING PAREN: US/08/175,069A
FILING DATE: December 29, 1993
PRICE APPLICATION NUMBER: US 07/529,951
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/529,951
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/529,951
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: MAY 29, 1990
ATTORNEY/AGENT INFORMATION:
 387 AA.
 ALIGHMAN TO THE MANAGEMENT OF
 INFORMATION FOR STO ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 387 As: 41660 MW; 736967 CN;
 Sequence 72, Application US/08175069A
Patent No. 5775751
GENERAL INFORMATION:
APPLICANT: ROGETS, Bruce
 Sequence 72, Application US/08296448A
Sequence 72, Application US/08175069A
 STANDARD;
 109 IFERDMVIRLDKEMVVNSDK 129
 1 IFSKNINIKLNMPLYIAGNK 20
 US-08-290-448A-72
 SECTIONS
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 Solution of the control of the contr
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Gaps
 Sequence 72, Application US/08290448A
Patent No. 5698304
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rogers. Bruce
APPLICANT: Rapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Ruo, Mei-chang
ITILE OF INVENTION: Allergenic Proteins From Ragweed and Uses
CORRESPONDENCE STORES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Strc., suite 510
 0
 COMMUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: Fishppy disk

COMPUTER: IBM PC COMPUTIBLE

APPLICATION NUMBER: 197/529,951

FILING DATE: May 29, ...

APPLICATION NUMBER: CS 7/325,365

FILING DATE: March: 7, 1989

ATTORNEY/AGENT INFORMATION:
 Query Match 43.4%; Score 62; DB 1; Length 387; Best Local Similarity 25.0%; Pred. No. 1.60e+01; Matches 5: Conservative 10; Mismatches 5; Indels
 387 AA
 suite 510
 IMI - 018CN
 P.K.1
 CITY: Boston
STATE: Massachusetts
CUUTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: USA PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 MOLECULE TYPE: protein
FENCE 387 AA: 41660 MW; 736967 CN:
 Sequence 72, Application US/08290448A
 ADDRESSEE: LAHIVE & C KFIELD STREET: 60 State Street suite
 NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36.207
REFERENCE/DOCKET NUMBER: IMI
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
IELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 72
SECJENCE CHRACTERISTICS:
LENGTH: 387 amino acids
 STAND. 400
 109 IFERDMVIRLDKEMVVNSDK 1.~
 1 IFSKNLNIKINMPLYIAGNK 20
 STREET: 60 State Stri
CIIY: Boston
STATE: Massachusetts
CORRESPONDENCE ADDRESS:
 amino acid
 linear
 US-08-290-448A-72
 TOPOLOGY:
 COUNTRY:
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 Sequence 59. Application US/08290448A
Patent No. 567694
SENERAL INFORMATION:
APPLICANT: Register, Based
APPLICANT: Rather, David G.
APPLICANT: Rather, Thering
APPLICANT: Rather, Thering
APPLICANT: Runs Antering
APPLICANT: Nuc. Antering
APPLICANT:
 ..
0
waery March 43.4%: Score 62: UB 1: Length 387:
Bost Local Similarity 25.0%: Pred. No. 1.80e-01:
Matches 5: Conservative 10: Mismatches 5: Indels
 STATE: MASSACHUSELTS
CCUNTRY: USA
21P: 0109-12P: COMPUTER: 10109-12P: COMPUTER: EACH PC COMPUTER: 1010PF PC COMPUTER: COMPUTER: 1010PF PC COMPUTER: Patentin Release = 1.0; Version #1.25
CCREWER APPLICATION DATA
 391 AA
 APPLICATION NUMBER: US/08/290,448A FILING DATE: Addist 15, 1994
PRICE APPLICATION DATE: 1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: MACE: 17, 1989
ATIONNEY/AGENI INFORMATION:
 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suito 510
 FRT
 MOGECULE TYPE: protein
SEQUENCE 387 AA: 41660 MW: 736967 CN:
 Sequence 59. Application US/08290448A
 Amy E. Mandragouras
 STANDARD:
 109 IPERDMVIRLPKEMVVNSDK 128
 1 IPSKNINIKONPUYIAGNK 20
 SIREET: 60 St
 US-08-290-448A-59
 XXXXXX
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Saps
 Sequence 59, Application US/08290449A
Patent No. 5698204
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Klapper, David 3.
APPLICANT: Rainar, Thorum.
APPLICANT: Rainar, Thorum.
APPLICANT: Nathar, Signature 510
STREET: 60 State Street, suite 510
 STREET 6 State Sireht suite 510
STREET 6 State Sireht suite 510
STATE Massachusetts
JOUNING 188

JOHN 188

 Query Match
Best Local Similarity 40.3%; Prod. No. 1.80e-31:
Matches 8; Conservative 5; Mismatches 7, Indees
 391 AA
 1MI-018CN
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п.
 MOLECULE TYPE: protein
UENCE 391 AA: 42864 MW: 754645 GN.
 Sequence 59, Application US/UN290448A
REGISTRATICN NUMBER: 36,207
REPRENCE/DOCKET NUMBER: IMI-
IELECOMMUNICATION INFORMATION:
IELEPHONE: (617)227.746.)
IELEFAX: (617)227.594
INFORMATION FOR SEQ 1D NO: 59:
SEQUENCE CHARACTER:371CS
LENGTH: 391 amino act.
 INFORMATION FOR SEQ IS NO: 59, SECUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acids
TOPCLOSY: linear
 STANDAKU
 i: 391 amino aci-
 113 IFKRNMVIHLNQELVVNSDK 132
 1 IFSKNINIKINMPLYIAGNK 20
 MOLECULE TYPE: protein
 inear
 LT 8
US-08-290-448A-59
 OPCLOGY:
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US-08-175-059A-74
 SECUENCE
 xxxxxx
 XXXXXX
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 Gaps
 Gaps
 APPLICANT: Rogers, Bruce
APPLICANT: Rapper, David G.
APPLICANT: Rapper, David G.
APPLICANT: Rapper, David G.
APPLICANT: Ruo, Mel-chang
APPLICANT: Ruo, Mel-chang
TITLE CF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE SS:
ACDRESSPONDENCE SS:
ACDRESSPONDENCE STREET
CORRESPONDENCE STREET
CORRESPONDENCE STREET
CITY: Boston
STATE: Massachusetts
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 .:
0
 / Match 43.4%: Score 62: DB 1; Length 391; Local Similarity 40.0%: Pred. No. 1.80e+01; conservative 5: Mismatches 7: Indels
 Length 391;
 / Match 13-4%; Score 62; Du 1; Length 391;
Local Similatity 40.0%; Pred. No. 1.80e+51;
ies 8; Conservative 5; Mismatches 7; Indels
 COUNTRY USA
ZIP: 02169-1875
COMPUTER REACRABLE FORM:
REDICH TYPE: Floppy
GOMPOTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patent': Re-case #1.6, Version #1.25
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/175.069A
FILING DATE: December 29, 1993
 391 AA
 APPLICATION NUMBER: US/08/175,069A FILING DATE: December 29, 1993 FRICA PAPPLICATION DATE: APPLICATION NUMBER: US 07/25,365 FILING DATE: May 29, 1990 APPLICATION NUMBER: US 07/125,365 FILING DATE: MAICH 17, 1969 ALIGNBY/AGENT INFORMATION:
 REGISTRATION NUMBER: 36.207
RECIESTRATION NUMBER: 36.207
REPERENCE/JOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227.7460
 PRT
 LE TYPE: protein
391 AA: 42864 MW: 754045 CN:
391 AA; 42864 MW; 754C45 CN
 Sequence 39, Application US/08175069A Patent No. 5776761
GENERAL INFORMATION:
 Sequence 59. Application US/08175069A
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ 1D NO: 59:
SEQUENCE CHARACTERISTICS:
 STANDARD;
 . 391 amino acids
amino acid
 113 IFKRNMVIHINQELVVNSDK 132
 113 IFKRNMVIHLNQELVVNSDK 132
 1 IFSKNUNIKUNMPLYIAGNK 20
 1 IFSKNINIKINMPLYIAGNK 20
 linear
 US-08-175-069A-59
 TELEPHONE:
 TOPOLOGY:
 MOLECULE
SECUENCE 39
 SEQUENCE
 Query Match
 Query Match
 XXXXX
 Best Loca
Matches
 Matches
 RESULT
 ò
```

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Gabs
 APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorun.
APPLICANT: Rafnar, Thorun.
TILLE OF INVENTION: Allergenic Profeins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
 OPERATING SYSTEM: PC-DCS/MS-DUS
SOFTWARE: Patentin Release #1.C. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/175.069A
FILING DATE: December 29, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529.931
FILING DATE: May 29, '990
APPLICATION NUMBER: US 07/325.365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
 Query Match

43.4%; Score 62; DB 1: Lengtl 398;
Best Local Similarity 40.0%; Pred. No. 1.80e+01;
Matches 8: Conservative 5; Mismatches 7: Indels
 398 AA.
398 AA
 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & CCCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 NAME: Amy E. Mandrago.:das
REGISTRATICN UNMBER: 36,201
REFERENCE/DOCKET UNMBER: IMI-0183V
TELECOMMUNICATION: INFORMATION:
 PRT;
 MOLECULE TYPE: protein
JENCE 398 AA, 43664 MW, 779006 CN;
 Sequence 74, Application US/C8175069A Patent No. 5776761
GENERAL INFORMATION:
 Sequence 74. Application US/08296448A
Patent No. 5676954
 Sequence 74, Application US/08175059A
 Seguence 74, Application US/08290448A
 MEDIUM TYPE: Floopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-FGS/WG-
 15 NO: 74:
 TELEPHONE: (617)227-7400
 STANCARD
 STANDARD;
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NOT
SEQUENCE CHARACTERISTICS
 120 IFKRNMVIHLNQELVVNSDK 139
 1 ITSKNENIKENMPLYIAGNK 20
 J 11
US-08-290-448A-74
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LT 13
US-08-175-069A-75
 TOPOLOGY:
 LENGTH:
 xxxxxx
 Ωp
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 Gaps
 Pate:: T No. 5698204
GENERAL INFORMATION:
APPLICANT: ROGERS, Bruce
APPLICANT: Rapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Ruo, Mei-Chang
TIILE OF INVENTION:
NUMBER OF SEQUENCES: 93
GENERAL INFTERATION:
APPLICANT: Rogers. Bruce
APPLICANT: Rogers. David G.
APPLICANT: Rafaper: David G.
APPLICANT: Kuc, Mei-chang
APPLICANT: Kuc, Mei-chang
APPLICANT: Ruce ANJURGENIC Proteins From Ragweed and Uses
NUMBER CF SEQUENCE: 93
CORRESPONDENCE ADDRESS:
 ö
 STREET: 66 State Street, suite 513
STREET: 66 State Street, suite 513
CITY: Boston
STATE: Massachusetts
COUTHER PADABLE FORM:
MEDULM TYRE: Flopky disk
COMPUTER: IRM PC COMPATIBLE
OPERATIOS SYSTEM: PC-COOS/MS-DOS
SOFTWARE: PATENTIA RE-EASE #1.0. Version #1.25
CURRENT AFFLICATION DATA:
PRIOR DATE: Auqust 15, 1994
PROR APPLICATION OATA:
APPLICATION NUMBER: US 07/525,951
 Match 43.4%; Score 62: DB 1: Lentin 398; Local Similarity 40.0%; Pred. No. 1.80e+61; es 8; Conservative 5; Mismatches 7; Indels
 FILING FATE: May 29, 1990
APPLICATION NUMBER: US 07.7325.365
FILING ATE: Warch 17, 1989
ATTORNEY/ACRT INFORMATION:
NAME: AND E. MAIGRAGOLIAS
REGISTATION NUMBER: 36,207
REPERENCE/POCKET NUMBER: 36,207
REPERENCE/POCKET NUMBER: 36,207
REPERENCE/POCKET (617)27.7400
IELEFAX: (617)227.7400
IELEFAX: (617)227.5941
INFORMATION FOR SEQ ID NO: 74:
 CORRESPONDENCE ADDRESS:
ADDRINSSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 5:0
 E: LAHIVE & COCKFIELD
60 State Street, suite 510
 PRT;
 JOSY: linear
LE TYPE: protein
398 AA: 43664 MW: 779006 CN:
 Sequence 74, Application US/08290448A
Patent No. 5698204
 Sequence 74, Application US/08290448A
 STANDARD:
 SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
IYPE: amino acid
TOPOLOGY: linear
 120 IFKRNMVIFINGELVVNSUK 139
 1 IPSKNENIKINMPIKIAGNK
 CITY: Boston
 JT 12
US-08-290-448A-74
 ADDRESSEE:
 SEQUENCE 39
 Query Match
 XXXXXX
 Matches
 RESULT
```

```
Sequence 70. Application 18/PRISTANA
Determ No. 577671
Determ No. 577671
Determ No. 577671
DENERAL INFORMATION:
APPLICANT: Riapper, David G.
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STRIE: Massarbir-7
 Gabs
 MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC TOUGHTELS
SOFTWARE: PRIORITY Release #1.0. Version #1.25
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/06/240.448A
PRIOR APPLICATION NUMBER: US/06/240.448A
PRIOR APPLICATION NUMBER: US 07/25/9/51
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/32/365
FILING DATE: MARCH 17, 1989
ATTORREYAGENT INFORMATION:
NAME: AMY E. MANDERS: US 07/32/365
REDISTRATION NUMBER: US/07/32/365
REDISTRATION NUMBER: US/07/32/365
 Ouery Match 43.4%; Score 62: UB 1: Length 398:
Best Local Similarity 46.0%; Pred. No. 1.85e+61;
Matches 8: Conservative 5: Mismatches 7: Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: December 29, 1993
 397 AA
 REGISTRATION NUMBER: 3£.207
REFERENCE/JOCKET NUMBER: 1M1-019CN
TELECOMONUNICATION:
T.LEPHONE: (617)227-7405
TELEFAX: (617)227-594.
INFORMATION FOR SEQ ID NC: 74:
SEQUENCE CHARATERISTICS:
 PKT
 MOLECULE TYPE: protein
SEQUENCE 398 AA; 43664 MW: 779006 CN:
 STANDAR
 398 amino acids
 120 IFKRYMVIHLNOELVVNSDK 139
 1 IFSKALNIKLNMPLYIAGNK 20
 COUNTRY: USA
Massachusetts
 ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
 amino acid
 02109-1875
```

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STANDARD:
TELEFAX: (617)227-5941
INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
 (2)
**:
 CITY: Boston
STATE: Massachusetts
COUNTRY: USA
 ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 1 IFSKNINIKINMPLYIAGNK
 119 IFKNDMVININGELVVNSI
 linear
 RESULT 15
ID US-08-290-448A-76
 TOPOLOGY:
 XXXXXX
 2
 ð
 888888888
 Gaps
 Sequence 76, Application US/08290448A
Patent No. 5976954
GENERAL INFURMATION:
APPLICANT: Reperty Bruce
APPLICANT: Rapper David G.
 ..
 COMPINE READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBA. PC COMPATIBLE
COMPOTER: IBA. PC COMPATIBLE
CORPOTER: IBA. PC COMPATIBLE
CORPOTER: IBA. PC COMPATIBLE
CORPOTER: IBA. PC COMPATIBLE
SOFTAME: PATENTIAN PRICE
CORRENT APPLICATION DATA:
FILING DATE: AUGUST: 15, 1994
PRIOR APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTOMNEY/AGENT INFORMATION:
NAME: AMANDREMENTIAN NUMBER: 36,207
RECINTRATION NUMBER: 33,207
REFERENCE/COMPATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 Query Match

41.3%: Score 59: DB 1: Length 397:
Best Local Sirilarity 35.0%: Pred. No. 3.59e+01;
Matches 7: Conservative 7: Mismatches 6: Indels
 397 AA
 APPLICATION WOREEN: US 0/722,791
FILING DATE: May 29, 1990
APPLICATION WOREEN: US 07/325,365
FILING DATE: March 17, 1999
ATTORNEY/AGENT INFORMATION:
NAME: MANGEN: ABOUTES
REGISTRION WORBER: 36,207
REFERENCE/DOCKET WOMBER: IMI-018DV
IELEPHONE: (617)227-740C
INFORMATION FOR SEC,120 MORBATION:
FELERAX: (617)227-5941
 PRT:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
 JOCK: linear
UE TYPE: protein
397 AA; 42947 MM; 781425 CN;
 Sequence 76, Application US/08290448A
 COLEMB 197 amino acids TOPCLOSE amino acids TOPCLOSE amino acid
 STANDARD
 119 IFKNOMVININGELVVNSDK 138
 1 IFSKNINIKLNMPLYIAGNK 20
 Massachusetts
 Soston
 USA
 J 14
US-08-290-448A-76
 COUNTRY
 CITY: B
 MOLECULE
 SEQUENCE
 xxxxxx
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Ċ
 Gaps
 Sequence 76, Application U./ :8290448A

Batert No. 5688204

GENERAL INFORMATION

APPLICANT: Rogers. Bruc.
APPLICANT: Rapper, David 3.
APPLICANT: Rafnar, florum
APPLICANT: Ruo, Mei-chang
IIILE OF INVENTION: All ergenic Proteins From Ragweed and Users
NUMBER OF SEQUENCES 9.
CORRESPONDENCE ADDRESS:
 3
 Ouery Match 41.3%; Score 59; DB 1; Length 397;
Best Local Similarity 35.0%; Pred. No. 3.59e+01;
 vue.y match
Best Local Similarity 35.0%: Pred. No. 3.59e+01;
Matches 7; Conservative 7; Mismatches
 WEDCOM TYPE: Floppy disk
COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COTTAIL LE COMPUTER: TW PC COMPUTER: TW
 397 AA
 ADDRESSEE: LAHIVE'S COCKFIELD
STREET: 60 State Street, suite 510
CIIY: Boston
 IMI-018CN
 PRT
 MOLECULE TYPE: protein
SEQUENCE 397 AA: 42947 MW; 781425 CN;
TOPCLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 397 AA; 42947 MW; 781425 CN;
 REFERENCE/DOCKET NUMBER: 36.207
REFERENCE/DOCKET NUMBER: IMI-6
TELECOMMUNICATION IMFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
NFORMATION FOR SPO.22
 Sequence 76, Application US/08290448A
 INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
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Matches 7: Conservative 7: Mismatches 6: Indels 0: Gaps 0:

OB 119 TERNDMVINLNGELDVNSDK 138 OF 1 TERNINGELDVNSDK 20

Search completed: the Jun 20 14:36:45 2000 Job time : 5 sect.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Mon Jun 19 16:27:09 2000; MasPar time 15.49 Seconds 130.125 Million cell updates/sec Run on:

Tabular cutput not generated.

>CS-09-142-524A-11 (1-20) from USO9142524A-pep 143 ! IFSKNINIKLNADIYIAGNK 20 Description: Perfect Score: Sequence:

Scoring table:

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721208 segs, 100765575 residues

Searched

Post-processing:

Database

Minimum Match 3% Listing first 45 summaries

a-pending liecz 2:06 3:06C 4:07 5:U°) 6:U81 7:U82 8:U83 9:U84A 10:0848 11:U85 12:U86 13:U87 14:U83 15:U89 16:U90 17:U91 18:U82 19:U93 20:U94 21:U95 22:NEWP 23:NEWD60 24:NEWU8 25:NEWU9

Mean 22.853; Variance 66.203; Scale 0.345 Statistics: Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 4, Applicatio 3.48e-08
Sequence 95, Applicatio 1.26e-05
Sequence 95, Applicati 1.26e-05
Sequence 97, Applicati 1.26e-05
Sequence 37, Applicati 1.26e-05
Sequence 37, Applicati 2.25e-04
Sequence 33, Applicati 2.25e-04 Description US-09-142-US-5-1109-US-08-467-US-08-226-US-08-250-US-08-467-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-US-08-266-Length. Cuery 

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 APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION 424
PRIOR APPLICATION ATA:
APPLICATION NUMBER: UP/350.225
FILING DATE: December 6, 1994
ATOMEN/ADATE: December 6, 1994
ATOMEN/ADATE: DECEMBER: UP/350.225
FILING DATE: DECEMBER: UP/350.225
FILING DATE: DECEMBER: UP/350.225
FILING DATE: DECEMBER: UP/350.225
FILING DATE: DECEMBER: US. (BMI-028CPE2)
FELEPAR: GATION NUMBER: US. (GAT)
FILEPAR: GAT) 227-746C
FILEPAR: GAT) 227-5941
INFORMATION FOR SEQ 1D NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 Amino Acids
TYPE: mino Acids
 Length 357.
 • Match 86.0%: Score 123: CH 10: Lendt! 3% Local Similarity 75.0%; Pred. No. 1.25e-65; cs 15: Conservative 4: Mismatches 1: Indeis
 ADDRESSEE: ImmuLogic Pharmaceutical Corporation,
PIREET: 61D Lincoln St
CITY: Waltham
STATE: MA
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,940
 357 AA
 ..
3.
 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 367 AA: 39846 MW; 695078 CN:
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: 68/256,225
FILLING DATE: December 6: 1994
APPLICATION NUMBER: 68/226,248
 Sequence 95, Application US/08468940 GENERAL INFORMATION:
 Sequence 95. Application US/U6468940
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 STANDARD:
 92 IFSONMNIKIKMPLYVAGHK 111
 I I FILLITITION IN 1 STATE IN 1 S
 CORRESPONDENCE ADDRESS:
 USA
 FILING DATE:
 SECUENCE
 Query Match
 a
 8888888888888888888888888
 ô
 APPLICANT: GROADS EDWARD G.
APPLICANT: GROADS EDWARD G.
APPLICANT: HIGGS-HORUTI. TERUMI
APPLICANT: MIGGS-HORUTI. TERUMI
TITLE OF INVENTION: FAMILY OF PLANI PATHOGENESIS RELATED PROTEINS
FILE REFERENCE: USSG-23-E-Z.
CURRENT APPLICATION NUMBER: US/6C/109,165
CURRENT PILLMG DATE: 1998-1-ZG
CURRENT PILLMG
 ..
O
 Gaps
 Sequence 95. AFFIleation FFCR467.27

GENERAL INFORMATION:
APPLICANT: Grifteth, Irwin J.;
APPLICANT: Grifteth, Irwin J.;
APPLICANT: Bond, Julian F.;
APPLICANT: Sarman, Revibang,
APPLICANT: Yeung, Sistered D.;
APPLICANT: Yeung, Sistered H.;
APPLICANT: Yeung, Sistered H.;
APPLICANT: Exievy, Mark A.;
APPLICANT: Exievy, Mark A.;
APPLICANT: Exievy, Mark A.;
APPLICANT: Powers, Sieven P.;
IIILE DE INVENTION: Japanese Cedar Pollen
NUMSER CF SEQUENCES: 261
 ..
 E: Immulogic Pharmaceutical Corporation, Inc. 610 Lincoln St.
 Length 346:
 Score 123; DB 3; Length 340. Pred. No. 1.26e-05;
 COUNTRY: USA
ZIP: 00154
COMPUTER READBRIE FORM:
MEDUIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERALING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
 367 AA
 346 AA
 .;
С.
 1. Juniperus ashei
345 AA: 37639 MW: 616983 CN:
 PRT
 Sequence 95. Application US/08467023
 Sequence 1, Application 08/60109165
GENERAL INFORMATION:
 Sequence 1, Application US/60109165
 STANDARD;
 STANDARD;
 71 IFSONMVIKLKMPLYVAGHK 90
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Immulogio
 Ouery Match 86.0%;
Rest Local Similarity 75.0%;
Matches 15; Conservative
 1 IFSKNENIKENMPLYTAGNK
 waltham
 05-08 467-023-95
RESULT 2
ID US-60-109-165-1
XX
 STATE
 TYPE: PRI
 ORGANISM
 SEQUENCE
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 XXXXXX
 RESULT
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ADDRESSEE: Immu
STREET: 610 Lin
CITY: Waltham
 USA
 02154
 38-380-228-95
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 COUNTRY:
 XXXXXX
 RESULT
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 ö
 Gaps
 Sequence 95. Application US/08226248A
GENERAL INFORMATION:
APPLICANT Griffeth. Irwin J.;
APPLICANT POLIOCK, Joanne;
APPLICANT Bond, Julian F.;
APPLICANT Garman, Richard D;
APPLICANT Kuo, Mei-Chang;
APPLICANT Kuo, Mei-Chang;
APPLICANT Bracer, Andrew;
APPLICANT BRACERS;
CFREESPONDENCE ADDRESS;
APPLICANT BRACES;
APPLICANT BRACES;
 E: Immulogic Pharmaceutical Corporation, Inc. 610 Lincoln St.
 Query Match 86.0%; Score 123; DB 10: Length 367; Best Local Similarity 75.0%; Pred. No. 1.26e-05; Matches 15: Conservative 4; Mismatches 1; Indels 9
 STATE: MA

SUNDING: USA

ZUNDING: USA

ZUNDITER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PARTICATION DATA:

APPLICATION NUMBER: US/08/26,248A

FILING DATE: APPLICATION: A14,

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/938,990

FILING DATE: SEPERMER I. 1992

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: January 15, 1993
FILING DATE: April 8, 1994

APPLICATION NUMBER: 67/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 67/938,990
FILING CATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/00139
FILING CATE: January 15, 1993
ATTORNEY/AGET INFORMATION:
NAME: DATAGNE A: VASIGNE
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 055.6 US (IMI-026CP2)
TELECOMUNICATION: NEDRIALION:
TELECOMUNICATION: NEDRIALION:
TELECOMUNICATION: 165-6000
INFORMATION FOR SEQ 10 No: 95.
SEQUENCE CHARACTERISICS:
LENGTH: 357 Amino acids
TYPE: maino acid
NOTOWEN INFORMATION: 10-001
 367 AA.
 PRT;
 MCLECULE TYPE: protein
SEQUENCE 367 AA: 39846 NW; 695078 CN;
 Sequence 95. Application US/08226248A
 STANDARD:
 92 IFSONMNIKLKMPLYVAGHK 111
 1 IFSKNINIKLNMPLYIAGNK 20
 CITY: Waltham
STATE: MA
 US-08-226-248A-95
 ADDRESSEE:
STREET: 61
 XXXXX
```

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0
 Saps
 Sequence 95, Application US/U8350225
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin 3...
APPL CANT: Pollock, Joanne:
APPL CANT: Bond, Julian F.:
APPLICANT: Garman, Rithard 3...
APPLICANT: Yeung, Sluch: H.:
APPLICANT: Yeung, Sluch: H.:
APPLICANT: Brieven P.
ITLE OF INVENTION: Allerenic Proteins And Poptides From ITLE OF INVENTION: Allerenic Proteins And Poptides From ITLE OF INVENTION: Allerenic Proteins And Poptides From ITLE OF INVENTION: Allerenic Proteins And Poptides Conserved Professor Conserved Proteins And Poptides From ITLE OF INVENTION: Allerenic Proteins And Poptides From ITLE Pro
 D. Immulouis grainmasser real Corporation. Inc
616 Lincols St.
 Length 367
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-705/Ms-D05
SOFTWARE: PATENTIN PC-705/Ms-D05
SOFTWARE: PATENTIN PAPA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,225
FILING DATE: December 6, 1994
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/225,248
FILING DATE: APPLICATION NUMBER: 07/380,990
FILING DATE: SEPTEMBER: 07/380,990
FILING DATE: PCT/US93/00139
APPLICATION NUMBER: PCT/US93/00139
 Indeis
ATTORNEY/AGENT INFORMATION:
NAME: Darlege A: Vanstone
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACIERISTICS:
LENGTH: 357 amino acids
IYPE: amino acids
IOPOLOGY: linear
 Query Match

86.0%; Score 123; 28.7; Le
Best Local Similarity 75.0%; Pred. No. 1.26e-05;
Matches 15; Conservative 4; Mismatches 1;
 367 AA
 PRT:
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 367 AA: 39846 MW: 695078 CN;
 Sequence 95. Application US/08350225
 FILING DATE: January 15, 1993
ATDORNEY/AGENT INFORMATION:
NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
 STANDARE
 92 IFSQNMNIKLKMPLYVAGHK 111
 111 ':111::111:'::F
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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 Gaps
 Sequence 95. Application US/08467006
GENERAL INFERMATION:
APPLICANT: POLICOK, Journel
APPLICANT: Bond, Julian F.:
APPLICANT: Bond, Julian F.:
APPLICANT: Bond, Julian F.:
APPLICANT: Woo, Mei-Chang:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Steven P.
TILLE OF INVENTION: Albergenic Proteins And Replicant APPLICANT: Brauer, Steven P.
TILLE OF INVENTION: Japanese Godar Polien
NUMBER OF SECONOCES: 221
CORRESPONJENCE ADDRESS:
ADDRESSLE: Fundlingiv Phaimaceutical Corporation: Inc.
STREET: 610 Lincoln St.
COUTY: Waitham
STATE: MA
 MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
CFREATING SYSTEM: PCLOSCANS-DOS
SCTUMARE: Datentin Release #1.0. Version #1.25
SCTUMARE: Datentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/467.006
FILING DATE: June 6, 1995
CLASS:FICATION: 424
PRIOR DATE: June 6, 1995
CLASS:FICATION: A24
PRIOR DATE: December 6, 1994
ATTORNEYAGEN: INFORMATION:
NAME: Jane E. Remillard
REDIENCE/DOCKEN UNMBER: 38.872
REPERENCE/DOCKEN UNMBER: 38.872
REPERENCE/COMPANION INFORMATION:
TILEPPONE: (617) 227-7406
TILEPPON
 3
 Cuery Match
Hest Local Similarity 75.0%; Pred. No. 1.25e-65;
Matches 15; Conservative 4; Mismatches 1: Indels
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-028CP2)
TELECOMMUTOMION INFORMATION:
TELEPHONE: (617) 466-6000
TELEPHONE: (617) 466-6040
INPORMATION POR SEQ. ID NO: 95:
SEQUENCE CHARACIERISTICS:
LENGTH: 367 amino acids
 367 AA
 ...
2.
 TOPOLOGY: linear NCLECULE TYPE: protein JENCE 367 AA: 39946 MW: 695678 CN:
 Sequence 95, Application US/08457006
 SIANDARD;
 92 IFSONMNIKLKMPLYVAGEK 111
 ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TYPE: amino acid
 CS-C8-167-C06-95
 SEQUENCE
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 Sequence 95, Application US/08467597

SENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GAPPLICANT:
GAPPLICANT:
POLICOK, Joanne:
APPLICANT:
GATMAN:
APPLICANT:
MONG Siu mei H.)
APPLICANT:
APPLICANT
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 Length 367;
 Query Match

86.0%; Score 123; DB 10; Lenath: 367;
Best Local Similarity 75.0%; Pred. No. 1.256-05;
Matches 15; Conservative 4; Mismatches 1; Indels
 NAME: Jane E. Remillard
REGISTRATION NUMBER: 38.872
REGISTRATION NUMBER: 38.872
TELECOMMUNICATION INFORMAL: 0.25.6 USD4 (IMI-028CPD4)
TELEPHONE: (617) 227-74 URLEFEAX: (617) 227-594
INFORMATION FOR SEG IS NO: 95: SEQUENCE CHARACTERISTICS:
 Score 123: DB 10;
Pred. No. 1.26e-05;
 STEMMENT APPLICATION DATA
CORRENT APPLICATION DATA
APPLICATION NUMBER: US/US/4477.(97
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PROOF APPLICATION DATA:
APPLICATION NUMBER: 08/350.225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
 TOPOLOGY: linear
MCLECULE TYPE: protein
JENCE 367 AA: 39846 MW: 695078 CN:
 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 367 AA, 39846 MW; 695078 CN;
 ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatitity
OPERATING SYSTEM: POTE: SZW: 1 S
 Sequence 95. Application US/08467697
 : 367 amino acids
amino acid
 STANDARD:
 92 IFSQNMNIKLKMPLYVAGHK 111
 86.08;
75.08;
TYPE: amino acid
TOPOLOGY: linear
 USA
 Query Match
Best Local Similarity
 US-08-467-697-95
 CITY: Wal
STATE: MA
 LENGIH:
 SEQUENCE
 SEQUENCE
 XXXXXX
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370 AA

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STANDARD:

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US-08-457-697-97
 Sequence 97,
 GENERAL
 Query Match
 XXXXXX
 Matches
RESULT
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 DEPLICANT GILIGET ITWIN 5.:
APPLICANT GILIGET ITWIN 5.:
APPLICANT BONG, Julian F.:
APPLICANT BONG, Julian F.:
APPLICANT Garran, Richard D.:
APPLICANT Garran, Richard D.:
APPLICANT Garran, Richard D.:
APPLICANT Woung, Siu-mei H.;
APPLICANT Woung, Siu-mei H.;
APPLICANT EXIBY, MARK A.:
APPLICANT EXIBY, MARK A.:
APPLICANT EXIBY, MARK A.:
APPLICANT STAUCK, Steven P.
TITLE DE INVENTION: Alergenic Proteins And Peptides From TITLE DE INVENTION: Japanese Cedar Poilen
NUMBER CF SEQUENCES: 261
CORRESSONDENCE ADDRESS:
ADDRESSONDENCE ADDRESS:
ADDRESSONDENCE ADDRESS:
ADDRESSONDENCE ADDRESS:
ADDRESSONDENCE ADDRESS:
ACTUAL OF INVENTION INC.
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 Length 370;
 Ouery Match 86.0%; Score 123; DB 10; Length 37 Best Local Similarity 75.0%; Pred. No. 1.26e-05; Matches 15; Conservative 4; Mismatches 1; Indels
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Indels
 025.6 USD2 (IMI-028CPD2)
 370 AA
Mismatches
 PRT
 MOLECULE TYPE: protein
SEQUENCE 370 AA: 40191 MW: 725506 CN:
 Sequence 97. Application US/08467023 GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin 3.:
 NAME: Jane E. Remillard
REGISTRATION NUMBER: 38.872
REFERENCE/DOCKET NUMBER: 025.6
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227.7400
TELEFAX: (617) 227.7541
INFORMATION FOR SEQ 1D NO: 977.
SEQUENCE CHARACTERISTICS:
 Sequence 97, Application US/08467023
15: Conservative 4:
 370 amino acids
 STANDARD
 IFSONMNIKLKMPLYVAGHK 111
 92 IFSQNMNIKLKMPEYVAGHK 111
 I IFSKNENIKLNMPLYIAGNK 20
 COUNTRY: USA
21P: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 amino acid
 linear
 US-08-467-023-97
 TOPOLOGY:
 XXXXX
 Matches
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 APPLICANT CALIFORN CONTROL APPLICANT POLIOCK, JOSEPH CANTER BONDOCK, STUTMER BL. APPLICANT BRAVEN MARK AND APPLICANT POWERS, Steven P. TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Allergenic Proteins And Peptides From NUMBER OF SEQUENCES: 261
 0
 Immulogic Pharmaceutical Corporation, Inc
 COMPUTER REACABLE FORM:
MEDICH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-D>S/MS-DOS
SOFTWARE: Patentin Ro-wase #1.0. Version #1.25
CURRENT APPLICATION DATA
RPLICATION NUMBER: Us 78/467,697
FILING DATE: June 6, 1.95
CLASSIPICATION: 424
PRIOR APPLICATION DATA
APPLICATION NUMBER: 1859,225
 FILING DATE: Decembe 1994
ATTORNEY/AGENT INFORMATI ...
NAME: Jane E. Remil and
REGISTRATION NUMBER: 38,872
REPERENCE/OCKET NUMBER: 025.5 UND4 (IMI-UZBRFD4)
TELECCAMMUNICATION INFORMATION
 370 AA
 PRI;
 TOPOLOGY: linear
MCLECULE TYPE: protein
SEQUENCE 370 AA; 40191 MW: 725536 CN;
 ...we 97, Application US/08467697
ENERAL INFORMATION:
Sequence 97. Application US/08467697
 :EEEAX: (617) 227-5441
:NESHATION FOR SEC 1D : 5
SEQUENCE CHARATERISTICS:
LENGIH: 370 amino acids
TYPE: amino acid
 STANDARD;
 92 IFSONMNIKLKMPLYVAGHK 111
 STREET: 610 Lincoln St
CITY: Waltham
 CORRESPONDENCE ADDRESS:
 JSA.
 US-08-226-248A-97
 02154
 ADDRESSEE:
 TELEPHONE
 COUNTRY:
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STATE: MA
COUNTRY: USA
ZIP: 02154
 US-08-467-006-97
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 VENERAL INFORMATION:
APPLICANT DISIGNATION:
APPLICANT POSSOCIAL DISIGNATION OF THE BOND OF
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 ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St. CITY: Waltham
 Cuery Match #6.0%; Score 123; DB 7; Longth, 370; Best Local Similarity 75.0%; Pred. No. 1.26e-05; Matches 15: Conservative 4; Mismatches 1: Indels
 CATIVITY OATSA

COMPUTER FRAABLE FCRM.
MEDIUM TYPE: Floppy disk
COMPUTER: IMM FOR COMPALIBLE
COERAING SYSTEM: POR DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/226,248A
FILING DATE: APTI 8, 1994
APPLICATION DATA
APPLICATION DATA
APPLICATION DATA
APPLICATION DATA
APPLICATION NUMBER: PCT/US/93/00139
FILING DATE: January 15, 1993
ATTOSNE FOR THE January 15, 1993
ATTOSNE FOR THE January 15, 1993
ATTOSNE DATICERE A VARSHORE
REGISTRATION WIMBER: G25.5 US (IMI-028CP)
FELECOMMINGTORION UNMBER: G25.5
FELECOMMINGTORION 1909
FELENCOMINGTORION 1909
FELENCOMINGTOR
 par:
 MOLEGOLE TYPE: protein
SEQUENCE 370 AA: 40191 MW: 725506 CN:
 Sequence 97, Application US/08225248A GENERAL INFORMATION:
APPLICANT. Stiffeth, Irwin J.:
 Sequence 97, Application US/08468940 GENERAL INFORMATION: APPLICANT: Griffeth, Irwin J.;
Sequence 97. Application US/38226248A
 Sequence 97, Application US/08468940
 STANDARD
 92 IFSONMNIKLKMPLYVAGHK 111
 1 TESKNINIKLNMPLYIAGNK 20
 TOPOLCGY: Inner
 USA
 02154
 DS-08-468-640-65
 STATE: MA
 COUNTRY
ZIP: 02:
 XXXXXX
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APPLICANT: Pollock, cc...
APPLICANT: Garman, Rich D. APPLICANT: Garman, Rich D. APPLICANT: Garman, Rich D. APPLICANT: Kuo, Mei-Cha...
APPLICANT: Yeung, Siu-mer, H., APPLICANT: Brauer, Andrew: APPLICANT: Brauer, Andrew: APPLICANT: Powers, Sie-we, P. TITLE OF INVENTION: Allergenia Proteins And Peptidus irun APPLICANT: Powers, Sie-we, P. TITLE OF INVENTION: Allergenia Proteins And Peptidus irun APPLICANT: Powers, Sie-we, P. TITLE OF INVENTION: Allergenia Proteins And Peptidus irun APPLICANT: Powers, Sie-we, P. TITLE OF INVENTION: Applicant Follow NUMBER OF SIQUENES: 26. CORRESPONDENCE ADDRESS. 26. CORRESPONDENCE ADDRESSEE: Immuloque Printmenentinal Corporation. Inc. Address ADDRESSEE: Inmuloque Printmenentinal Corporation. Inc.
 Gaps
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 Query Match 86.0%; Score 123; UB 10; Length 370; Best Local Similarity 75.0%; Pred, NU, 1.26e-05; Matches 15; Conservative 4; Mismatches 1; Indels
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.940
 REFERENCE/DOCKEI NUMBER.
TELECOMMUNICATION INFORM: 0.05 f US (IMI-028CP2)
TELEPHONE: (617) 466-b.c.
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 97.
SEQUENCE CHARACTERISTIPS
LENGTH: 375 amino acid
 376 AA.
 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATE:
RILING DATE: December 6, 1994
APPLICATION NUMBER: 08/255,225
FILING DATE: December 6, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: POT/US93/00139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
 PRT:
 TOPOLNOY: Libear
MOLECULE TYPE: Protein
SEQUENCE 370 AA; 4019! MW: 1255- N
 Sequence 97, Application US/)8467006
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Jaanne;
 Sequence 97. Application US/C 457006
 NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
 Floppy d.sk
 STANDARE;
 92 IFSQNMNIKLKMPLYVAGHK 11:
 1 IFSKNINIKLNMPLYIAGNK 20
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
```

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Sequence 33, Application US/28467006
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Pollock, Joanne,
APPLICANT: Bond, Julian F.:
APPLICANT: Kuo, wat-Chang:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Exley, Mark A.:
APPLICANT: Exley, Mark A.:
APPLICANT: Dowers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From IIILE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SECUENCES: 561
IITLE OF INVENTION: Allergenic Proteins And Peptides From NUMBER OF INVENTION: Japanese Cedar Pollen NUMBER OF SEQUENCES: 26.
CORRESPONDENCE ADDRESS: And ADDRESSE: Immuloque Pharmacoutical Corporation. Inc SIREET: 610 Lincoln S'STREET: 610 Lincoln S'STREET: MA COUNTRY: USA COUNTRY: USA 21P: 02154
 Match 86.0%; Score 123; DB 8; Length 370; Local Similarity 75.0%; Fred. No. 1 24e-05.
As 15: Conservative 4: Missur Ass 1: 10361s
 CCMPUTER: ALJUAN TYPE: FLOPPY disk MEDIJUM TYPE: FLOPPY disk MEDIJUM TYPE: FLOPPY disk COMPUTER: TBM PC COMPATIBLE SOFTWARE: TBM PC COMPATIBLE SOFTWARE: PATENTIN Release #1.0. Version: #1.25 SOFTWARE: PATENTIN NOTE: PATENTIALION DATA: APPLICATION UNBER: 35/68/350,225 FLING DATE: December 6, 1994 CLASSIFICATION NOTE: 424 PRIOR APPLICATION NOTE: 62/938 990 FLING DATE: APPLICATION NUMBER: 07/938 990 FLING DATE: SEPTEMBER: 07/938 990 FLING DATE: SEPTEMBER: 07/938 990 FLING DATE: SEPTEMBER: 07/938 990 FLING DATE: APPLICATION NUMBER: PAT/05/938 990 FLING DATE: APPLICATION NUMBER: PAT/05/938 990 FLING DATE: ABNARTION: 2993 APPLICATION: 2993
 NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35.729
REGISTRATION NUMBER: 25.729
RECENCENCE NUMBER: 225.6 US (IMI-028GP2)
IELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6050
IELEPHONE: (617) 466-6040
INFORMATION FOR SEQ 1D NO: 97:
SEQUENCE CHARACIERISTICS;
 20 AA.
 LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
UENCE 370 AA: 40191 MW: 725506 CN:
 53.5
 Sequence 33, Application US/08457605
 STANDARD;
 92 IFSUNWIRCKMPLYVAGER [1]
 1 IESKNINIKLNMPINIAJNK Z.
 .T 15
08-08-467-006-33
 SEQUENCE
 Query Match
 XXXXXX
 Matches
 RESULT
 APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D.
APPLICANT: Kuo, Marchant
APPLICANT: Yeung, Siummel H.;
APPLICANT: Brauer. Andrew:
APPLICANT: Bray Mark A.;
APPLICANT: Appanese Cedar Poilen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
 Ö
 STREET: Limmilogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St CITY: Maltham STATE: MA
 query Match 85.0%, Scoro 12% 08.30; Identifi 370-88st Local Similarity 75.0%; Pred. No. 1.258-05;
Matches 15: Conservation 4: Mishatches I: Indels
 PRI;
 MOLECULE TYPE: protein
SEQUENCE 370 AA: 40191 KW: 725506 CN:
 Sequence 97, Application US/08350225 GENERAL INFORMATION:
 Griffeth, Irwin J.;
Pollock, Joanne:
Bond, Julian F.;
Garman, Richard D;
Kuo, Mei-Chang;
 Sequence 97. Application US/08350225
 Yeung, Siu-mei H.;
Brauer, Andrew;
Exley, Mark A.;
Powers, Steven P.
 TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: acino acid
 STANDARD;
 linear
 USA
 2IP: 02154
 .T :4
US-08-350-225-97
 APPLICANT
APPLICANT
APPLICANT
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APPLICANT
 TOPOLOGY
 APPLICANT:
 APPLICANT:
APPLICANT:
 COUNTRY
 XXXXX
 RESULT
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CURRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutica Corporation, Inc.
SIREET: 610 Lincols St.
CITY: Waitham
STATE: Waitham
COMPUTER RADABLE FORM:
WADJUM TYPE: FORMY CORPORATION BRIDGE
SOBTRATE: TOWN PC COMPUTER: TOWN WER: US/08/467.306
FILING CATE: June 6 1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/950,225
FILING CATE: December 6 1994
ANIORNEY/AGENT INFORMATION:
NAME: Jane E. Remilland
REFERENCE/DOCKET NUMBER: 025.6 URD6 (IMI-028CPD6)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 38.
FELECOMMUNICATION NUMBER: 025.6 URD6 (IMI-028CPD6)
TELECOMMUNICATION NUMBER: 027-5941
INPORMATION CALL ON 0: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: anino acids
TYPE: anino acids
TYPE: Anino acid
TYPE: Anino acid
TYPE: Anino acid
TOPOLOGY: Linear
MCLECULE TYPE: PEPLINGE
TYPE: Anino acid
 Cuery Match
Pest Local Similarity 75.0%; Pred, No. 2.25e-34;
Matches 15; Conservative 3; Mismatches 2; Indels 0;
 SECUENCE
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Saps

Search completed: Mon Jun 19 16:27:27 2000 Job time : 18 sers.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrob\_pp = protein - protein database search, using Swith-Waterman algorithm

Mcm Jun 19 16:13:48 2000; MasPar Lime 5.53 Seconds 170:634 Million cell updates/sec Tabular output not generated. Run on:

>US-09-142-524A-11 (1-20) from USC9142524A.pep 143 1 IFSKNLNIKLNMPLYIAGNK 20 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Subring table:

142080 segs, 47172405 residues searched:

Postrprocessing: Minimum Match 0% insting first 45 summaries

pir62 I:pirl 2:pir2 3:pir3 4:pir4

Database

Mean 29,146; Variance 45,738; scale 0.637 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| d. No.                | .35e-09        | .35e-09  | .52e-03  | .02e-01           | .11e+00                                                      | .63e+00        | .40e+00 | .09e+00         | .38e+00         | .38e+00         | .38e-00               | .05e+01               | .05e-01         | .05e+01        | .06e+01        | .06e+01        | .06e+01 | .06e+Cl               | .06e-01              | .53e+01            | 536-01             | .53e+01         |   |
|-----------------------|----------------|----------|----------|-------------------|--------------------------------------------------------------|----------------|---------|-----------------|-----------------|-----------------|-----------------------|-----------------------|-----------------|----------------|----------------|----------------|---------|-----------------------|----------------------|--------------------|--------------------|-----------------|---|
| Pred                  | Cry 1 2        |          | EC 4.2 5 | a                 | EC 4.2 1                                                     | I.4 pr :       |         | protein 5       | hypothetica 7   | protein 7       | sphate 7              | ucible 1              | 3,4-d 1         | 7.             | 1.2 - 1        | I.2 pr 1       | 4       | hetica 1              | otein 1              | ase (u             | ase (" 1           | protein 1       |   |
| Description           | major allergen | allergen | ·        | probable membrane |                                                              | allergen Amb a | yase    | hypothetical pr | conserved hypot | hypothetical pr | ribulose-bisphosphate | osmotically inducible | protocatechuate | allergen Amb a | allergen Amb a | allergen Amb a | yase (  | conserved hypothetica | hypothetical protein | NADH dehydrogenase | NADH dehydrogenase | hypothetical pr |   |
| QI QI                 | 302124         | JC2123   | S25211   | \$59837           | T00856                                                       | D53240         | 829612  | E64320          | E64638          | D7:875          | 847236                | B64250                | DAPSAA          | A39099         | B39099         | B53240         | T07058  | G70350                | T16416               | H58850             | S41827             | G71243          |   |
| 77.                   | 7              | ~        | 7        | 7                 | 7                                                            | ~              | 7       | ~               | C)              | 7               | ~                     | 1                     |                 | ~              | ~              | ~              | ~       | ~                     | ~                    | ~                  | ~                  | ~               |   |
| osery<br>Match Length | 374            | 374      | 5.<br>5. | 347               | 5.05<br>5.05<br>5.05<br>5.05<br>5.05<br>5.05<br>5.05<br>5.05 | 392            | 434     | 395             | 150             | 150             | 452                   | 155                   | 201             | 396            | 398            | 398            | 398     |                       | ~                    | 115                | 115                | 131             |   |
| e<br>Query<br>Match   | 0.62           |          | 56.6     |                   | 47.6                                                         | 46.9           | 46.2    | 44.8            | 44.1            |                 | 44.1                  | 43.4                  | 43.4            | 43.4           | 43.4           | 43.4           | 43.4    | 43.4                  | 43.4                 | 42.7               | 42.7               | 42.7            |   |
| Score                 |                | 213      | 81       | 7.                | 6.8                                                          | 29             |         | 64              | 63              | 63              | 63                    | 52                    | 52              | 62             | 62             | 62             | 62      | 62                    | 62                   | 51                 | 9                  | 61              |   |
| Result<br>No.         |                | 5        | 3        | 4                 | 5                                                            | 9              | 7       | 80              | 6               | 10              | ננ                    | 12                    | 13              | 14             | 15             | 16             | 17      | დ)<br>r:1             | 19                   | 20                 | 21                 | 22              | , |

| GTP-binding protein h 1 534-01 conserved hypothetical 534-01 deoxyribodipyilmidine 1 534-01 hypothetical protein 5 546-01 hypothetical protein 5 546-01 ning protein 2 196-01 ning protein 2 196-01 probable type II UNA 2 196-01 probable type II UNA 2 196-01 ribulose bisphosphate 2 196-01 | # 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | plete<br>I precursor (clone pCCI.2-2) - Japanese<br>eria japonica #common_name Japanese cedar<br>e_revision 14-Jul-1994 #text_change |
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| ス 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | RESULT FILE ORGANISM DATE ACCESSIC REFERENCE FALLS FILLS FELL SEL SEL SEL SEL SEL SEL SEL SEL SEL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | RESULT<br>ENTRY<br>TILLE<br>ORGANISM                                                                                                 |

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*domain signal sequence *status predicted *labe: SIGN *product major allergen Gry j i (clone pGG1-2-2) *status predicted *labol MATN *binding_site carbohydrate (ASn) (covalent) *status
 *authors Sone, I.: Komiyama, N.: Shimizu, K.: Kusakabe, T.: Morikubo, K.: Kino, K.: Kino, K.: Sonemus, D.: Morikubo, K.: Kino, K.: Biophys. Res. Commun. (1994) 159:619-625
*title closing and sequencing of CDNA coding for Cry j I. a major aliergen of Luganese cedar polien.
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 translation of the nucleotide sequence is not complete
 $26.211 *type compiete perfate types (EC 47.2.2.2) - common tobacco effectate lyase (EC 47.2.2.2) - common tobacco *formal_name Noctional tabacur *common_name common tobacco 12.Feb-1993 *text_change 12.Feb-1993 *text_change
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**Pexperimental_source pollen
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 29-Sep-1999
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 193/1: 293/2
#superfamily pectate lyase LAT59
carbon-oxygen lyase
 92 IFSGNMNIKLKMPMYIAGYK 111
 predicted
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 1 IPSKNENIKUNMPLYIAGNK 20
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JC2123
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 $21933
 158, 191, 293, 354
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 **residues 1-347 **label PAU
**cross-reterences EMBL:U25842* NID:9786312; PID:9786317; MIPS:N:R:R:P-W
 Rounsley, S.D.; Lin, X.: Ketchum, K.A.; Crosby, M.L.:
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M..
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
 S59837 #tyro complete
probable membt - protein YPRINUW - yeust (Saccountomyres
 cerevisiae)
hypothetical profein P9705.5
*formal_name Saccharomyces cerevisiae
13-Jan-1996 *sequence_revision 07-Mar-1996 *text_chanae
 *domain transfembrane *status predicted *label 1KM *longth 347 *moltivilat-weidh: 19223 *checksim 329.
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 *submission submitted to the EMBL Data Library, March 1998 *description Arabidopsis thaliana chromosome II BAC 720F6 genomin
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**cross-references EMBL:AC002521; NID:92947056; PIDN:AAC0535G.
PID:92947069
*length 397 *mc.ecular-weight 4435; *checksum
 Pauley, A. submitted to the EP -1 Data Library, April 1995 submitted to the EP -1 Data Library, April 1995 sequence of S. erevisiae cosmid 9705. 559837
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 Score 81: DB 2: LO
Pred: No. 5:52e-03;
 **eross-references SGD:S00063 4: MITS:YPR160W *map_position 16R transmembrane ordinals
 ranslated from GB/EMBL/DDBJ
 W. smatches
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 transmembrane protein
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 56.68;
 51.7%;
Similarity 52.9%;
9; Conservative
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-has 10; Conservi
 *accession S5983/
**molecule_type_DNA
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CLASSIFICATION *superfamily pectate lyase LATS9
KEYWORDS **-arbon-cxygen lyase
 ##ICS: dues 1-392 ##label GRI ##Cross-references GB:M80562; NID:g156444; PIEN:AAA32670.1; PID:g166445 KEYWORDS pollen pollen pollen signerate lyase : T59 SUMMARY # Forest CATANTON pollen Poll
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 Kim, S.: Finkel, D.J.: An, G.
submitted to the EMBL Data Library, October 1992
Abundancy patterns of lily pollen cDNAs: characterization
three pollen-preferential cDNA clones.
 $25612 *type romplete pecdate lyase (EG 4.2.2.) - trumpet lilly stormal name Lillum longiflorum scormon, name trumpet lily 19-Mar.1997 *sequesce_revision 19-Mar.1997 *text_connections.
 A53240
Griffith, 1.5.: Pollock, J.: Klapper. D.G.: Rogers, B.L.:
 D53240 *Lype complete
allerged Amb a 1.4 precursor - common ragweed
*formal_name Ambrosia artemisiifolia *common_name common
 #journal Int. Arch. Allergy Appl. Immunol. (1991) 96:296-304
#title Sequence polymorphism of Amb a I and Amb a II, the major allergens in Ambrosia artemisiifolia (short ragweed).
#cross-references MUD:92234570
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 19-May-1994 #sequence_revision 19-May-1994 #text_change 29-Sep-1999
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O
 Score 66; DB 2; Length 434;
Pred. No. 2.40e+00;
6; Mismatches 6; Indels
 46.9%: Score 67: DB 2: Length 392: 35.0%: Pred. No. 1 43e-00: 42tive 7: Mismat: 45 5: Indexsets
 Length 455;
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 1 LESKNINIKLNMPLYIAGNK 20
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Rauthors Balt, C.C.; White O.: Disen. S.C.; Zhou. L.: Fletschmann.
Rauthors Balt, C.C.; White O.: Disen. J.C.; L.M.: Clayton,
R.D.; Sutton, J.: Blake, J.A.: FitzGerald, L.M.: Clayton,
R.D.; Sutton, J.: Blake, J.A.: FitzGerald, L.M.: Clayton,
R.D.; Sutton, J.: Reich, C.L.; Cverbeek, R.:
Kirkness, E.F. Weisstock, R.G.; Merrick, J.M.: Glodek, A.:
Scott, J.L.; (Haggen, N.S.M.: Weidman, J.E.; Futrnain,
J.L.; Nguyen, C. Jtterback, T.R.: Kelley, J.M.: Peterson,
J.D.; Sadow, F.M.; Hanne, M.C.; Cotton, M.D.; Roberts,
R.M.: Hurst, M.A.: Smith, H.O.; Weese, C.R.: Venter, J.C.
#journal Schence (1996) 273:1058:1073
#title Methanococcus Jannaschii, the methanogenic archaeon,
Methanococcus Jannaschii.
 Toob, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, S.G.; Eleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quarkentush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Godayne, J.D.; Utrerback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, T.M.; Fulli, C.; B.wman, C.; Hatthey, L.; Wallin, E.; Hayes, W.S.; Bordodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter,
 conserved hypothermal semicing protein HF044 - Helicobacter pylori (strain 2665)
#formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
26-Aug-1999
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 E64320 *type complete hypochetical pricein MJ0164 · Methanococcis jannaschil aformaliame Methanococcus jannaschil 13:5ep-1996 *sequence_revision 13:5ep-1996 *text_change 10-oct-1997
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 Nature (1997) 38 :539-547
The complete gen me sequence of the gastric pathogen
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 preliminary: nucleic acid sequence not shown
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SUMWARY *length 395 **molecular-weight 45273 *checksum
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Hilmatches 3: Indels
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 Ouery Match
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 Alm. R.A.: Lind. L.S.L.: Moir, D.T.; King, B.L.: Brown, E.D.: 5019, P.C.; Smith, D.R.: Noonan, B.: Guild, B.C.; deJonge, S.L.: Carmel, G.: Tummino, P.J.: Carmen, A.: (tra-Nickelsen, M.: Mills, D.M.: Ives, C.: Gibson, R.: Metberg, M.: Mills, D.M.: Jiang, C.: Taylor, D.E.: Vovis, G.E.: Tust, T.S.
Nature (1999) 397:176-180
 #fittle Genomic sequence comparison of two unrelated isolates of the human quartic pathogen Helicobacter pylori.
 **residues="'| I-150 **!abel ARN
##Cross-references 38.Ab001518; GB:Ab001439; NIO:q4155454: PID:q4155464
**#experimental_source strain 39
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 Manen, J.F.; Nataii, A. Submitted to the EMBL Data Library, July 1994 Comparison of the evolution of the rbcL sequence and of the atpB-rbcL non-coding spacer in a recent plant group, the Rubieae tribe (Rubiaceae).
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 D71875 #type complete
hypothetical protein jhp0883 - Helicobacter pylori (strain
hypothetical protein jhp0883 - Helicobacter pylori (strain
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Flenath 150 Froledular-Weight 17321 Fohecksum 8226
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 4: Indels
 2: Length 150
 Score 63: DB 2: Le
Pred. No. 7.38e+00:
4: M:smatches 4:
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 ##molecule_type DNA ##residues
 Guery Match
Pest Local Similarity 52.3%.
Matches 9: Conservation
 Owery Match
Sest Local Similarity 52.9%;
Matches 9: Conservative
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 85 FSKMLENBLNINFFIAG 101
 2 FSKNINIKINMPLYIAG 18
 2 FSKNINIKLNMPLYIAG 18
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Maner, J.F.; Natali, A.; Ehrendorfer, F
submitted to the EMBL Data Library. December 1994
Phylogeny of Rubia-Rae-Rubiea inferred from the sequency of
CPDNA intergene region.
$39292
 catalyzes the reaction of carton dioxide with D rithiose 1. 5-bisphosphate to form two molecules of 3-phospho-L-quyceric and superfamily rithiose-bisphosphate carboxylase large could calvin cycle. Carbox dioxide fixations catbon catbon dioxide fixations carboxylase. Mioroplast: magnesiam remonstrations photorespiration photosynthesis
 ##cross-references GB:U39732; GB:L43967; NID:q1046169; PID:q1046173:
##cross-references GB:U39732; GB:L43967; NID:q1046169; PID:q1046173:
TIGR:M6454
 osmotically indicible protein csmc horoloa - Mycoplasma
qenitaliam (SGC3)
#formal_namc Mycoplasma aenitaliam
10.5ep-1999 #sequence_fevision 10.5ep-1999 #text_change
 4.100
 *Superfamily hypothetical protein yklA
*length 155 *molecular-weight 17376 *checksum 8910
 preliminary, nucleic acid sequence not shown:
translation not shown
 **residues 1-52,"X'.54 67 **;346; MAN2
**cross-references EMBL:X76- 5; NIC.44'4895; PIUN:CAA5405'.1.
PID:4434436
 Match 44.1%; Sivre 63. 1952; Longth 452; Local Similarity 33.3%; Picd. No. 7.38e-00; es 6. Conservative is Mishatches 5; Indels
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 #type complete
 **experimental_source strain G-37
 B64250
A64290
Fraser, T.M. Dictor
 255 VFARELAVPIVMHDYITG 272
 : |:::| : | ':|
: IFSKNLNIKLNMPLYIAG 18
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 364250
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 *description
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 Fourthors Kohlmiller, N.A.: Howard, J.B.
Fjournal Chem. (1979) 254:7309-7315
Fille The primary structure of the alpha subunit of protocatechuate 3.4-dioxygenase. II. Isolation and sequence of overlap peptides and complete sequence.
Forcession A00505
 ###notecule_type protein
##residues 2-59, 'D',61-76, 'D',78-201 ##labe! KOH
##residues 2-59, 'D',61-76, 'D',78-201 ##labe! KOH
##rexperimental_source ATCC 23975
##note this is the second of two papers giving the experimental
 Fauthors Oblendorf, D.H.: Orville, A.M.: Lipacino, J.D.
#Sournal J. Mol. Biol. (1994) 244.586-608
#title Structure of protocatechuate 3.4-dioxyvanase from Pseudomonas aeruginosa at 2.15 angstroms resolution.
#cross-references MuiD:95082024
 FERENCE A50309
**Bauthors Oblendorf, D.H.; Weber, P.C.
**Submission submitted to the Brookhaven Protein Data Bank, September 1990
**Cross-references PDB:1PCD
 #authors Fraze, R.W.: Livingston, D.M.: LaPorte, D.C.: Lipscomb, J.D. #journal J. Bacteriol. (1993) 175:5194-5202 *Litle Cloning, sequencing, and expression of the Pseudomonas putida protocatechuate 3,4-dioxygenase gends. #Cross-refer nces_MUD:94012480
 catalyzes the oxidative cleavage of 3.4-dihydroxybenzoate to (E.2)-1,3-butadiene-1,2,4-tricarboxylic acid by dicxygen this is the second step in the conversion of
 ##rcsidues 1-201 ##labe: FRA ##cross-references GB.Li4936: N.D.q294343; PIDN:AAB41025.1; PID:g294345 ##experimental_source AICC 23975 AND:G294345; A00505 A00505 A00505
ö
 *authors Ohlendorf, D.H.; Orville, A.M.; Lipscomb, J.D. *asubmission submitted to the Brookhaven Protein Data Bank, June 1994 across:references PDB:2PCD acontents annotation: X-ray crystallography, 2:15 angstroms, residues
 annotation: X-ray crystallography, 2.8 angstroms, residues 2-24,'G',25-59,'D',61-76,'D',78-135,'G',136-173,175-201
 protocatechuate 3.4 dioxygenase (EC 1.13.11.3) alpha chain
Pseudomonas putida
#formal_name Pseudomonas putida
 strain ATCC 23975 was formerly classified as Pseudomonas
Gaps
 31-Jan-1980 *sequence_revision 14-Feb-1997 *text_change 11-Jun-1999
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 annotation; X-ray crystallography, 2.8 angstroms
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#authors Smith, J.J.; Olson, J.R.; Klapper, D.G.
#journal Mol. Immusol. (1988) 25:555-365
#title Monoclonal antibodies to denatured ragweed police allergen
Amb a I: characterization, specificity for the denatured
allergen, and utilization for the isolation of immunoqunic
peptides of Amb a I.
#accession A60895
 ##residues 1-36 ##label GRI
##cross.references GB:M8058; NID:q166434; PIDN:AAA32665.1; PID:q166435
FICATI N #superfamily pectite lyase LAT59
DS glycoprotein; pol en
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 #journal J. Biol. Chem. (1991) 266:1229-1236
#title Cloning of Amb a I (antigen E). the major allerace family
#cross-references WJID:91093235
#accession A39699
 *product protocatechuate 3.4-dioxygenase alpha chain
status experimental fiabel MAI)
*binding_site substrate (Arg) *status producted
*length 201 *molecular-weight 22387 *checksum 486
4-hydroxybenzoate to succinate and acetyi-COA *superfamily protocatechuate 3,4-dioxygenase alpha chaim aromatic hydrocarbon catabolism; dodecamer: heterodimer.
 Nail, A.K.
Int. Arch. Allergy Appl. Immunol. (1991) #6:296-304
Sequence polymorphism of Amb a I and Amb a II. the major
allergens in Ambrosia artemisiifolia (short ragweed).
 aliergen Amb á 1.1 precursor - cormon ragweed
#formal_name Ambrosia artemisinfolia #common_name common
 *binding_site carbohydrate (Asn) (covalent) *status
 T.) Griffith, 1.3.: Kuc. M.; Bond, J.F.; Rogers,
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 27-Nov-1991 #sequence_revision 63-Apr-1992 #text_chande
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Griffith, Lidis Pollork, die Klapper, DiGis Roqurs, B.
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O
 Query Match
43.4%; Score 62: DB 2; Length 395;
Best Local Similarity 25.0%; Pred. No. 1.06e+01;
Matches 5; Conservative 10; Mismatches 5; Indels
 6: Indels
 Parolegule_type_profess
##residues 256-273:292-353, W. 305-306 ##lakel SMI
 Ouery Match 43.4%: Score 52: DB 1: Lenath 201
Best Local Similarity 31.5%; Pred. No. 1.05e-61:
Matches 5: Conservative 7: Mismatches 6: Indels
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 #Type complete
nb a I.1 precura
 RAF
 A39099; A60895; A53240
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NCE A60895
 *cross-references MUID:92234570
 118 IFERDMVIRLDKEMVVNSDK 137
 preliminary **molecule_type mRNA **residne
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 1 IFSKNINIKLNMPLYIAGN 19
 29-Sep-1999
 ##molecule_type mRNA
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whery Match 43.4%; Score 62; DB 2; Length 398; Pest Local Similarity 40.0%; Pred. No. 1.05e+01; Matches 9; Conservative 5; Mismatches 7; Indels

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyrigh: (c) 1993-1998 University of Edinburgh. U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 3.84 Seconds 158.450 Million cell updates/sec Mcc Jun 19 16:12:55 2000; Tabular output not generated. MPsrch\_pp Rith On:

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FAM 150 Gap 15 Sporing table:

Minimum Match 0% Listing first 45 summaries Post-processing:

83857 seqs, 30454973 residues

Scarched:

swiss-prot38 1:swissprot Catabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Variance 43.129; scale 0.691

Mean 29.800;

Statistics:

Query Result

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| Score       | ~                      | . 18                   | 7.4                    | 67                    | 99                     | 54                     | 63                    | 63                    | 63                    | 63                    | 63                    | 63                    | 62                     |                        | 62                     | 62                    | 62                     | 62                    | 62                     | 51                     | 61                     | 61                    | 63                    |
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| BL_CORSA<br>RBL_IRIGE<br>RBL_VERBO<br>RBL_ABIVE<br>RBL_ABIVE<br>RBL_CALDI<br>PESS_LYCES<br>RBL_CARANA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CRAMA<br>RBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_CASCU<br>BBL_C                                                                                                                                                          | RBL_CICIN                                    |
| аненанисминистичен                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 4                                            |
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| 48000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ት 4 4<br>ሁ ፋ የህ                              |

## ALLONMENTS

01-NOV-1990 (Rel. 16, Create 01-NOV-1995 (Rel. 32, Last so ence update) 15-DEC-1996 (Rel. 37, Last an italion update) SUGI BASIC PROTEIN PRECISCR (SBP) (MAJOR ALLENGEN GRY 11) (GRY 11). Cryptomeria japonica (Japanese cedar). Eukaryota: Viridipiantae: Streptophyta: Embryophyta: Tracheophyta: euphyllophytes: Spermatophyta: Coniferopsida: Coniferales; "N-terminal amino acid sequence of a major allergen of Japanese cedar pollen (Cry  $\{-1\}$  ).": Some I., Komiyama N., Shimizu K., Kusakale I., Morikubo K., Kibo K., "Cloning and sequencing of CDNA coding for Cry () I. a major alterage of Japanese redar pollen ". TISSUE-POLLEN:
TENDINE: 89031257.
Taniai M., Ando S., Usui M., Kurimoto M., Sakaguchi M., Inolye S., Matuhasi T.; Terracy K., Fukuda S., Kurimoto M., to the EMSL/Danbank/DDBJ databases of Japanese cedar pollen."; Biochem. Biophys. Res. Commun. 199:619-625(1994) 374 AA SEQUENCE FROM N.A., AND PARTIAL SECTION PRT; FEBS Lett. 239:329-332(1988). Taxodiaceae; Cryptomeria STANDARD: TISSUE=POLLEN: Namba M., Kurose M., Submitted (JUL-1994) SEQUENCE OF 22-41. TISSUE-POLLEN: MEDLINE: 94183234 SECUENCE FROM N.A. CARBOHYDRATES. SBP\_CRYJA P18632; OCCOCCENTARY REPRESENTATION OF STREET OF STREE

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EMBL; U25842: AAB68113.1; -
 Lyase: Signal
 RH31_YEAST
Q05524;
 ACT_SITE
CARBOHYD
 CONFLICT
 CONFLICT
 SEQUENCE
 Query Match
 CARBOHYD
 SIGNAL
 Matches
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 8
 This SWISARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.

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 Gaps
 Rogers H.J., Harvey A., Lonsdale D.M.; Isolation and characterization of a tobanco gene with homology to pectate lyase which is specifically expressed during
 #Lorosporogenesis.":
plant Mol. Biol. 20:493-502(1992).
-:- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
-:- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
-:- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
-:- CATALYTIC NON-REDUCTIVE HAND BENDS.
AT THEIR NON-REDUCTING ENDS.
-:- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED LATE IN POLLEN
 Enaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta:
euphyllophytes, Spermatophyta, Magnollophyta, endroctyledons,
core endicots, Asteridae, enasterids I: Solundies, Solunaroac,
 :
:
 uery Match
Pest Local Similarity 75.0%; Pred. No. 2.31e-10;
Matches 15; Conservative 3; Mismatches 2; Indeis
 POIENTIAL.
POIENTIAL.
74AB25950248F56F CRC64;
 SUGI BASIC PROTEIN.
L > F (IN CRY J 1-b).
S + Y (IN CRY J 1-b).
L > S (IN CRY J 1-b).
L > S (IN CRY J 1-b).
Q > + H (IN CRY J 1-b).
R > Q (IN CRY J 1-b).
POTENTIAL.
 RESULT 2

(D PELICBAC STANDARD; PRT: 397 AA. AC P4C92.

AC P4C972.

AC P4C972.

AC P4C972.

AC P4C972.

AC D4C972.

AC D4C972.

AC D4C972.

AC D4C973.

AC D4C973.

AC D4C973.

AC D4C973.

AC D4C973.

AC D4C973.
 AMB A I/AMB A II/CRY J I SUBFAMILY
 Nicotiana tabacum (Common tobacco)
 SEQUENCE FROM N.A.
STRAIN-CV. SAMSUN, TISSUE-POLLEN,
MEDLINE: 93043039.
 40645 MW:
 IFSGNMNIKLKMPMYIAGYK 1:1
 EMBL: D26544; BAA05542.1; ...
EMBL: D26545; BAA05543.1; ...
EMBL: D34639; BAA07020.1; -...
PIR: A44773; A44773;
 1 1FSKNINIKUNMPLYIAGNK 20
 293
293
374 AA;
 DEVELOPMENT.
 Nicotiana.
 CARBCHYD
 CARBOHYD
 SEQUENCE
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 VARIANT
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 VARIANT
VARIANT
 VARIANT
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 ö
 CHARACTERIZATION.
MEDLINE: 97248684.
Shayeghi M., Does C.L., Tavassoli M., Watts F.Z.;
"Characterisation of Schizosaccharomyces pombe rad31, a UBA-related
 Sapo
 -:- FUNCTION: COULD BE INVOLVED IN A 'UBIQUITIN-RELATED PROCESS IMPORTANT FOR DNA DAMAGE TOLERANCE.
-:- SIMILARITY: 10 THE N-TERMINAL OF UBIQUITIN-ACTIVATING ENZYME -:- SIMILARITY: STRONG, TO S.POMBE RAD31.
 's yeast).
Gotharomydetes: Saccharomydetales
 SEQUENCE FROM N.A.
STRANGESCON A AB972:
Underson A. AB972:
STRANGESCON A AB972:
Johnston A. Fulton L., Gattung R., Cooper J., Ding H., Du Z.,
Ravello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Billier L., Jier X.,
Johnston D., Johnston L., Landsron Y., Lailfellie P., Le T.,
Mardis E., Menezos S., Miller N., Whan M., Paniey A., Felisc L.
Stifkon L., Siles L., Jard, P., Trivasky R., Vegdath D.,
Wilcox L., Wohldman P., Va. H. M., Milson R., Waterston R.,
Submitted (MAY-1995) to the EMHL/Johnshik/DDBJ databases.
 ..
ن
 3; Indels
 Length 397
 S -> D (IN MRNA).
H -> R (IN MRNA).
H -> N (IN MRNA).
EFUA82CE5CA7643F CRC64:
 CONTROL 1997 (Rel. 35, Created)
(1-NOV-1997 (Rel. 35, Last sendence update)
(1-NOV-1997 (Rel. 37, Last sendence update)
DNA DAMAGE TOLERANCE PROTEIN F-(31 (RAD31 HUMOLOG)).
ACSI OR RHC31 OR YPR18CW OR P⁽¹⁾ (5.5
Saccharomyces cerevisiae (Bake'' S' yeast).
Eukaryota: Fungi: Ascomycota.
Saccharomycetaceae; Saccharomycetes: Sacch
 PECTATE LYASE.
POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> C (IN MENA).
GS -> SG (IN MENA).
 Score 81; DB 1; L Pred, No. 1.55e+03;
 (IN MRNA)
 K.sma.ches
 347 AA
 gene required for DNA damage tolerance.";
Nucleic Acids Res. 25:1162-1169(1997).
or send an email to licensedisb-sib.ch)
 POTENTIAL.
 Pred.
 EMBL: X67158; CAA47630.:: -.
EMBL: X67159; CAA47631.: -.
EMBL: X61102; CAA43414.:: -.
PIN: S2621:: S2621:
PFAM: PF00644; Pec_lyase: 1.
PRINTS: PR00807; AMBALLERGEN
 44351 MW:
 116 IFGKNMKIKLSRELIVISNK 135
 1 IFSKNINIKLNMPLYIAGNK 20
 56.6%:
50.0%;
 Local Similarity 50.0%;
les 10; Conservative
 STANDARD;
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15-DEC-1998 (Rei. 37, Last annotation update)
PECIATE LYASE PRECURSOR (EC 4.2.2.2).
 . .
.E.
 1 22
23 434 8:18
312 312 8:18
68 69 97
434 AA: 48457 Mk
 156 IFGKSMVIRLKQELIINNDK 175
 EMBL. L18911: AAA33398.1:
PIR; S29612: S29612:
PFAM: PFO0544: PCC_IVASC: I
PRINTS: PRO0807: AMBALLERGEN
 EMBL: 217328; CAA78976.1: -.
 Science 273:1058-1073(1996).
 Query Match
Best Local Similarity 40.0%;
Matches 8: Conservative
 1 IFSKNINIKLNMPLYIAGNK
 Conservative
 STANDARD
 Methanococcus jannaschii
 Methanococcus.
 Lyase: Signal
 111 6
Y164_METJA
C57628:
 jannasch11
 ACT_SITE
CARBOHYD
 CARBOHYD
 SECUENCE
 CHAIN
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P8144 AWRAR
STANCARD: FRT: 392 AA.

P28744:
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1998 (Rel. 37, Last annocation update)
POLLEN ALIERGEN AMB A 14 PRECISSOR (ANIGEN E) (ANTIGEN AMB A I).

Ambrosia artemisifolia (Short ragweed).

Eukaryotar Viridiplantae: Streptophyta: Erbryophyta: Tracheophyta: euphyllophytes: Spermatophyta: Magnoliophyta; eudicctyledons;
core eudicots: Asteridae: euasterids II: Asterales: Asteraceae:
Asteriodeae: Heliantheae: Ambrosia.
 ·;
 ..
 DB 1,
5.68e-31;
-haq 6; Indels
 Antigen: Allergen: Signal: Multigene family: Polymorphism.
SIGNAL 1 25
 3; Indels
 POTENTIAL.
POLLEN ALLERGEN AMB A 1.4.
 SHDGPPV -> CNDGPPA.
7B6219C12F365DA9 CRC64:
 347 AA; 39273 MW; IADB7B817BA27F3E CRC54;
 Score 74; DB 1; Li
Pred, No. 3.49e-02;
 46.9%; Score 67; DB 1; 35.0%; Pred. No. 5.68e-0
 PEL_LILC STANDARD; PRT: 434 AA. P40973: 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update)
 5; Mismatches
 7; Mismatches
 SEQUENCE FROM N.A., AND VARIANTS.
 26 392 PO.
226 726 BL/
182 188 SHI
392 AA; 42842 MW:
SGD: L0004031; AOS1.
PFAM: PF00899; ThiF_family: 1.
 119 IFARDMVIRLDRELAINNOK 138
 EMBL: M8C562: AAA32670.1; ...
PIR; D53246; D53246; D53246; PPRA: PF05244; PPC21yase;]
PRINTS: PRC0807; AMBALLERGEN.
 Query Match
Rest Local Similarity 52.9%:
Matches 9: Conservative
 140 NTLTRKLNIPLYVAGSN 156
 7; Conservative
 4 KNENIKENMPLYIAGNK 20
 Local Similarity
 DNA damage.
 SEQUENCE
 SEQUENCE
 Query Match
 MOD_RES
 VARIANT
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Matches

RESULT 

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 ő
 SEQUENCE FROM N.A.
STRAIN-JAL-1, DSM 2661 / ATCC 43057;
MEDLINE, 96337999.
Bult C.J., White O., Clsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Switton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Switton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
 | [1]
| SEQUENCE FROM N.A.
| STRAIN-CV. NELLIE WHITE: TIS "DE-POLLEN;
| STRAIN-CV. NELLIE WHITE: TIS "DE-POLLEN;
| Kim. S. R., Finkel D.J., An G.
| Submitted (JUN-1993) to the EMBL/Genbank/DDBJ databases.
| SUBMITTED (JUN-1993) to the EMBL/Genbank/DDBJ databases.
| CATALYTIC ACIVITY: ELIMINATIVE CLEANAGE OF PECTATE TO SIVE
| CATALYTIC ACIVITY: ELIMINATIVE CLEANAGE OF PECTATE TO SHUCKS
| AT THEIR NON-FEDUCING ENDS.
| SIMILARITY: BELONGS IO THE POLYSACCHARIDE LYASE FAMILY IS
| THE TIME OF THE TOTAL ACIVITY OF THE TOTAL ACIVITY ACIVITY OF THE TOTAL ACIVITY ACIVITY ACIVITY OF THE TOTAL ACIVITY A
 Sdro
Lilium longiflorum (Irumpet lily).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnollophyta: Liliopsida: Liliales:
Liliaceae: Lilium.
 Archaea: Euryarchaeota: Methamococcales: Methanococcaceae;
 Score 66: DB 1: Length 434;
Pred. No. 1.00e+00;
 Indels
 CIFYE30AD2BBD064 CRC64:
 .
S
 UL-NOV-1997 (Rel. :5. Creatal)
UL-NOV-1997 (Rel. :5. Lust and reservation)
UNIV-1997 (Rel. :5. Lust annotation update)
HYDCHETICAL PROTEIN MODI64.
 OTENTIAL.
FECTATE LYASE.
POTENTIAL.
FCTENTIAL.
 Mismatches
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
 Ö
 CI-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEF: 1998 (Rel. 37, Last annotation update)
RTBULGSE BISPHOSPHATE CABOXYLASE LARGE CHAIN PRECURSOR (EC 4.1.1.39)
(RUBISCO LARGE SUBUNIT) (FRAGMENT).
 Saps
 Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: euphyllophytes: Spermatophyta: Magnollophyta: eudloctyledons: core eudlocts: Asteridae; euasterids I: Gentlanales; Rubiaccae;
 ..
 -. CATALYTIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHATE - CO(2)
2 3-PHOSPHG-O-GLYCERATE.
-!-CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2)
3-PHOSPHOT-CGLYCERATE - 2-PHOSPHOGLYCCLATE.
-!-SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
-!-SUBCELLULAR LOCATION: CHLOROPLAST.
-!-SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
 PFAM, PF00016, RuBisCO_large, 1.
Photosynthesis, Carbon dioxide fixation: Photorespiration;
 Score 64, DS 2; Length 395; Pred, No. 2.23e-00; 2; Mismatches 3; Indels
 Hypothetical protein.
SECUENCE 395 AA: 46273 MW: 5EA460ABDCC9A412 CRC64:
 RUBISCO_LARGE: 1.
 PRT;
 EMBL: X81104: CAA57010.1; -. HSSP: P00876; IRLC.
 44.8%;
larity 64.3%;
Conservative
 EMBL: U67473; AAB98152.1; -.
 MENDEL: 4673; RUBLi;rbcL:1.
PROSITE: PSG0157; RUBISCO_L
 Rubla tinctorum (Madder).
 STANDARD;
 129 IVERYLNIKLDIPL 142
 : FESKNENIKLNMPL 14
 Local Similarity
 SEQUENCE FROM N.A. MEDLINE: 96139025
 Chloroplast.
 RBL_RUB11
033050:
 SECTENCE
 Query Match
 Matches
```

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 ं
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytas, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids 1, Fabales, Fabancae, Papiliomedeum
 Kaess E., Wink M.:
"Molecular phylogeny of the Papillonoldose (Fumily Leguminosse). Incl.
 sequences versus chemical taxonomy.

Bot. Acta 108:49-102(1995).

-!- FUNCTION: RUBISCO CATALVEES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOREES TWO PRIMARY EVENT IN PHOTOSYNHEETING CARBON DIOXIDE FIXATION. AS WELL AS THE CXIDATIVE FRAGMENTATION THE PRIMARY EVENT IN PHOTOSSY HOTHOR THE PRIMARY EVENT IN PHOTOSSY HOTHOR FRAGMENTATION PROCESSY HOTHOR FRACTIONS OFFICE AND THE SAMP ACTIVE SITE.
 BY SIMILARITY.
RIBULOSE BISPHOSPHATE CARBOXYLASE LANGE
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
LARBUCGE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.11.19) (RUBLISCULARGE SCHONII) (FRAGMENT).
 3
 RINDING OF CO(2) ACTIVATES THE ENZYME.
Monooxygenase: Chloroplast: Acetylation
 11)
11:
1--
 A MANTIC ANTICLE FOR THE FEBRUARY OF THE STREET OF THE STR
 PFAM: PF00016; RuBisCC_large: 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lyase: Oxidoreductase; Monooxygenase; Chloroplast.
 Score 64: DB 1: Length 453:
Pred. No. 3.31e+00:
7: Mismatches 5: Indeis
 ACETYLATION (BY SIMILARITY)
PINDING OF CO(2) ACTIVATES
 50265 MW; 461DCF5DF6145933 CRC64;
 453 AA: 50263 MW: 888536EA72F849A0 CRC54;
 455 AA
 Score 63:
 ..
...
...
 PROSITE; PS00157; RUBISCO_LARGE: 1.
 255 VEARELAVPIVMHDYITG 272
 Match 44.18;
Local Similarity 33.38;
 1 IFSKNINIKLNMPLYIAG 18
 EMBL: 270063; CAA93922.1;
 Conservative
 STANDARD:
 Lyase: Oxidoreductase;
PROPEP 1 2
 201
 >453
 Lupinus microcarpus.
Chloroplast.
 192
455
455 AA;
 SEQUENCE FROM N.A.
 IISSUE-LEAF
 RBL_LUPMI
P92406;
 NON TER
ACT SITE
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 ACT_SITE
NON_TER
 SEQUENCE
 SEQUENCE
 Query Match
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Length 455;

DB 1;

44.28;

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RESULT

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 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (EC 4.1.1.39)
 01-NOV-1995 (Rel. 32, Created)
C1-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBGLOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (EC 4.1.1.39)
(RUBISCO LARGE SUBUNIT).
 REQUENCE FROM N.A.

Rettig J.H., Wilson H.D., Manhart J.K.;

Submitted (Xxx.1994) to the EMBL/Genbank/DDBJ databases.

-i- FUNCTION: RUBISCO CAFELYZES IWG REACTIONS: THE CARBGXVIATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNIHETIC CARBON DIOXADE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENIATION CARBON DIOXADE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENIATION OF THE BENTOSE SUBSTRATE IN THE PHOTOSESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
 PROSITE: PSUGIST, NOTICE | PROSITE | PROBLEM |
 euphyllophytes; Spermatophyta: Magnollophyta: eudicotyledoms:
core eudicots; Caryophyllidae; Caryophyllales: Caryophyllaceae;
 Score 53: DB 1; Length */5.
Pred. No. 3.31e+00;
....marches 5; Indels
 ACEINIALIEN (BY SIMILARITY)
BINDING OF CO(2) ACTIVATES
 D865E53BC7B585F1 CRC64;
 476 AA.
 475
 HSSP; P00875; 1AUS.
MENDEL; 2993; STEME:rbcL;1.
PROSITE: PS00157; RUBISCO_LARG:: 1.
 201 201 F
475 AA; 52675 MW;
 EMBL: M62570; AAA84620.1: -
 255 VFARELGVPIVMHDYITG 272
 44.18;
33.38;
 | :|:::| : : | ||::
| IFSKNLNIKLNMPLYIAG 18
 Conservative
 STANDARD;
 STANDARD;
 Local Similarity
 Stellaria media.
 ACTI E SITE
 Chloroplast.
 RBL_AREDR
P25827;
RBL_STEME
P46820;
 MOD_RES
ACT_SITE
SEQUENCE
 Stellaria.
 Query Match
 Matches
 RESULT
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 ö
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 Manhart J.R., Hugh J.H., Wilson D.:
Submitted (XXX-1992) to the Emal/Genbank/DDBJ databases.
Submitted (XXX-1992) to the Emal/Genbank/DDBJ databases.
In EUGLICOR. RUBISCO CATALYZES TWO REACTIONS: THE CARROXYLATION OF
D-RIBUTOSE 1,5-BISPHOSPHATE, THE PRIMARY EVEN IN PHOTOSYNTHETIC
CARBON DIOXIDE FIXALION, AS WELL AS THE OXIDATIVE PRAGMATATION OF
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 RBL_CERGL STANDARD; PRT: 475 AA. pp28810; 01-MAY-1992 (Rcl. 22, Created) 01-MAY-1992 (Rcl. 22, Last sequence update) 15-DEC-1998 (Rcl. 37, Last annotation update) RTBULOSE BISPHOSPHATE CARBCXYLASE LARGE CHAIN PRECURSOR (EC 4.1.1.39) (RUBISCO LARGE SUBUNII).
 Photosynthesis: Carbon dioxide fixation; Photorespiration;
Lyase; Oxidoreductase; Monooxygenase; Chloropiast; Acetylation.
PROPEP 1 2 BY SIMILARITY
PROPEP 3 475 REBUIOSE BISPHOSPHATE CARBOXYLASE LARGE
 Gaps
 Gaps
 ENZYME
 Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyladons:
core eidicots: Caryophyllidae; Caryophyllaceae:
Cerastium.
 .;
O
 ö
 CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CC(2) =
 2) ACTIVATES THE
 2 3-PHGSPHO-D-GLYCERATE.
-: CATALYTIC ACTIVITY: D-RIBULGSE 1.5-BISPHGSPHATE + O(2);
3-PHGSPHO-D-SLYCERATE + 2-PHGSPHGGLYCCLATE.
-: SUBUNT: 8 LARGE CHAINS + 8 SMALL CHAINS.
-: SUBCELLULAR LOCATION: CHILOROPLAST.
-: SUMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
 Score 63; DB i; Length 475;
Pred, No. 3.32e+00;
7; Mismatches 5; Indels
 ACETYLATION (BY SIMILARITY).
BINDING OF CO(2) ACTIVATES 1
 Indels
 OD9BF646BE50211B CRC64:
 No. 3.31e+00:
Mismatches 5:
 MENDEL, 2754; CESQLITECLIL.
PROSITE: PS00157; RURISCO_LARGE: 1.
PFAM: PFC0016: RUBISCO_large: 1.
 Pred.
 475 AA; 52656 MW;
 255 VFARELGVPIVMHDYITG 272
 Best Local Similarity 33.3%;
Matches 6; Conservative
 33.3%;
 245 VFARELGVPIVMHDYITG 263
 IFSKNLNIKLNMPLYIAG 18
 EMBL; M83542; AAA84173.1;
 1 IFSKNUNIKLNMPLYIAG 18
 Best Local Similarity 33.3%:
Matches 6; Conservative
 201
 Cerastium glomeratum.
Chloroplast.
 P00875; 1AUS.
 SEQUENCE FROM N.A.
 ACTIVE
 ACT_SITE
SEQUENCE
 Query Match
 MOD_RES
 HSSP; P(
MENDEL;
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Gaps

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(RUBISCO LARGE SUBUNIT).

Arenaria drummondii

RESULT

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ENZYME

CO(2) ACTIVATES THE

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Y454_MYCGE
P47692;
 ACT_SITE
SEQUENCE
 Query Match
 MOD_RES
 CHAIN
 Matches
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 HERER REPRESENTATION OF THE PROPERTY OF THE PR
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 Ö
 Manhart J.R., Budh J.H., Wilson D.;
Submitted (XXX-1992) to the EMBLGenbank/DDBJ databases.
Submitted (XXX-1992) to the EMBLGenbank/DDBJ databases.
-!- FUNCITON: RCBISCO CAIALYZES TWO REACITONS: THE CAKBOXYLATION OF
-!- FUNCITON: ACBISCO CAIALYZES TWO REAMARY EVENT IN PHOTOSYNTHETIC
CARBON DICKIDE FIXATION. AS THE DATABASE TRADIATION OF
THE PRACTICES SUBSTRATE IN THE PHOTORESPYRATION PROCESS. BOTH
REACITONS GOOUR SIMULIANDGOUSLY AND IN COMPETITION AT THE SAME
 RBL_AVESA STANDARD: PRI: 477 AA.
P48684.4
01-FBB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC:1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (EC 4.1.1.39)
(RUBISCO LARGE SUBUNIT).
 Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lyase; Oxidoreductase, Moncovygenase; Chioreplast; Acetylation.
PROJEP 3 SY SIMILARITY
CHAIN 476 RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE
 Saps
 Garcia P.G.:
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
 ACETYLATION (BY SIMILARITY).
BINDING OF CO(2) ACTIVATES THE ENZYME.
: B4B913647EF81589 CRC64:
 Chloroplast.

Eukaryota: Viridiplantue: Streptophyta: Embryophyta: Tracheophyta: Eukaryota: Viridiplantue: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Caryophyllidae: Caryophyllales: Caryophyllaceae:
 Eukaryota, Viridipiantae, Streptophyta, Embryophyta, Tracheophyta,
euphyilophytes, Spermatophyta, Magnollophyta, Lillopsida, Poales,
 ::
 -i - CATALYTIC ACTIVITY: D-R:BULOSE ::S-SISPHOTE + CO(2)
2 3 PHOSPHO-U-GLYCRARIE
-i - CATALYTIC ACTIVITY: D-RIBULOSE ::S-SISPHOSEHATE + O(2) =
3 -PHOSPHO-D-GLYCRATE + 2 -PHOSPHOGLYCOLATE
3 -PHOSPHO-D-GLYCRATE + 2 -PHOSPHOGLYCOLATE
5 - SUBCELULAR : B LARGE CHAINS + 8 SMALL CHAINS.
-i - SUBCELULAR ::CCATION: CHIONEDLAST
-i - SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
 Score 63: 38 1: Length 476:
Pred. No. 3.31e+00:
7: Mismatches 5: Indels
 MENDEL 2732: AMEdrirbotii.
PROSITE: PS00157; RCBISCO_LARGE: I.
PFAM: PFCC016: RuBisCO_large: 1
 201 201 B 476 AA: 52562 WW:
 EMBL: M93541: AAA84023.1; ...
HSSP: P00875: IAUS.
 Match
Local Similarity 33:38:
Nes 6; Conservative
 255 VEARELGVPIVMHDYITG 272
 1 IFSKNINIKLNMPLYIAG 18
 Avena sativa (Cat).
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 ACTIVE SITE
 Poaceae: Avena
 Chloroplast.
 MOD_RES
ACT_SITE
SEQUENCE
 Cuery Match
 Ma, ches
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DARIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CARBON DIOXIDE STATION, AS THE DAYBDATTRE FRAGMENATION OF
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS, BOTH
REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 SEQUENCE FROM N.A.
STRAN-ATCC 33330 / G-37;
MEDLINE: 96626346.
MEDLINE: 96626346.
Fleischmann R.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Keliey J.M., Frictoman J.L., Weidman J.F., Srill K.V., Sandusky M., Fuhrmann J.L., Neidman J.F., San iek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III. Venter J.C.; Science 270:397-403(1995).
 RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE
 Sapt
 Protosynthesis: Carbon dioxide fixation: Photorespiration:
Lyase: Oxidoreductase: Monooxygenase: Chloroplast: Acetylation
PROPEP BY SIMILARITY.
 Mycoplasma genitalium.
Bacteria: Firmicutes: Bacillus/Clostridium group: Mollicutes
 -:- CATALYTIC ACTIVITY: D-RIBULINEE 1.5-BISPHOSFHATE - CO(2)
2 3-PHOSPHO-D-GLYCERALE
-:- CATALYTIC ACTIVITY: D-RIBULINEE 1.5-BISPHOSPHATE - U(2) -
3 -PHOSPHO-D-GLYCERATE - 2-PHONSPHOGLYCOLATE
-:- SUBMIT: 8 LARGE GHAINS + 8 SMALL CHAINS.
-:- SUBMILLULAR LOCATION: CHICHOPLAST
-:- SUBMILLULAR LOCATION: CHICHOPLAST
-:- SIMILARITY: BELONGS IO THE RUBING LANGE CHAIN FAMILY
 BINDING OF CO(2) ACTIVATES THE F1058ED95AED05DD CRC64;
 Score 63: DB 1: Length 477:
Pred. No. 3.31e+00:
7: Mismatches 5: Indels
 ACETYLATION (BY SIMILARITY)
 01-001-1996 (Rel. 34, Orested)
01-001-1996 (Rel. 34, Last Septence (pdate)
01-001-1996 (Rel. 34, Last annotation update)
HYPCHELICAL PROTEIN MA454
 PAT: 155
 MENDEL: 2735; AVESA;rbcl;.
PROSITE; PS00157; RUBISCO_LARGE: 1.
PFAM; PF00016; RUBISCO_large; 1.
 201 B
 EMBL; L15300; AAA84028.1; -. HSSP; P00876; 3RUB.
 Mycoplasmataceae: Mycoplasma
 44.18:
33.38:
 255 VFARELGVPIVMHDYIIG 272
 1 IFSKNINIKLNMPLYIAG 18
 5; Conservative
 STANDARU:
 201 2
477 AA;
 Local Similarity
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 ö
 PCNA_PSEPU STANDARD: PRI; 260 AA.
P00436;
21-JUL-1986 (Rcl. 01, Created)
61-NCV-1995 (Rel. 32, Last sequence update)
15-JUC-1999 (Rel. 38, Last annotation update)
PROTOCATECHGAIE 3,4-DIOXYGENASE ALPHA CHAIN (EC I.13.11.3) (3.4-PCD).
 Gaps
 STRAIN-AICC 23975;
MEDLINE: 79216432.
Kohimiller N.A., Howard J.B.;
The primary structure of the alpha subunit of protocatechuate 3.4-dioxygenase. II. Isolation and sequence of overlap peptides and
 Orville A.M., Elango N., Lipscomb J.D., Ohlendorf D.H., "Structures of competitive inhibitor complexes of protocatechuate 3.4-dioxygenase: multiple exogenous ligand binding orientations
 Pseudomonas pitida.
Bacteria; Protcobacteria: gamma subdivision: Pseudomonas group:
 Fraze R.W., Livingston D.M., Laporte D.C., Lipscomb J.D.;
Fraze R.W., Livingston D.M., Laporte D.C., Lipscomb J.D.;
"Cloning, sequencing, and expression of the Pseudomonas putida
protocatechuate 3.4-dioxygenase genes.";
J. Bacteriol, 175:6194-6202(1993).
 Oblendorf D.H., Orville A.M., Lipscomb J.D.:
"Structure of protocatechuate 3,4*dioxygenase from Pseudomonas aeruginosa at 2.15*A resolution.";
J. Mol. Biol. 244:586-608(1994).
 X-RAY CRYSTALLOGRAPHY (2.8 ANGSIRCMS).
MEDLINE: 89057125.
Obleadorf D.H. Lipscomb J.D. Weber P.C.:
Structure and assembly of protocalechuate 3.4-dioxygenase.";
Nature 336:403-405(1998).
 .
0
 Score 62: DB 1: Length 155: Pred: No. 4.88e+60: 4: Mismatches 2: Indels
 IIGR: W3454:
Hypothetical protein.
SEQUENCE 155 AA: 17376 MW: F231FE2A31FCAC39 CRC64:
 RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
 X-RAY CRYSTALLOGRAPHY (2.13 ANGSTROMS).
STRAIN-AICC 23975;
 X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
STRAIN-AICC 23975:
MEDLINE: 95082024.
 complete sequence.";
J. Biol. Chem. 254:7309-7315(1979).
 within the active site.";
Biochemistry 36:10039-10051(1997).
 EMBL; U39727; AAC72474.1; -. SMBL; U39732; AAB01644.1; -.
 Query Match
Best Local Similarity 57.1%:
Matches 8: Conservative
 5 IFTKILSILINMAL 18
 1 IFSKNLNIKLNMPL 14
 SEQUENCE FROM N.A. STRAIN-AICC 23975;
 MEDLINE: 97400460
 STRAIN-ATCC 23975
MEDLINE: 97400451
 Pseudomonas.
 STRAIN-ATCC
 14
 SEQUENCE
 RESULT
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 ċ
 -!- CATALYTIC ACTIVITY: 3.4-DIHYDROXYSENEGATE + 0(2) - 3-CARBUSY-CIS.6TS.4CONATE.

-!- CORACTOR ACCOUNTE.

-!- COPACIOS. FERRIC ION. EACH PROTOMER APPEARS TO CONTAIN 1 ATOM OF PERRIC IRON, FORMING THE ACTIVE SITE OF THE ENZYME.

-!- PATHWAY. SECOND SIEP IN THE CONVERSION OF P-HYDROXYBENZORIE TO SUCCINATE AND ACETYL-COM.

-!- SUBUNIT: THE ENZYME IS AN OLIGOMER OF 12 COPIES OF THE ALPHA AND
Orville A.M., Lipscomb J.D., Ohlendorf D.H.;
"Crystal structures of substrate and substrate analog complexes of protocatechuate 3.4-dioxygenase: endogenous Fe3+ ligand displacement in response to substrate binding.":
Biochemistry 36:10052-1006(1997).
 "Crystal structure and resonance Raman studies of protocutechuate 3.4 dioxygenase complexed with 3.4 dibydroxyphenylacetate.") Blochemistry 36.11504-11313(1997).
-1. FUNCTION: PLAYS AN ESSENTIAL ROLE IN THE UTILIZATION OF NUMEROUS AROMATIC AND HYDROAROMATIC COMPGENOS VIA THE BETA-KETCADIERIE
 Aromatic hydrocarbons catabolism: Oxidoreductase; Dioxygenase: Iron;
 MEDLINE: 97444342.
Elgren T.E., Orville A.M., Keily K.A., Lipscomb J.D., Ohlendoit D.R
 Gaps
 ö
 Query Match 43.4%; Score 52; DB 1; Length 200: Best Local Similarity 31.5%; Pred. No. 4.88e+00; Matches 6; Conservative 7; Mismatches 5; Indels
 PROTOCATECHUAIE (POTENTIAL).
N -> D (IN REF. 2).
N -> D (IN REF. 2).
S -> D (IN REF. 2).
 PS00083: INTRADIOL_DICKYGENAS: 1.
 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
 133 133 PR
133 133 PR
59 6 N
76 76 76 N
200 AA: 22256 MW:
 130 LFARGINIHLHTRLYFDDE 148
 EMBL; L14836; AAB41025.1; -. PIR; A00505; DAPSAA.
 1 IFSKNENIKLNMPLYIAGN 19
 3PCL: 21-JAN-98.
3PCM: 21-JAN-98.
3PCM: 25-FEB-98.
 29-APR-98
20-DEC-94
27-MAY-98
27-DAR-98
07-JAR-99
07-JAR-99
07-JAR-99
21-JAR-99
21-JAR-99
21-JAR-99
 3PCB; 21-JAN-98
3PCB; 29-APR-98
 3D-structure.
INIT_MET
 3PCC;
2PCD;
3PCD;
3PCE;
3PCE;
3PCE;
 3PCH:
3PCL:
 STRAIN-ATCC
 PATHWAY
 CONFLICT
CONFLICT
SEQUENCE
 PROSITE;
 BINDING
 PDB;
PDB;
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 -1- SUBUNIT: HETEROTETRAMER OF TWO SUBUNITS A AND TWO SUBUNITS B.
 ö
 STRAIN-BLZ:
MEDLINE: 97238659.

*An atypical topoisomerase II from Archaea with implications for melotic recombination."

"An atypical topoisomerase II from Archaea with implications for melotic recombination."

"An atypical topoisomerase II from Archaea with implications for melotic recombination."

"An atypical topoisomerase II from Archaea with implications for melotic recombination."

"I fortune 386-414-417 (1997).

"FUNCTION: RELAXES BOTH POSITIVE AND NEGATIVE SUMERTURNS AND EXHIBITS A SIRGO DECALEMBER ACTIVITY.

"OF DOUBLE-STRANDED DNA.
 Saps
 .;
0
 Isomerase: Topoisomerase: DNA-binding.
ACT_SITE 106 106 DNA CLEAVAGE (HY SIMILARITY).
SEQUENCE 389 AA; 45055 WW: 6F6170B8231431B7 CKC64;
 # Match 43.4%; Score 62; DB 1; Length 389; Local Similarity 46.7%; Pred. No. 4.8 --03; Conservative 4; Mismatches 4; Indexs
 1+;
SEQUENCE FROM N.A., AND SEGUENCE OF 212-22; AND 344-352
 15-302-1998 (Re). 36, Created)
15-302-1998 (Rel. 36, Last sequence update)
15-302-1998 (Rel. 36, Last annotation update)
TYPE II DNA IPPOISOMERASE VI SURGNIT A (EC 5.99.1.3)
 Archaea: Crenarchaeota: Sulfolobales: Sulfolobus.
 389 AA.
 PRI;
 EMBL: Y10582: CAA71605.1:
 244 FVRRINEELKLPVYI 258
 STANDARD;
 2 FSKNLNIKINMPLYI 16
 TOP6A.
Sulfolobus shibatae.
LI :5
TP6A_SULSH
005208;
 Cuery Match
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Search completed: Mon Jun 19 15:13:01 2000 Job time : 6 secs.

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|-----------------------------------------|-----|
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| ******                                  |     |
| ********                                |     |
| ********                                |     |
| ********                                |     |
| *******                                 |     |
| *************************************** | 1.2 |

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Mon Jun 19 16:13:19 2000; MasPar time 9.14 Seconds 15:.746 Million cell updates/sec Run on:

Tanular output not generated.

>05-09-142-524A-11 (1-20) from US09142524A.pep 143 1 IFSKNINIKLNMPLYIAGNK 20 Description: Perfect Score: Sequence:

РАМ 150 Gap 15 Scoring table:

225878 segs, 69334122 residues Searched:

Post-processing:

Minimum Match 08 Listing first 45 summaries Database:

spirembil2 lisp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_buman 5:sp\_invertebrate 5:sp\_mammai 7:sp\_mhc 8:sp\_organeile 9:sp\_phage 10:sp\_plant il:s \_rodent 12:sp\_unclassified i3:sp\_vertebrate 14:sp\_viru scale 0.610 Mean 29,386; Variance 48,203 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result<br>No. | Score | Query<br>Match | Query<br>Match Length | aq | GI.    | Description            | Pred. No |
|---------------|-------|----------------|-----------------------|----|--------|------------------------|----------|
| 7             | 143   | 100.0          | 375                   | 10 | 095385 | CHAC1 PRECURSOR,       | 9.15e-15 |
| 7             | 123   | ુ.98           | 367                   | 10 | 092NU7 | POLLEN MAJOR ALLERGEN  | 1.476-10 |
| m             | 69    | 47.5           | 444                   | ဆ  | 058879 | RIBULOSE BISPHOSPHATE  | 3.04e-00 |
| ಶ             | 6.8   | 47.6           | 455                   | 10 | 064510 | PUTATIVE PECIATE LYASE | ω.       |
| Ŋ             | 69    | 47.6           | 1202                  | S  | 021303 | KO7G5.3 PROTEIN.       | 3.04€+0  |
| 9             | 67    | 46.9           | 430                   | ထ  | 078617 | RIBULOSE BISPHCSPHATE  | 4.39e-0  |
| 7             | 67    | 46.9           | 459                   | 10 | 023565 | PUTATIVE PECTATE LYASE | 4        |
| ထ             | 29    | 5.94           | 555                   | Ś  | 018771 | PROTEIN.               | 4        |
| 6             |       | 45.5           | 414                   | 80 | 03:954 | RIBULOSE BISPHOSPHATE  | 9.08e+00 |
| 10            | 65    | 45.5           | 449                   | സ  | 033403 | RIBULOSE BISPHOSPHATE  |          |
| 113           | 65    | 45.5           | 466                   | œ  | O9XOF1 | RIBULOSE BISPHCSPHATE  | 9.086+00 |
| 12            |       | 45.5           | 467                   | œ  | P93920 | BISPHOSPHAT            | 9.08e+00 |
| 73            | 65    |                | 475                   | Ø  | Q31807 | RIBULOSE BISPHOSPHATE  | 9.08e+00 |
| 74            | 65    | 45.5           | 475                   | œ  | P92302 | RIBULOSE BISPHOSPHATE  | 9.08e+00 |
| 15            | 65    | 45.5           | 475                   | 80 | 009485 | RIBULOSE BISPHOSPHATE  | 9.08e+00 |
| 16            | 64    | Ξ.             | 449                   |    | 036373 | RIBULOSE BISPHOSPHATE  | 1.30e+01 |
| ۲.            | 64    | 44.8           | 459                   |    | 045932 | RIBULOSE BISPHOSPHATE  | 1.30e+01 |
| œ<br>~1       | 64    | 44.8           | 473                   |    | 036638 | RIBULOSE BISPHOSPHATE  | 1.30e+0] |
| 61            | 64    | 44.8           | 473                   |    | 036641 | RIBULOSE BISPHOSPHATE  | 1.30e+01 |
| 20            | 64    | 44.8           | 475                   | 80 | 019878 | RIBULOSE BISPHOSPHATE  | 1.30++01 |

Created) Last sequence update) Last annotation update)

| BISPHOSPHATE 1.85 | BISPHOSPHATE : 85e+ | BISPHOSPHATE 1.85e+ | BISPHOSPHATE 1.85e- | SE BISPHOSPHATE 1.85e+ | BISPHOSPHATE 1.85e. | BISPHOSPHATE 1 85e+ | BISPHOSPHATE 1.85e- | BISPHOSPHATE : 85e- | BISPHOSPHATE : 85e- | BISPHOSPHAIE 1.85e- | BISPHOSPHATE : 856- | BISPHOSPHATE 85e- | BISPHOSPHATE : #5e+ | BISPHOSPHAIE 1.85e- | BISPHOSPHATE 1856. | BISPHOSPHATE : 85E+ | BISPHOSPHATE 1.85e+ | BISPROSPHATE 1.85e- | BISPHOSPHATE 1.85e+ | BISPHOSPHATE 1.85e- | BISPHOSPHATE : 85e+ | BISPHOSPHATE 1.85e- | BISPHUSPHATE 1.85e+ | LLUCAR A-AMYLAS 1.65e+ |             |   |        |              |        |              | ite)                  | odate)        |
|-------------------|---------------------|---------------------|---------------------|------------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|--------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|------------------------|-------------|---|--------|--------------|--------|--------------|-----------------------|---------------|
| RI                | I &                 | RI                  |                     | RIBULO                 | ₩,                  | Ω,                  | òr.                 | æ                   | æ                   | æ                   | æ                   | æ.                | æ                   | æ                   | x                  | æ,                  | ar.                 | 3159 RIBULOSE       | æ                   | æ                   | ar,                 | a.                  | RIBULC              | NIRAC                  | S ENGENOTIN |   |        | PRT: 375 AA. |        | reated)      | Last sequence update) |               |
| 394 8 047         | 8 *6                | 94 8                | 94 B                | 94 B                   | 94 8                | 46 10               | 30<br>83<br>83      | 58 9                | 58 B                | 58<br>83            | 58 6                | 58 8              | 58 8                | 65 8                | 8 69               | 8 69                | 8 69                | 8 69                | 8 69                | 69 8                | 73 8                | 76 8                | 8                   | 86 2                   | .:<br>4     |   |        | PRELIMINARY: |        | 02, €        | 5                     | 3             |
| •                 | 3 44                | 3 44                | 3 44                | 3 44                   | 3 44.               | 3 44.               | 3 44                | 3 44.               | 3 44.               | 3 44.               | 3 44.               | 3 44.             | 3 44.               | 3 44.               | 3 44.              | 3 44.               | 3 44.               | 3 44.               | 3 44                | 3 44                | 3 44.               | 3 44.               | 3 44                | 3 44.                  |             | , | - 1    | 5385         | 6385;  | FEB-1997 (Tr | -FEB-1997 (Tr         | XI) 6661-AON- |
| 21                | 22                  | 23                  | 24                  | 25                     | 25                  | 27                  | 28                  | 29                  | 33                  | 3.1                 | 32                  | 33                | 34                  | 35                  | 36                 | 37                  | 3.8                 | 39                  | 40                  | 4                   | 42                  | £ 4.3               | 4                   |                        |             | 1 | KESUL. | o oi         | $\sim$ | 100          | $\overline{}$         | $\sim$        |

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 SUZUKI M., KOMIVAMA N., ITOH M., HITH H., SONE T., KUND K., TAKANI J., CHIA M. N.,
CHIA M. N.,
PLILILIDATION, CHARACTERIZAT, C. GRID SCHOOL TONION CONTRACT
PLILIDATION CHARACTERIZAT, C. GRID SCHOOL TONION CONTRACT
MAINTENANCE, 33:451-450(15%)
MAINTENANCE, 7450 Chaobellos
MENDEL 7450 Chaobellos
PEMAI PRO044; pec_lyase, 1.
PRINTS, PRO0807; AMBALLERGEN.
 50.55
CHAOI PRECURSOR.
Chamaecyparis obtusa.
Chamaecyparis obtusa.
Eukaryota. Viridiplantae; Streptophyta: Embryophyta: Trachecphyta:
euphy.lophytes: Spermatcphyta: Coniferopsida: Coniferales:
Taxodiaceae: Chamaecyparis.
 0)
 Query Match 100.0%; Score 143; DB 10; Length 375; Best Local Similarity 100.0%; Pred. No. 9.15e-15; Matches 20; Conservative 6; Mismatches 0; Indels
 SIGNAL 1 21 POTENTIAL.
CHAIN 22 375 CHACI.
SEQUENCE 375 AA: 40258 MM; A0961492 CRC32;
 367 AA.
 PRT:
 092NU7 PRELIMINARY;
092NU7;
01-MAY-1999 (TEMBLEEL 10, Cr
01-MAY-1999 (TEMBLEEL 10, Le
01-NOV-1999 (TEMBLEEL 10, Le
 92 IFSKNENIKINMPEYIAGNK 111
 1 IFSKNENIKENMPERIAGNK 20
 SEQUENCE FROM N.A.
TISSUE-POLLEN;
MEDLINE; 96265194.
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AC 09
DT 01
DT 01
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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PRANCE G.T., KAROL K.S., CHASE M.K.;

PROPION C.M., MORI S.A., PRANCE G.T., KAROL K.S., CHASE M.K.;

PROPION C.M., MORI S.A., PRANCE G.T., KAROL K.S., CHASE M.K.;

WASHING IN CONTROL SEQUENCE AND METAL S.A.

FUNCTION RESERVED TO THE PRIMARY EVENT IN PROCESSING THE PROPERTY CARBON DISCRESSING OF ALMARY EVENT IN PROCESSING THE PROPERTY OF THE
 Gaps
 MIDGRO-HORIOTH I.M., GOLDBLUM R.M., KUROSKY A., WGOD T.G., BROOKS E.G.,
BROOKS E.G.,
"Molecular close of mountain cedar (Judiperus ashei) pollen major alleraes, Jun al.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL. AF105662: AAE03669.1: -
EMBL. AF105662: AAE03669.1: -
MENDEL; 36544; Junas:1288;3654.
BRENDEL; 36545; Junas:1288;3654.
SEQUENCE 36734: 39924.WW: 40208630.0F.32;
 BINDING OF CO(2) ACTIVATES THE ENZYME C98E6781 CRC32;
 Juniperus ashei (Ozark white cedar).
Bukaryota, Viridoplantae: Streptophyta: Em ryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Conlferopsi a: Conlerales:
Taxodiaceae: Juniperus.
 Chloropiast.

Eukaryota Vir.diplantae: Streptophyta: Embryophyta: Tracheophyta: euphyllophytes: Spermatophyta: Magnoliophyta: eudictyledons: euphyllophytes: Asteriatophyta: Ecythilaceae: Conratari.
 -i-CATALYTIC ATTUTY: D-RIBULOSE 1.5-BISPHOSPHATE + O(2) = 3-PHOSPHOGLYCOLATE.
-i-SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS.
EMBL: 280177: CABO2224.1;
MENDEL: 3684: Couta;rbcL: 3684.
MENDEL: PROJECTS TRUBSCC_LARGE.
CHOTOplas:: Photographhesis: Carbon dioxide !ixation:
Photographration: Lyase: Carbon dioxide !ixation:
 ö
 098879;
01-XAY-1999 (TEMBLEEL 10, Created)
01-MAY-1999 (TEMBLEEL 10, Last sequence update)
01-MCV-1999 (TEMBLEEL 12, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39)
 Length 367
 Score 68; DB 8; Length 444; Pred. No. 3.04e+00;
 Score 123: DB 10; Length 36
Pred. No. 1.47c-10;
4: Mismatches 1: Indels
 -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE PHOSPHO-D-GLYCERATE.
 444 AA
 PRT;
 49296 MW;
 92 IFSCNM IKLKMPLYVAGHK 111
 Query Maich
Rest Local Similarity 27.8%:
 puery Match
best_Local Similarity 75.0%;
 1 IFSKNINIKINRPLYIAGNK
 15: Conservative
POLLEN MAJOR ALLERGEN 1-2
 PRELIMINARY:
 444 AA;
 SEQUENCE FROM N.A.
 Couratari tapari.
 (FRAGMENT)
 ACT_SITE
SEQUENCE
 .T
098879
 Matches
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MEDGINE: 94150718

MEDLINE: 94150718

AMULISON R., BURNES C., BERKS M., MELSON R., BURNES C., BERKS M., MILSON R., BURNEL M., COPSEY T., COOPER J., COLLIGN A., BONFELD J., CONNELL M., COPSEY T., COOPER J., COLLIGN A., CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., A GARDNER N., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON I., JONES M. KERSHAW J., KIRSTEN T., LAISTER N., LAITHELLE P., LIGHTXING J., LLOYD C., MENTRY A., MORTINORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEIN R., SHALDON N., SMITH A., SONNHAWMER F., STABDN R., SULSTON J., HILBERY-MIEG J., THOMAS K., VALDIN M., VAUGHAN K., WATERSTON R., MATESON A., WEINSTOCK L., MILKINSON-SPROAT J., WOHLDMAN P.:
 Silve
 Cacobrhabditis elemans.
Būkaryota: Metapoa: Nematoda - Secenteries. Ababditia: Krahditida:
Rhabditina: Krabditoidea: Malditidae, Peludoffuae: Geomitialditis.
 Arabidopsis thaliana (Mouserear cress)
Brayopara Viriablandee, Streptophyta: Erthyophyta: franheophyta:
euphyllophytes: Spermatchhyta: Magnollophyta: eudicotyledus:
core eudicots: Rosidae: eurosids II: Brassicales: Brassicane.
 SEQUENCE FROM N.A.
STRAIM-CV. COLUMBIA:
STRAIM-CV. COLUMBIA:
SYRES S.M. LIN X., KETCHUM K.A., CRUSHY M.L., BRAND-N R.D.,
SYRES S.M. A. MASON T.M., KERLAVAGE A.R., AGAMS M.D.,
SOMERVILLE C.R., VENTHR J.C.,
Submitted (MAR-1998) to the EMBL/GenBank/DURJ databases.
BMBL, RG002521, AAC05356.13.
PRODEL 26565: Arath;1088:28565,
PFAM: PF0644: pec_lyase: 1.
 ä
 Length 455
 6. Indels
 Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 271264: CAÀ95830.1: -.
NCE 1202 AA: 138469 MW: 6F9C9E53 CRC32:
 Score 68; DB 10;
Pred, No. 3.04e-00;
 SEQUENCE 455 AA; 51257 MW; EBACH82D CRG32;
 Mishatches
 01-NOV-1996 (TEMBLREL 01, Created)
01-NOV-1996 (TEMBLREL 01, Last seq
01-NAV-1999 (TEMBLREL 09, Last ann
KC7GS.3 PROTEIN.
 FRT
 171 IFARSMIIKLQQELIITNDK 19
 1 IFSKNLNIKLNMPLYIAGNK 20
 07.
07.
12.
 Query Match
Best Local Similarity 40.0%;
Matches 8: Conservative
 PRELIMINARY:
 PRET. IMINARY
 01-AUG-1998 (TrEMBLIEL)
01-AUG-1999 (TrEMBLIEL)
61-NOV-1999 (TrEMBLIEL)
PUTATIVE PROTATE LYASE.
 elegans.";
Nature 368:32-38(1994).
EMBL: 271264: CAA95830.
SEQUENCE 1202 AA: 13
 SECUENCE FROM N.A.
 Arabidopsis
 MCMURRAY
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064510
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Gaps

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5: Indels

Mismatches

231 VFARELGVPIXMHXYLTG 249

5: Conservative

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RESULT
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                                                                                                                                                                           Eukaryota, Viridiplantae: Stroptophyta: Embryophyta: Tracheophyta;
euphyllophytes: Spermatophyta: Magnollophyta: Lillopsida: Asparagales;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                Gaps
                                                                                                                                                                                                                                                     BINDING OF CO(2) ACTIVATES THE EN2YME 708E695E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                   01-NCV-1998 (TrEMBLrel. 08. Created)
01-NCV-1998 (TrEMBLrel. 08. Last sequence update)
01-NCV-1999 (TrEMBLrel. 12. Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4 1.1.39)
Score 58; DB 5, Length 1202; Pred. No. 3.04e+00;
                                                                                                                                                                                                                                                                                                                                                                        Score 57: DB 8; Length 435;
Pred. No. 4.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TEMBLEEL 05, Created)
01-JAN-1998 (TEMBLEEL 05, Last sequence update)
01-NOV-1999 (TEMBLEEL 12, Last annotation update)
PUTATIVE PECIATE LYASE.
               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               459 AA
                                                                      430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                      182 182 B
430 AA: 47681 WW:
                                                                                                                                                                                                                                                                                                                                                                                                     235 VFARELGVPIIMPDYLIG 252
Query Match
Best Local Similarity 61.5%:
                                                                                                                                                                                                                                                                                                                                                                      Cuery Match
Best Local Similarity 33:3%:
                                                                                                                                                                                                                                                                                                                                                                                                                   8
                8; Conservative
                                                                                                                                                        Orchidaceae; Metracyllium
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                               1 IFSKNLNIKINMPLYIAG
                                                                                                                            Meiracyllium trinasutum
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                                      9 IKENMPLYIAGNK 20
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                                                                                                                                    Chloroplast
                                                                                                               (FRAGMENT).
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                                                                               KULIKAUSKAS R., MCCORMICK S.:
*Identification of the tobacco and Arabidopsis homologues of the pollen-expressed LAT59 deace of torato.":
Plant Mol. Blob. 34.869 e14(1997).
EMBL. 03559; Arathilo88.25559.
PRAM: PF00544; pec.14ysee: 1.
PRINTS: PROBGY: AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoaː Nematoda: Secernontea: Rhabditia: Rhabditida:
Rhabditina: Rhabditoidea: Rhabditidae: Peloderinae: Caenorhabd::
euphyllophytes; Spermatophyta: Magnollophyta: eudicotyledons;
core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                           Length 459
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                                                                                                                                                                                                                                       Score 67: DB 10, Length 459
Pred. No. 4.396+60;
7: Mismatches 5: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1996) to the East/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scc e 67; DB 5; L
Pre No. 4.39e+00;
7; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
EMBL: 278410; CAB01641.1: -.
SEQUENCE 555 AA: 60315 MW: 4D90D542 CRC32:
                                                                                                                                                                                                               459 AA: 51420 MW: 41EB5908 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                      555 AA
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1 :FSKNINIKINMPLYIAGNK 20
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01-JAN-1998 (TrEMBLrel. 05,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                       46.9%;
Local Similarity 46.0%;
ies 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 46.9%;
Local Similarity 35.3%;
les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                     MEDLINE; 97422403
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C51E3.6 PROTEIN.
                core eudicot
Arabidopsis.
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Best Local 9
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Q31994;
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Q18771
Q18771;
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Chloroplast.
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- FUNCTION: AUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF CRIBULOSE 1.5-BISPHOSPHATE: THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PROTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULIANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                       KONDO K., TEPASAYASHI S., OKALA M., YOAN C., HE S., "Phylogenetic relationship of medicinally important Chidium offcinale and japanese apiaceae besed on rbcL sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta: euphyllophytes; Spermatophyta; Magnollophyta: eudicotyledons; core eudicots; Asteridae; elasterids II; Asterales; Donatiaceae;
                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) + 2 3-PHOSPHO-D-GLYCERATE.
                                                                                    Enkaryota Viridiplantae: Streptophyta: Embryophyta: fracheophyta: esphyllophytes: Sperratophyta: Magnollophyta: eldicotyledons; core eudicots; Asteridae; cuasterids II: Apiales: Apiaceae;
                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHOTO-C-CLYCRATE + 2-PHOSPHOGLYCOLATE.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: CHLOROPLAST.
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(NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RIBULOSE BISPHOSFHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39)
01-NOV-1996 (TrEMBLrel. 01, Created)
(01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
(01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RIBULOSE BISPHOSPHATE CARHCXYLASE LARGE CHAIN (EC 4.1.1.39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65: DB 8: Length 414:
Pred. No. 9.08e-00:
Fred. Wirmatches 5: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING OF CO(2) ACTIVATES F581E0BD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                          Photorespiration: Lyase: Oxidoreductase: Monooxygenase
                                                                                                                                                                                                                                                                                                                                                                               tixation:
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Chloropiast; Photosynthesis; Carbon dloxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 AA
                                                                                                                                                                                                                                                                                                                                             MENDEL; 21634; Coegm;rbcL;21634.
PROSITE; PSC0157: RUBISCO_LARGE: 1.
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414 AA; 45839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                    D44563; BAA07967.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY:
                                                                  Coelopleurum grelinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Donatia fascicularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                         Coelopleurum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast
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RBCL.
                                                                              Chloroplast
                                             (FRAGMENT)
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NON_TER
ACT_SITE
SEQUENCE
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Q33403
Q33403:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euphylophytes. Spermatophyta: Magnóllophyta: eudicotyledons; cure
eudicots: Asteridae, edasterids II: Asterales: Donatlaceae: fonatla
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-:- CAIALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) - 3-PHOSPHO-D-GLYCERATE - 2-PHOSPHOGLYCOLATE.
-:- SUBBNIT: 8 LARGE CHA'NS + 8 SMALL CHAINS.
EMBL: AC225058: CAB39389.1; -
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SLY AND IN COMPETITION AT THE SAME
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ن
                                           -i- CATALYTIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHAIE - CO(2)
PHOSPHO-D-GLYCERATE
--- CATALYTIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHAIE - O(2) -
PHOSPHO-O-GLYCERATE - 2-PHUSPH-GLYCOLAIE.
--- SUBDNIT: 8 LARGE GRAINS + 8 SMALL CHAINS.
--- SUBCELLULAR LOCATION: CHUIR-PLAST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12. Greated)
01-NOV-1999 (TREMBLEL. 12. Last sequence update)
01-NOV-1999 (TREMBLEL) 12. Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                   CO(2) ACTIVATES
CO(2) ACTIVATES
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                                                                                                                                                                                                                                                                                                                   Photorespiration; Lyase; Oxid reductase; Monooxygenase.
                                                                                                                                                                                                                                                                   PFAM: PF00016; RubisCC_large; 1.
Chloroplast; Photosynthesis: Carbon dioxide fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast: Photosynthesis: Carbon dicxide fixation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.5%; Score 65; DB 8; 1
38.9%; Pred. No. 9.08e+00;
ative - 1, Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 AA
                                                                                                                                                                                                                                                                                                                                                                 SO SNICKIE
                                                                                                                                                                                         EMBL; X87385; CAA60839.1; ...
MENDEL; 21722; Donfa:rbcL:21722.
PROSITE: PSC0157; RUBISCO_LARGE: 1.
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  REACTIONS OCCUR SIMULTAN
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38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 IFARELGVPIVMHDYITG 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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ACTIVE SITE.
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ACT_SITE
SECUENCE
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P92302
P92302;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: KUBISCO CATALYSES TWO REACTIONS: THE CARROXYLATION OF D-RIBULOSE 1.5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXALION, AS WELL AS THE CXIDALIVE FRACHENTATION OF THE PENTOSE SUBSIFACE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULIANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridipiantae, Streptophyta, Embryophyta, Iracheophyta, euphyllophytes, Spermatophyta, Magnollophyta, Lillopsida, Asparagales; Tecophilaeaceae, Odontostomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnollophyta; eudicotyledons:
core endicots: Asteridae: euasterids II; Apiales: Apiaceae: Angelica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i. CATALYTIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHATE + CO(2) = 2 3-PHOSPHO-D-GLYCERATE.
-: CATALYTIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCCLATE.
-: SUBGNIT: 8 LARGE CHAINS + 8 SMALL CHA NS.
-: SUBGNIT: 8 LARGE CHAINS + COATION: CHLCROPLAST.
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Lyase; Chioropiast; Photosynthesis; Carbo.. dioxide fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING OF CO(2) ACTIVATES THE BINDING OF CO(2) ACTIVATES THE
                                                                                                                               CI-NCV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RIBU:ODE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39)
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Photorespiration: Oxidereductase: Monoexydenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 8; L
Pred, No. 9.08e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51835 MW; 1F18A356 CRC32;
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PROSITE: PSO0157; RUBISCO_LARGE: 1.
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27.8%;
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HSSP: P00880; 1RSC.
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  246 IFARELGVPIVMHDYITG 253
                                            : IFSKNENIKLNMPLYIAG 18
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les 5: Conservative
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193
167
467 AA;
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                                                       FUNCTION: RUBISCO CATALYS TWO REACTIONS: THE CARBUXYLATION OF RIBULOSE 1.5-BISPHOSPHATE HE PRIMARY EVENT IN PROTOSNYTHETTO CARBON DIOXIDE FIXATION. A. WELL AS THE OXIDATIVE FRAGMENIATION THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS: BATHER REACTIONS OCCUR SIMULTANFOUSLY AND IN COMPETITION AT THE SAME
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euphyllophytes: Spermatophyta: Magnollophyta: eudicotyledons:
Core eudicots: Rosidae: euros ds I: Cucurbitales: Begoniaceae.
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PHOSPHO-D-GLYCERATE.
-:- CATALYTIC ACTIVITY: D-RIBULOSE 1.5-BISPHOSPHATE + C(2) - 3-
PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-:- SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS.
-:- SUBCELLULAR LOCATION: CHLOROPLAST.
--- BMBL, 1059821 ARA41157.1;
--- HSSP: PO0975: IRCX
--- MENDEL: 21804: Hilsa:rbcl,218
--- PROSITE: PS00157: RCBISCO_LARA : 1.
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-!- CAIALYTIC ACTIVITY: D-RIE:LOSE 1,5-B:SPHOSPHATE + O(2)
PHOSPHO-D-CLYCERAIE + D-RIE:LOSE 1,5-B:SPHOSPHATE + O(2)
-!- SUBURIT: 8 LARGE CHAINS + SMALL CHAINS.
-!- SUBCELLULAR LOCATION: CHI. + PLAST.
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01-MAY-1997 (TIEMBLEEL. 03. Last sequence update)
01-NCV-1999 (TIEMBLEEL. 12. Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXY: ANE LARGE CHAIN (EC 4.1.1.
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Chloroplast; Photosynthesis; Carbon dioxide fixation;
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Pred, No. 9.08e+00;
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                        S TIS P.S.;
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SEQUENCE FROM N.A.
PLUNKETI G.M., SOLTIS D.E., S.
Am., J. BOL. 83:499-515(1996).
-!- FUNCTION: RUBISCO CATALYS
RIBULOSE 1,5-BISPHOSPHATE
                                                                                                                                                                                                                                                                                         EMBL. USOZZI; AA498935.]; -...
MENDEL: 21616; Anglu:rbcL:21;
PROSITE: PSOSI57; RUBISCO_LAR
PFAM: PSO016; RUBISCO_LAR
Chioropiast: Photosynthesis;
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475 AA: 52676 MM:
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38.9%;
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SEQUENCE FROM N.A.
STRAIN-CCLL. BREMER 3089 (UPS);
BACKLUND A., BREMER B.;
Plant Syst. Evol. 200:0-0(1997).
Plant Syst. Evol. 200:0-0(1997).
Plant Syst. Evol. 200:0-0 CATALYSES TWO REACTIONS: THE CARBOXYLATION OF D.-FUNCTION: FUBLICOS. 15-BISPHOSPHAPE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIGXIDE FIXATION. AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PRINACE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS COUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE.
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Usukaryota: Tracheophyta: Embryophyta: Tracheophyta: eukaryota: Tracheophyta: euphyllophyta: Spermatophyta: Magnolicphyta: eudicotyledons: core eudicots: Asteridae: Cornaics: Hydrostachyareae: Hydrostachys
BINDING OF CO(2) ACTIVATES THE ENZYME: DC40A579 CRC32;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence (pdate)
01-JUNOV-1999 (TrEMBLrel. 12, Last annotation update)
RIBULOSE BISPHUSEHATE CARBOXYLASE LARGE CHAIN (EC 4.11.139)
(FRACMENT).
                                                                                                                                                           Guery Match

45.5%: Score 65; DB 8: Length 475;
Best Local Similarity 38.9%: Pred. No. 9.08e-30;
Matches 7; Conservative 6; Mismatches 5; Indels
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475 AA; 52775 MW;
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Search completed: Mon Jun 19 16:13:30 2000 Job time : 11 secs.

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Felease 3.1A John F. Collins. Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh. U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm WPsrch_pp

MasPar time 4.03 Seconds 117.455 Million cell updates/sec Mon Jun 19 16:15:53 2000: 3u'. on:

Tabular output not generated.

(1-20) from USO9142524A.pep 125 >US-09-142-524A-12 Description: Perfect Score:

1 SSGKNEGINIYNNNEAFKVE 20 Scoring table: se ineuce:

188963 segs, 23686106 residues PAM 150 Gap 15 seirched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-qeneseq35 I:geneseqp Database:

scale 0.316 Variance 59.693 Mean 18.891; Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.10e-06	1.100-06	.10e-0	.13e-0	1.10e-05	.18e-0	.61e-0	6.51e-03	.61e-0	6.51e-03	. 51	٠.	6.51e-03	φ,		6.61e-03	6.51e-03	6.61e-03	6.51e-03	1.45e-02	1.90e-02	3.21e-02	1e-0
Description	I-cell epitope peptide	Ω.	Japanese cypress polle	g	secyparis obtusa	14	• •	F-1	rol peptid	allergen	j I pollen	se Ced	j I polien a	nese cedar	ar pollen al	ry) I.	iese cedar	I polien	: Japanes	Sugi allergen protein	ide used for	ide used for	ide used for
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Score	125	125	125	(7	10.7	Ö	93	63	63	69	65	66	66	93	63	66	66	66	93	06	68	87	82
Result No.		5	3	4	S.	Q	7	æ	s.	0.1	:1	12	13	14	15	16	17	80	57	20	2.	22	23

9.096-02	1.97e - 01	1.976.01	4.036+00	5.216.00	5.210+00	3.616.01	4.570-01	5 3 20.02	۲~۰	9.230-01	4.23ee.C.	s	9.250-01	1.156+02	1.560-02	1.150-02	1.150.02	1.456-02	1.466+02	1.450+02	1 450.02
Peptide used for the t	Cry j I pollen allerge	Cry j I pollen allerde	I-cell epitope peptide	Cedar pollen allergen	Peptide used for the t	50K-celiulase from Mel	Jun v I.	I-cell epitobe peptide	KRES.	Human RNA editing enzy	P. falciparum Projs.	Plasmodium Proj3.	Plasmodium var-7.	Arabidopsis saccharopi	Ceilular Receptor 2 li	W09904265 Seq ID No: 6	Arabidopsis lysine ket	Sequence of ARV-2 env	ARV-2 env protein segn	Canine herpes virus pr	env gene decoded from
¥01+03	R4 10	F4 -	5.	885	¥01805	W16543	K45578	W4 2153	R36783	25022M	87-236	W22192	W22.15	9 ·8M	ች]	X J.	о 8 м	26]	¥. 51.3	Wilbed	R29706
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83	80	80	58	67	67	59	58	57	56	55			55			54	54	53	53	53	53
24	25	56	27	28	58	30	33	32	33	34	35	36	37	8 8	36	40	. 1	42	*	7 7	4.5

ALIGNMENTS

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Claim 1: Page 12: 7ipp: Japar ie.

Claim 1: Page 12: 7ipp: Japar ie.

Claim 1: Page 12: 7ipp: Japar ie.

The present sequence represent a Threel epitope peptide from Japanese cypress poblen antigen Chaol. The present invention describes peptides extraorespond to the Three epitope sites on Japanese cypress pollen antigens Chaol and Chaol. The reptides can be used as a respect for the diagnosis of alleray to Japanese cypress pollen, and as an antigen of the treatment and prevention of spring tree pollen disease in which the pollinosis involves reactivity to Japanese cypress pollen.
                                     16-JUN-1998 (first entry)
IT-cell epitope peptide 34 from Japanese cypress polien antigen Chaul.
Japanese cypress pollen: antigen: I-cell epitope: Chaol: Chaol:
Glagnosis: allergy: spring tree polien disease: politiosis.
Chamaeyparis obtusa.
                                                                                                                                                                 18-DEC-1997.
14-JUN-1995. JP-153527.
14-JUN-1996. JP-153527.
(MEIP ) MEDIX MILK PROD GO LTD.
MAIN 98-05242/05.
1-cell epitope peptide portio. Jf Japanese Cypress polle: antiwens Chaol and Chaol - used for diagnosis and treatment of spring tree
W42154 standard; peptide; 20 AA
                                                                                                                                                 W09747648-A1
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Gabs .. ; Query Match 100.0%: Score 125; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.10e-06; Matches 20; Conservative 0; Mismatches 0; Inde.s

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20 20 | SSGKNEGTNIYNNNEAFKVE 1 SSGKNEGTNIYNNNEAFKVE g ò

24-MAR-1998 (first entry)
Multi-epitope peptide used as mmunotherapeutic agent #5.
Multi-epitope peptide; immunot erapeutic agent; allergic disease:
T-cell epitope region; allergen; lymphocyte; immunoglobuiin E.
Synthetie.
W09732600-A1.
12-SEP-1997. W27373 standard; peptide; 3: AA RESULT 1D #2 AC #22 DT 24 DE MU KW HC KW TI-OS SI PD #C

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                                                                                                                                                                                                                                                                                   Claim 9; Page 42; 58pp. Japanese.

The present sequence represents a multi-epitope peptide which is used as a new immunctherapeutic agent. It comprises I cell epitope regions from 2 or more different allergens (preferably incked via arginine or lysine dimers), where the T cell epitope regions; have a positivity index allergen; have at least 70% reactivity index allergen; have at least 70% reactivity with lymphocytes from patients responding to the allergen; and are not restrive with immunoglobulin E (IEE) antibodies from patients responding to the allergen and are not restrive with immunoglobulin E be used to prevent and treat a wide variety of allergic diseases, e.g. by desensitisation, side effects, e.g. those mediated by 1gs, are reduced.
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(MEIP ) MELLI MILK PROD CC LTD
Dairiki K, Kiro K,
WPI: 99-65242/02 poptide portion of Japanese cypress police antigens
Chaol opicope poptide for diamosis and treatment of spring tree.
10-MAR-1997, C:0740.
10-MAR-1996, JF-284702.
10-MAR-1996, WEDIN HIK PROD CO LTD.
DAILKE K, TWARGA A, KINO K, KUME A, Sone T;
WPI: 97-470495/43.
PPPEALE Immuno:Therapeutic agent to treat allergic diseases -
contains multi-epitope poptide containing I cell epitope regions
from different allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W04344:
28.NOV-1996 (first entry)
Chamacyparis obtusa pollen allergen Cha o I (A)
Pollen allergen: Cha o I: 7-cell epitope: prevention: treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W42121 standard: protein: 354 AA.
W42121.
16-JUN-1998 (first entry)
Japanese cypress pollen antigen Chaol.
Sapanese cypress pollen: antigen; Treel epitope: Chaol: Chao2:
diagnosis: allerqy: spring tree pollen disease: pollinosis.
Chamaeyparis cutusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 160.0%; Score 125; DB 1; Longth 31; Rest Local Similarity 160.0%; Pred. No. 1.10e-06; Betches 20; Conservative 0; M.smatches 0; Indels
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WC4344 standard; Protein; 354 AA
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1D WG-
AC W0
07 28
0E CF
KW PC
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               요품절님중한다다고요인원인원인원인원인원
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                                                                                                                                                                                                                DNA encoding thamaecyparis obt..a pollen aliergen - I cell, epitope(s) of which are useful in development of preventative unit treating agent for C. obtusa pollen pollinosis Claim 2: Pages 10-11: Jopp: Japanese.

The present sequence is the C. obtusa pollen aliergen Cha C.; the Treeli epitopes of which can be used in the development of preventive and treating agent for C. obtusa pollen pollinosis.

C. obtusa pollen (2.4 kg) was devreased with diethyl ethyr and purified. RNA was extracted from C. obtusa pollen, and mkNA and conA derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding charactyparis obtasa polich allerge. T relices bytrope(s) of which are useful in development of preventative and treating acout for cutusa police policies.

Claim E. Pages 11-12 17pp. Japanose.

Claim E. Pages 11-12 17pp. Japanose of the milergen Claim E. Pagest sequence is the C. Obtasa police pricele epitopes of which can be used in the development of preventive and treating agent for C. Obtasa pollen pollinosis.

Preventive and treating agent for C. Obtasa pollen pollinosis.

Obtasa pollen (2.4 kg) was deereased with diethyl ether, and died at room temp. Overnight. Cha oliwas sept. from it and Duriffied, RNA was extracted from C. Obtusa pollen, and mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chamaecyparis obtusa polies allergen Cha c I cDNA (B).
Polies allerges: Cha o I: T-cell epitope: prevention: treatment
pollinosis.
Chamaecyparis obtusa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1: Length 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%: Sc re 125, DB 1: Le
Best Local Similarity 100.0%: Pr d. No. 1.10e-06;
Matches 20, Conservative C. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 5
W04345 standard; Protein: 375 AA.
W04345.
28-NOV-1996 (first entry)
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R45577 standard: Protein: 367 AA.
R45577:
13-JUD-1994 (first entry)
Jun s z.
                                                09-JUL-1996.
21-DEC-1994: 335089.
21-DEC-1994: JP-335089.
(MEIP ) MEIJI MILK PRCD CO LID
WPI: 96-368225/37.
N-PSUB: 138519.
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21-DEC-1994; JP-335O89;
(MEIP ) MEIJI MILK PROD CO
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Chamaecyparis obtusa.
J08176192-A.
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N-PSDB: T38519.
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US-09-142-524A-12.rag

1 SSGKYEGGNIYTKKEAFNVE 20

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Wolfied Cryptomeria Japonica (Cry j) I peptide(s) - useful for treating allergy to Japanese cedar pollen allergen or treating allergy to Japanese cedar pollen allergen or immucologically cross reactive allergens.

Sischosure: Floure 2: 60pp: English.

Novel peptides of cry j: have been modified as a part of a preformulation scheme to develop an optimised drug product for therapeutic treatment of humans suffering from allergy to Japanese cedar pollen allergen or an allergen witch is immunologically cross reactive with Japanese cedar pollen allergen which render them particularly possess certain characteristics which render them particularly cossess certain characteristics which render them particularly modified and unrodified, are given in RR84491/882525. This peptide fragment corresponds to amino acids 311-330 of the allergen mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                               allersy Disclosure: iq 16: 137pp: English. Disclosure: iq 16: 137pp: English. The sequence is that of Jun s I, a homologue of the Japanese cedar police allergen Cry j I. Antigenic peptides derived from it can be used for the treatment and diagnosis of allergies associated Sequence :57 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Cry 1 Japanese Cedar pollen allergen; modified; drug production;

Cry 1 I. japanese cedar pollen allergen; modified; drug production;

allergy; Crytpomeria japonica.
                                                                                                                                                                                                                                                                                                           Antioens derived from Japanese cedar pollen allergen Cry \beta : contain at least two I cell epitope(s), used to treat or diagnose
pollen allergen: allergy: 'reatment: diagnosis: sensitivity: detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.4%; Score 108; DB 1; Length 357;
85.0%; Pred. No. 1.18e-04;
/ative 1; Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 93; DB 1; Length 20;
Pred. No. 6.61e-03;
                                                                                                                                                                                                 10-JUL-1992: WO-U05661.
01-SEP-1992: US-93890.
UMMC-) IMMULDGIC PHARM CORP.
Rond JF. Garman RD. Griffith IJ, Kuo M. Pollock J;
WPI; 94-035:66/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Powers SP
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06-DEC-1994: US-350225.
(IMMU-) IMMULGGT PHARM CORP.
Chen X, Evans S, Franzen HM, Kuc M.
                                                                    1. .4.
/sote- "signal peptide"
22. .367
                                                                                                                              "mature peptide"
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R82522 standard; Protein: 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 SSGKTEETNIYNSNEAFKVE 351
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Best Local Similarity 70.0%;
Matches 14; Coreavaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17: Conservative
                    T cell epitope: sensi
Juniperus sabinoides:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )aponica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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06-APR-1995: 004249.
                                                                                                                                                               2C-JAN-1994.
15-JAN-1993: U00139
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WPI: 95-366391/47
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WO9527786-A:
                                                                                                                                               W09401560-A
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                                                                         peptide
                                                                                                           peptide
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Reference Example 6: Page 87: 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 1/2. Fig 13: 137pp; English.
The sequence is that of an isolated peptide of the Japanese cedar pollen allergen Cry j I (amino acids 311-330). The peptide. CJI-32, can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiqens derived from Japanese cedar pollen allergen {\tt Cry} ) I contain at least two I cell epitope(s), used to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Control peptide pi6.
Fast epitope: HFE7A: monoclonal autitody: numanised antibody: human: apoptosis; HFE7A: autoremente disease, Hastifictor's disease; systemic lupus erythematosis; oratt verses Nost disease; erythematosis; oratt verses Nost disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sjogren syndrome; permicrous anaemia, Addison's disease, scleroderma; Goodgasture syndrome; Cichr's disease; sterility: theumatoid arthritis; autoimanne haemolytic anaemia; myasthania gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; alopy; arteriosclerosis; myocarditis; cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
                                                                                                                                                              13-JUL-1994 (first entry)
Cry j I pollen allergen peptide CJI-32.
Apanese cedar: detection: alleray: treatment: diamosis.
T cell epitope; sensitivity.
Cryptomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93, DB 1, Length 20;
Pred, No. 6.61e-03;
3: Mismatches 3, Indels
                                                                                                                                                                                                                                                                                                                20-JAN-1994
15-JAN-1993: UOC139.
10-UGL-1992: WO-U05661.
01-SEP-1992: US-938990.
(IMMU-) IMMULOGIC PHARM CORP.
BOND TO CARRON ED. GRIEfith IJ. Kuc M. Pollock J:
WPI: 94-035066/04
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08-0CT-1998.
08-0CT-1998.
00-0CT-1527: CP-276064.
08-0CT-1527: CP-276064.
01-APR-1997: JP-1692953.
25-JUN-1997: JP-16908.
6ANY ) SANXXO CO LTD.
Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                     AA
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W83058 standard; Peptide: 20 AA
W83058;
                                                                                    RESULT 8

ID 845573 standard; Protein; 20 AA AC R45573; Delien allergen peptide ET 13-JUL-1994 (first entry)

ET 07y j polien allergen peptide EW Japanese cedar detection: aller EW T cell epitope; sensitivity.

SN WC94C156C-A.

PD 20-JAN-1993; W0-10561

PR 10-JUL-1992; W0-10561

PT Antiqens derived from Japanese PT Chain at least two T cell epit PT Antiqens derived from Japanese PT Chain it is contain at least two T cell epit PT Antiqens derived from Japanese CC Can be used for the treatment acc Can be used for the treatment acc Coult Japanese CC With Japanese cedar pollen. It cc but reduced side effects compares SQ Sequence 20 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07
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Match
Local Similarity 70.0%;
es 14: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1999 (first entry)
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Gaps

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3; Indels

Mismatches

US-09-142-524A-12.rag

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allergy claim 76, Fig 18: 137pp; English.

The sequence is that of an isolated peptide of the Japanese cecur; pollen allergen Cry 1. The peptide, CJI-44.1, can be used for the treatment and diagnosis of allerques associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens.
               Antigens derived from Japanese codar pollen allergen Cry ) : contain at least two T cell epitope(s), used to treat or diagnose
   WPI; 94-035056/04
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugi-pollinosis
Claim 8: Pages 19-20: Zipp: Japanese.
Claim 8: Pages 19-20: Zipp: Japanese.
W80339-58 represent epitopes for T ceils, derived from the sugi allergen
proteins Cryil (W80394-44, W80350-53 and W80356-58) and Cryj2 (W80345-49
and W80354-55). The peptides are useful for the treatment of
sugi-pollinosis, an allergic reaction of the body to pollen.
Sequence 21 AA:
                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                        See K83389 is a negative control having no homology with human Pas. P1-P16 were used in an ELISA, which demonstrated that novel murine anti-inman Fas monoclonal antibody HFDA specifically binds an amino acid sequence contained in P11. The epitope (see W8333) was subsequently identified. The invention provides humanised HFDA antibodies (see W8331-37) produced by CDR grafting. These antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting fas induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                               Gaps
Synthetic peptides P1-P15 (see W83043-57) are partial sequences of amino acids 1:157 of the extracellular domain of human Fas, with between 9 and 11 amino acid residues overlapping one another. P16
                                                                                                                                                                                                                                                                                                                                                                                                                    Sugi allergen protein Crýj2 derived epitope for T cells.
I cell epitope: sugi allergen proteins Crýj1; Crýj2: treatment:
sugi-pollinosis: allergic reaction; pollen.
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O
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... NO. 6.61e-03;
Mismatches
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Pred. No. 6.61e 0
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                                                                                                                                                                                                                                 Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
(SANY) SANKYO CO LTD.
WPI; 98-577037/49.
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R45599 standard; Protein; 26 AA.
R45599;
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15-JAN-1993: U00139.
10-JUL-1992: WC-U05661.
01-SEP-1992: US-93899.
(IMMC-) IMMU: OGL PHARM CORP.
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Hest Local Similarity 70.0%;
Matches 14; Conservative
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Fest Local Similarity 70.0%:
Matches 14: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                          W80355 standard: peptide:
W80355;
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22-DEC-1997; 353448.
24-DEC-1996; JP-343441.
                                                                                                                                                                                                        20 AA;
                                                                                                                                                                                        such diseases
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WPI: 95-366 J147.

Modified Cryptomeria japonica (Cry !) I peptide(s) - useful for treating allergy to japanese cedar pollen allergen or immunologically cross reactive Pleaders.

So Claim I: Figure 3: 66pp. Englis.

So Claim I: Figure 3: 66pp. Englis.

Novel peptides of cry i lavet ben modified as a part of a preformulation scheme to develor an optimised drug product for therapeutic treatment of humans suffering from allergy to Japanese cedar pollen allergen or an allergen which is immunologically cross reactive with Japanese cedar pollen allergen or an allergen which is immunologically cross centure with Japanese cedar pollen allergen from allergen by the allergen of modified periods situation. Such modified and uncodified, are given in RES491 RRESSS Tils peptide is one of three modified peptides (See R92178-60).
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                                                                     Saps
                                                                                                                                                                                                                                                                                                                                                                           Cry ) I Japanese Cedar pollen allergen modified peptide (CJI-44 E).
Cry ) I: japanese cedar pollen allergen: modified: drug production:
allergy: Crytpomeria japonica.
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R45598;
13-JUL-1994 (first entry)
Cry j I pollen allergen peptide CJI-44.
Japanese cedar: detection: allergy; treatment: diagnosis;
T cell epitope: sensitivity.
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         Length 26:
/ Match 74.4%: Score 93: DB 1: Le
Local Similarity 70.0%: Pred. No. 6.61e-03:
Nes 14; Conservative 3: Mismatches 3:
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Mismatches 3
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                                                                                                                                                                                                                                                                                               R92180 studard; Protein: 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-APR-1994; US-226248.
06-DEC-1994; US-350225.
(IMMU-) IMMCLOGIC PHARM CORP.
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15-JAN-1993; U00139.
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Best Local Similarity
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         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAK-1996 (first entry)
Japanese cedar pollen allerden Cryj I.
Japanese cedar pollen allergen; Cryj I. Trcell epitope; peptidos:
prevention: treatment: cryptomeria pollinosis.
Cryptomeria japonica.
                                                                                                                                                                                            Claim 75: Fig 18: 137pp: English.

The sequence is that of an isolated peptide of the Japanese cedar pollen alloraen Cry 7 1. The peptide, CJ144, can be used for the treatment and diagnosts of allorates associated with Japanese cedar pollen. It has enhanced therapeutic properties but reduced side effects compared to naturally occurring allergens.
                                                                                                                    Antigens derived from Japanese redar pollen allergen Cry j I - contain at least two T cell epitope(s), used to treat or diagnose allerny fs. Fig. 137gp. English.
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74.4%: Score 93: DB i: Length 30:
West Local Similarity 70:0%: Pred. No. 6.61e-03:
Matches 14: Conservative 3: Mismatches 3: Indels
10-JUL-1992: WO-U05661.
01-SEP-1992: US-93899C.
NOMU-) IMMUCGIC PHARK CORP.
FOMU -) CARMAN BD, GRIffith IJ, Kuo M, Pollock J:
WPI: 94-035065/04
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R75988 standard: protein: 353 AA
R75388;
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20-007-1993. 262026.
20-007-1993. 29-262626.
(MEIP.) MELUI MILK PROC CO LTD.
WPI: 95-203834/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 SSGKYEGGNIYTKKEAFNVE 30
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Hino K, Salto S. Tanigud. Annabad.

Hino K, Salto S. Tanigud. Annabad.

WPI: 96-140976/15

New Peptide(s) derived from cedar police allergens - activate

New Peptide(s) derived from cedar police allergenspecific [gE actitables.]

Tallergen-specific T-cells, but not allergen-specific [gE actitables.]

Softhetic peptides based on portions of cedar pollen allergens R.

Synthetic peptides based on portions of cedar pollen allergens R.

Synthetic peptides based on portions of their ability to activate cedar allergen specific T-cells but not allergen-specific [at antibodies. 6 Peptides (R8158) were includies. 6 Peptides (R8158) were includies. These peptides (R8158) were includies. These peptides (R8158) were includied as T-cell collinosis. avoiding side-effects such as anaphylaxis.

Sequence 353 AA:
cedar pollen allergen B.
Cedar pollen allergen B.
Cedar: pollen; allergen; immuncajobulin E; igE; T-ceil epitcen:
antibody; pollinosis; therapy: immuncaherapy.
Cryptomeria japonica.
13-Map-jec.
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Pest Local Similarity 70.0%: Pred. No. 6.6ie-03:
Matches 14; Conservative i: Nismutches 3: Indole
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                                                                                                                                                                                                                                                                                                      13-MAR-1996.
08-SEP-1995; 306295.
10-SEP-1995; JP-242137.
14-JUL-1995; JP-200221.
14-JUL-1995; JP-200204.
(HARB.) HAYASHIBARA SEIBUTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 SSGKYEGGNIYIKKEAFNVE 330
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Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

MPsrch_pp - protein - protein database search, using Smith-Waterman algorithm

Tue Jun 20 13:37:01 2000; MasPar time 2.38 Seconds 121.366 M:1lion cell updates/sec Topular output not generated. R.131 OC:

>US-09-142-524A-12 (1-20) from USC9142524A.pep 125 1 SSGKNEGTNIYNNNEAFKVE 20 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table: Searched:

145341 seqs, 14437480 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:5_COMF 4:PCT_COMB 5:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 17.862; Variance 55.722; scale 0.321

Statistics:

SUMMARIES

Pred. No.	1.630-01	3.39e+01	4.3.e+01	4.31e+01	4.31e+01	4.31e+01	6.95e+C1	6.95e+01	1.11e+02	1.11e+02	1.4;e+02	1.4le+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02
Description	atent No. 5204097	atent No. 5194600	Sequence 1, Applicatio	.5	12,	14,	58,	75,	10,	9	2:,	21.	21,	21.	ω,	۳,	٦,	7	Sequence 2, Applicatio	Sequence 2, Applicatio	1 C	Sequence 10, Applicati	
3:	5204097-1	5194630-4	.918-80-SD	ns-08-268-	US-08-487-	US-08-487-	ns-08-680-	PCT-US93-1	US-08-483-	CS-08-40C-	US-08-292-	3S-08-467-	US-C8-467-	US-08-467-	US-08-937-	JS-08-305-	US-08-021-	JS-08-919-	PCI-US94-0	JS-08-445-	US-08-462-	PCT-US95-0	US-08-441-
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Score	e) (A)	9 9	50	55			53	53	.15	51	() ()	50	50	50	50	50	50	() *3	4. Q/	(7) ਵਜ਼	4.9	4	σ ₁
Result No.	-	7	m	4	5	9	7	∞	6	10	11	12	13	14	15	16	17	18	19	20	2:	22	23

15-08-942- Sequence 6. Applicatio 1.778-02 15-08-849- Sequence 6. Applicatio 1.778-02 15-08-849- Sequence 6. Applicatio 1.778-02 1204-97-4 atent No. 5204097 2.280-02 1204-97-4 atent No. 5204097 2.280-02 121-1255-0 Sequence 24. Applicatio 2.140-02 15-18-18-19- Sequence 25. Applicatio 2.140-02 15-18-19-18-18-18-18-18-18-18-18-18-18-18-18-18-	AE GNWENIS PR 70 AA. HARARI, ILANA, KEUSCH, GERALD I. IGA TOXIN B CHAIN POLYPEPTIDES AND TA: US/01/x64.506 1989 77.24 1987	2%: Scure 59. Ub 5: Length 70. 9%: Pred. No. 1.63e-01: ve 5: Mismatches 6: Indels 0: Gaps 0: 23 19 PRT: 1365 AA. HULIP GENES WHICH PARTICIPATE IN B-GLUCAN
24 49 39.2 25 26 26 27 2	RESULT 1 STANDARD: B STANDARD:	Ouery Match Best Local Similarity 38.9%; practices 7; Conservative 5 Conservative 6 TGKVEEYTKYNDDDTFTV 23 CKNEGINIYNNEAFKV 19 CKNEGINIYNNEAFKV 19 CKNESUL 2 SGKNEGINIYNNEAFKV 19 CKNESUL 2 SGKNEGINIYNNEAFKV 19 CKNEST XX

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Indels

3: Mismatches

6; Conservative

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Matches
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                                                                                                                                                Score 56: 78 5: Length 1365: Pred. No. 3.39r-01: 3: Mismatches 5: indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baddman, Clqa
APPLICANT: Goli Surya K.
ITLE OF INVENTON: NUVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE AUDRESS:
ADDRESSEE: Incyte Pharmaceuticals, inc.
STREET: 3174 Porter Drive
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTE: SAM Compartble
OPERATING SYSTEM
OPERATING SYSTEM
OFFRICATION WASHER OF WINDOWS WITSHIG 200
COMPENT AFFLICATION WASHER US/OB/916,241
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                     190 AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, lucy J. REGISTATION NUMBER: 36.749
REFERENCE/DOCKET NUMBER: PF-0239 US FELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 1:
                                                                                                  LENGTH: 1365
SEQUENCE 1365 AA: 156637 MW: 9878636 CN:
ASSEMBLY AND USE THEREOF
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,316
FILING DAIE: 05-MAR-1990
SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2: 1645823
190 AA: 22826 MW: 191242 CN:
                                                                                                                                                                                                                                                                                                                     Sequence 1, Application 35/08816241 Patent No. 5804185
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08816241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 190 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                  44.8%;
Local Similarity 46.7%;
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE: LIBRARY: PROSTUT09
                                                                                                                                                                                                                       840 CCTHIYNNCIDYITE 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                     6 EGINIYNNNEAFKVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UN
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ID US-08-816-241-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
SEQUENCE 19
                                                                                                                                                       psery Match
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 888888888
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Sequence 12, Application US/3856459A
Patent No. 5849366

APPLICANT: Sim, Kim L.
APPLICANT: Chinchs. Chetan
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Willer, Thomas
TITLE OF INVENTION: BINDING FCMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIFARUM ENTHROLYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Pred. No. 4.31e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PU-DISYMETORS
SOFTWARE: PATENTIA PELEGATION FELGES FILE, Version #1.25
CURRENT APPLICATION DATA
CURRENT APPLICATION DATA
FILE
FILING DATE: 07-DEC-1995
CLASSIFICATION 445
ALICHENTYAGEN INFORMATION
NAME: 15574-5010 NOTE: 0.000
FELEPHONE: (619) 235-9550
TELEPHONE: (619) 235-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Knobbe Martels (1850) & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California COUNTRY: US 2.1P: 92660
                                                                                                                                                                        2715 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VISM: Plasmodium talciparum
2710 AA; 308038 MW; 37145344 CN;
                                                                                                                                                                           PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Bloppy disk
MEDIUM TYPE: BM PC compatible
OPERATING SYSTEM: PC-DGS/MS-109S
                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/38568459A
                                                                                                                                                                           STANDARCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPULOGY: linea:
MCLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%;
Similarity 38.5%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2205 EGKTIFDDDKTFK 2217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
161 VYNDNEPFK 169
                                                                                                                                    RESULT 4
ID US-08-568-459A-12
                                       10 IYNNNEAFK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                     XXXXXX
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RESULT

Score 55; DB 1; Length 190: Pred. No. 4.31e+01;

44.08;

Luery Match Pest Local Similarity

SYRXBXESSS

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APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Willer, Louis H.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHRUCYTE BINDING PROIEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/08680726A
Patent No. 5804197
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55: 05 2: Length 3060:
Pref. No. 4: (le-01:
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFTTER: IBM PC COMPATIBLE
OPEL MING SYSIEM: PC-D3C/MS-DOS
SOFTWARE: Patentin Relea: #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/C8/487,826B
FILING DATE: 10-SEP:1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3018
                                                                                                                                                                                                                                                                                                           STREET: Knobbe Martens Discn & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach Center Drive 16th Floor CITY: California COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE 3060 AA: 347049 MW; 46990904 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Sequence 14, Application US/08487826B
Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 58, Application US/08680726A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 3060 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.0%;
Best Local Similarity 38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2203 EGKTIFDDDKIFK 2215
                    Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Chitnis.
APPLICANT: Miller.
APPLICANT: Miller.
APPLICANT: Petersor
APPLICANT: SU, Xin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 EGINIYNNEAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-680-726A-58
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     Sequence 12, Application US/084878258
Patent No. 5993827
DENERAL INFORMATION:
APPLICANT: Sim L.
APPLICANT: Chitais, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 4.31e-01;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDIUM TYPE: Floppy disk
COMPUTER: 18W PC Compatible
COMPUTER: 18W PC Compatible
DEFAILNG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                        ...rARUM.
...cokES:
...cokESS:
STREET: 620 Newport Center Drive 15th Floor
CITY: Newport Beach
STATE: California
CCUTTY: US
CCUTTY: US
     2710 AA
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TELECOMMUICATION INFORMATION:
TELEPHONE: (619) 235-855
INFORTERAX: (619) 255-6176
INFORMATION FOR SEQ 10 NO: 12:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VISM: Plasmodium falciparum
2710 AA; 308038 MW; 37145344 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
     PRT:
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                                                                                                                                          Sequence 12, Application US/08487825B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Istaelsen. Ned
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92460
CCMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2205 EGKTIFDDDKTFK 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 EGTNIYNNNEAFK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SCURCE:
ORGANISM: Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
ID US-08-487-826E-14
     US-08-487-825B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 261 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sindle
                                                                                                                                                             Single
                                                                                                                                                                                                                                                                   Match 42.4%;
Local Similarity 40.0%;
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                              453 RDGGTNVINDTEVFR 467
                                                                                                                                      TYPE: amino acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                4 KNEGINIYNNEAFK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-483-857-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xxxxxx
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                              COMPUTER SELECTIONS

COMPUTER FLORMS

MEDIUM TYPE: Floppy disk
OFGNEUTER: EN PC COMPATIBLE
OFGNEUTER: EN PC COMPATIBLE
OFGNEUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Helease #1.0, Version #1.0
ORRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ANGENIE 12-JUL-1996
CLASSIFICATION: 424
ANJORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25.020
REGISTRATION NUMBER: 25.020
REGISTRATION NUMBER: 25.020
REGISTRATION NUMBER: 26.023
TELEPAN: (303) 863-9703
TELEPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upry Match
Hest Local Similarity 35.3%; Pred. No. 6.95e-01;
Matches 6; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.6, Version #1.308 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT: 1018 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 75, Application PCZIUS9411703
SENERAL INFORMATION:
APPLICANT: Chirot Mimotopes Pty Ltd.
TITLE DF INVENTION: 1-0511 Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/984.952
FILING DATE: 02-DEC-1992
ATTORNEY/ABONT INFCRMATION:
NAME: Green, Grant D.
NAME: Green, Grant D.
PERERRICE/DOCKET NUMBER: 31,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHLECULE IYPE: protein
JENCE 522 AA: 59930 MW: 1516583 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 75, Application PC/TUS9311703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 KNYHSHVFVPNDSFKIE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KNEGINIYNNEAFKVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4560 Hort
CITY: Emeryville
STAIE: CA
      Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4FSULT 8
1F PCT-US93-11763-75
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         STAIE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE
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                                                                                                                                                                                           Score 5s. DB 4: Length 1018
Pred. No. 6.95e+01:
5. Misratches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10. Application US/06483857
Patent No. 6026125
GENERAL INFORMATION:
GENERAL OCCUPATION:
APPLICANT: Chair, Wood Locing
APPLICANT: Chair, Word Louis, Releas
TITLE OF INVENTION: BASA! BIDY BG:
TITLE OF INVENTION: CAME "BAGTER
NUMBER OF SEQUENCES: 12
COHRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael 1.
REDISTRATION NUMBER: 24,93
REFERENCE/COCKET NUMBER: 3.98-6.04
FELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ 10 NO: 30: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-308/18/48:257
07-308-1995
08-408-1995
18-435
18-435
TOPOLOGY: Linear MoLECULE 1YPE: peptide SEGUENCE 1018 AR: 5.51:54 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .
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NCE 261 AA: 2765C MW: 357696 CN:
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STRANDEDNESS:
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                                                                                                                                                                                                                            APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Myat, Anna M.
APPLICANT: Myat, Anna M.
APPLICANT: Myat, Anna M.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Mann, Robert S.
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
IILE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
IILE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SUCENNESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
GITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.11e+02;
4: Mismatches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/400,159 FILING DATE: 07-MAR-1995
                                                                           1218 AA
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JENCE 1218 AA; 133810 MW; 7064054 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7326-029
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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ISh-BOTOWICZ, David
APPLICANT: Lewis, Julian H.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
21P: 10386-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             PRT;
                                                                                                                                                                            Sequence 6, Application US/08400159 Patent No. 5869282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ALTORNEY/AGENT INFORMATION:
NAME: MISTORY, S. GOSIGE
REGISTATION NUMBER: 18:72
REFERENCE/DOCKET NUMBER: 7326
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9990
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNEE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                    Sequence 6, Application US/08499159
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TYPE: amino acid
                                                                             STANDARD:
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Best Local Similarity 42.9%;
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109 DGTSAYIRDGSFGVD 123
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                          6 EGTNIYNNNEAFKVE 20
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ID US-08-292-968-21
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                                                                             US-08-400-159-6
                                                                                                                                                                                                                                                                                                                                                                                               CITY: N
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                                                                                                      XXXXXX
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                                                                  RESULT
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                                                                                          APPLICANT: STEIN, Penelope E
APPLICANT: STEIN, Penelope E
APPLICANT: COCKLE, Stephen A
APPLICANT: COCKLE, Stephen A
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBUFFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENI APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AA.
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 50: DB 2; L/44.4%; Pred. No. 1.41e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 193: (*110,947
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US '251,127
FILING DATE: 3: *MAY-196
ATTORNEY/AGENT INFORMATION
NAME: SIEWART MIChael
REGISTRATION NUMBER: 2...;
REFERENCE/DOCKET NUMBER: 2...;
REFERENCE/DOCKET WUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELECHOME: (416) 595-1153
INFORMATION FOR $EU 150
SECUENCE CHARACTERISTICS:
LENGTH : 69 amino dot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                     Sequence 21, Application US/C<sup>2</sup>··2968
Patent No. 5856122
GENERAL INFORMATION:
Seguence 21, Application US/08292968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOGY: linear
69 AA; 7691 MW; 25533 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08467974
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Matches 8; Conservative
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MODIFIT THON OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SCFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA
                                                                                                                                                                                                                                      ersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/08457976
Sequence 21, Application US/OB 153
Patent No. 5977304
GENERAL INFORMATION
APPLICANT: REAN, Randy J.
APPLICANT: COCKLE, Stephon A.
APPLICANT: COCKLE, Stephon A.
APPLICANT: COMEN, RAYMORG E.
APPLICANT: LOUSMORE, Sheena
APPLICANT: KLEIN, MICHOLE, E.
APPLICANT: HAZES, BATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 AA: 7691 MK: 25533 CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24...
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                      S: Sim & McBurne
Suite 701, 330 (
                                                                                                                                                                   TITLE OF INVENTION: MOCH.
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSES
ADDRESSES: SIM & MCBUTTO
STREET: SULLE-701, 330:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEWART, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 595-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino anida
                                                                                                                                                                                                                                              CITY: Toronto
STAIE: Ontario
COUNTR: Canada
2IP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Fioppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 artico actios
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Best Local Similarity 44.4%:
Matches 8: Conservative
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US-08-467-976-21
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                                        APPLICANT STEIN, Randy J.
APPLICANT STEIN, Penelope E.
APPLICANT COMEN, Raymond P.
APPLICANT COMEN, Raymond P.
APPLICANT LOSMONE, Shena
APPLICANT HAZES, Harl
APPLICANT HAZES, Harl
TILLE OF INVENTION: WODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SECUENCES, 46
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 2; Length 69;
Pred. No. 1.41e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
FILING DATE: CLASSIFICATION: 435
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PROGRAPHICATION 1974

APPLICATION NUMBER: US 08/467,536

FILING DATE: G6-UN-1994

PRICK PAPLICATION NUMBER: US 08/292,968

FILING DATE: 22-AUG-1994

PRICK PAPLICATION NUMBER: US 08/251,121

FILING DATE: 31-MAY-1994

PRICK PAPLICATION DATE: US 08/110,947

FILING DATE: 131-MAY-1994

PRICK PAPLICATION NUMBER: US 08/110,947

FILING DATE: 24-AUG-1993

ATORNEYAGEN: INFORMATION: NAME: 24,973

REGISTRATION NUMBER: 24,973

REFERENCE/OCKET NUMBER: 1038-454 MIS:VG
TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155

TELEPHONE: (416) 595-1165

TELEPHONE: (416) 595-1163

INPOMMATION FOR SEC 1D NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 AA.
                                                                                                                                                                                                                   Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.R.T.
                                                                                                                                                                                                                                                                                                                                        CCMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 21, Application US/08467974
Pation No. 5965383
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08467536
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69 AA: 7691 MW: 25533 CN:
                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                                                                                                  STREET: Suite 701, 330
CITY: TOFONICO
STATE: Octario
COUNTRY: Canada
ZIP: MSG 187
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single
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Best Local Similarity 44.4%;
Matches 8; Conservative
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STRANDEDNESS: sin
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Pred. No. 1.41e+02;
5: Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AA
APPLICATION NUMBER: US/08/467,536
FILING DAIE: 06-UN-1995
CLASS.FICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 09/292,368
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                       APPLICATION NUMBER: US 06/251.121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/110.947
FILING DATE: 24-A90-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI:
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OUTCHARE PATENTINE SYSTEM: PC'DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: C6-70N-1995
CLASSIFICATION: 435
PALOR DATE: C6-70N-1995
CLASSIFICATION: 435
PALOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/291,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 31-MAY-1994
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT: MATCHARI IN-
REGISTRATION NUMBER: 24,973
RECISTRATION NUMBER: 24,973
RECISTRATION NUMBER: 24,973
RECISTRATION NUMBER: 24,973
RECISTRATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEC 10 NO: 21:
SECOURDE CHARACTERISICS:
LENGTH: 69 aming acide
TYPE: aming acide
STRANDENESS: SINGLE
               APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE. Stephen A.
APPLICANT: COMEN. Raymond P.
APPLICANT: COMEN. Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: MAZES, Bart
ITILE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.0%; Score 50; DB 3; Length 69; Best Local Similarity 44.4%; Pred. No. 1.41e+62; Matches 8; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Sille 701, 330 University Avenue
CITY: Toronto
CITY: Toronto
CONTY: Canada
ZIP: MSC 187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 AA
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
ICE 69 AA: 7691 MW: 25533 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08937972
Patent No. 5932443
GENERAL INFORMATION:
APPLICANT: LAI, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08937972
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GENERAL INFORMATION:
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80 F.
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MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DCS SOFTWARE: FASSEG for Windows Version 2.0 CURRENT APPLICATION NUMBER: US/08/937,972 FILING DATE: Herewith CLASSIFICATION: 4.24 PRIOR APPLICATION THEREWITH APPLICATION TOWNER: FILING DATE: FILING DATE: APPLICATION NUMBER: SA.749 REFRENCE/AGRYI NUMBER: 36.749 REFRENCE/DOCKET NUMBER: 36.740 US TELLECOMMUNICATION: TELLECOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
40.0%; Scote 5gr 19 2. ..
Best Local Similarity 30 8%; Pred Mo. 1 41er.2
Matches 4: Conservative 6: Riscotches 3
                                                                                                                                                                             E: Incyte Pharm seuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: BLADNOTO4
CLONE: 1318190
GE 321 AA: 35892 MW; 544482 (7);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: Tue Jun 20 13:37:07 2000
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
IIILE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHRACTERISTICS: LENGTH: 321 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                     STREET: 3174 POR CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 INVESPHENENCE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TNIYNNNEAFKVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Job time : 6 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:27:44 2000; MasPar time 15:63 Seconds 128:946 Million cell updates/sec Run on:

Tabular output not generated.

>US-C9-142-524A-12 (1-20) trom USC9142524A.pep 125 I SSGKNEGINIYNNNEAFKVE 20 Intle: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

721208 segs, 100765575 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-pending liect 2:06 3:056 4:07 5:080 6:081 7:082 8:083 9:084A l0:084B 11:085 12:086 13:087 14:068 15:089 16:090 17:091 18:092 19:093 20:094 21:095 22:NEWP 23:NEWU66 24:NEWU8 25:NEWU9 Calabase:

Mean 20.905: Variance 54.342; scale 0.385 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SELECTIVES

	Pred. No.	1.39e-07	3.54e-05	4.09e-03	4.09e-03	4.09e-03	4.09e-03	4.09e-03	4.09e-03	4.05e-03	4.09e-03	4.09e-03	4.09e-03	4.09e-03	4.09e-03						
		Applicatio	Applicatio	_														2, Applicat			
	ion	Ŋ	- 1	95		95					57,						91,	132			131
	Description	Sequence	Sequence	Seguence	Sequence	Seguence	Sednence	Seguence	Seguence	Sednence	Sequence	Sequence	Sednence	Sedrence	Sequence	Sedneuce	Sequence	Sequence	Sequence	Sequence	Sequence
SOMMARIES	QΙ	US-09-142-	us-60-109-	CS-08-226-	US-08-467-	US-C8-467-	US-08-467-	US-C8-350-	US-08-468-	US-08-467-	US-07-938-	US-08-468-	US-08-350-	US-08-226-	US-08-226-	US-08-467-	US-08-468-	US-08-320-	CS-08-467-	CS-08-467-	CS-08-468-
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	& Ouery Match	0	47	4	7	86.4	4.	86.4	4	4	4	4	7	74.4	4	7	4	4	7	4	₹.
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	Score	125	108	108	108	108	108	108	108	93	66	66	66	93	65	66	85	93	რ	<u>«</u>	£,
	Result No.		~1	က	4	S	9	7	ക	s	10	11	12	13	14	15	16	17	18	19	3 C

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COUNTRY:
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                                                                                                Sequence 1, Application US/60109165
GENERAL INFORMATION:
APPLICANT GOLDBLUM, PANDALL M.
APPLICANT BROOKS EDWARD G.
APPLICANT: MIDDOO HORDIT! TERUMI
APPLICANT: MUDONO-HORDIT! TERUMI
APPLICANT: WURSKY, ALEX
TITLE OF INVENTION: FRAILY OF PLANT PATHOGENESIS RELATED PROTEINS
FILE REPERENCE: USG61230P21
CURRENT APPLICATION NUMBER: US/60/109,165
CURRENT APPLICATION NUMBER: US/60/109,165
SOFTWARE: PATENTIN USC: 2
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO. 3
SEQ ID NO. 3
SEQ ID NO. 3
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TITLE OF INVENTION: Japanese Cedar Pollen
                                                                                                                                                                                                                                                                                                                                                                 ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ImmuLogic Pharmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                      query Match 86.4%; Score 108: DB 3: Length 346: Rest Local Similarity 85.0%; Pred. No. 3.54e-05; Antches 17: Conservative 1: Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 95, Application US/D8225248A
GENERAL INFORMATION:
APPLICANT: STIFFIELD: ITALIO III
APPLICANT: POLICEK, JOSHON
APPLICANT: Bond, Johan E.
APPLICANT: Bond, Johan E.
APPLICANT: Koo, Mei-Chang:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Estey, Mark A.:
APPLICANT: POWETS, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.1
                                                                                                                                                                                                                                                                                                     d Cuniperus ashel
346 AA; 37639 MW; 616983 CN;
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 95. Application US/08226248A
                                                                                 Sequence 1, Application US/60109165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                       311 SSGKTEETNIYNSNEAFKVE 33C
            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              1 SSCKNEGINIYNNNEAFRVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-226-248A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Wald
RESCLT 2
ID US-60-109-165-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCUNTRY:
                                                                                                                                                                                                                                                                               LENGIH: 346
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                                                                                                                                                                                                                                                                                         TYPE: PRI
ORGANISM:
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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83.79
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APPLICAN: Sarman Return D.
APPLICAN: Young, Studen B.
APPLICAN: Young, Studen B.
APPLICAN: Exiger Andrew,
APPLICAN: Exiger Andrew,
APPLICAN: Alexand P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Allergenic Proteins And Peptides From NUMBER OF SEQUENCES: 261
ACCRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: ImmuLogic Pharmaceutical Corporation, Inc
610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.4%: Score 108: 0H 7: Legath 367
Best Local Similarity 85.0%: Pred. No. 3.54e-05:
Matches 17: Conservative 1: Mismatches 2: Indels
APPLICATION NUMBER: US/06/226.248A
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA: 424
APPLICATION NUMBER: 07/948.990
FILING DATE: September: 1, 1992
APPLICATION NUMBER: 07/944/00139
FILING DATE: Samuary 15, 1993
ATTORNEY/ABENT INFORMATION: NAME: DATABRE NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 059.5 JS (IMI-0483F)
TELECHONE: (617) 466-6040
INFORMATION FOR SEQ. JD NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 aming acids
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APPLICATION NUMBER: US/08/457,023
FILING DATE: Jane 6, 1995
FILING DATE: JAN 424
PRIOR APPLICATION A24
APPLICATION NUMBER: 08/350,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCPOLDGY: linear
MOLECULE TYPE: protein
JENCE 367 AA: 39946 MW; 695 78 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIJM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSIEM: PC-COS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 95, Application US/08467023 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 95, Application US/U8467023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffeth, Irwin J.:
Pollock, Joanne
Bond, Julian F.
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 367 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 SSGKTEETNIYNSNEAFKVE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SSGKNEGINIYNNNEAFKVE 20
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US-08-467-023-95
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TELEFAX: (617) 227-5541
INFORMATION FOR SEG ID NC:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
TOPOLOGY: linear
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LENGTH: 367 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD
                                                                                                                                                                                                                                                                                                                             332 SSGKTEETNIYNSNEAFKVE 35:
                                                                                                                                                                                                                                                                                                                                                      1 SSGKNEGTNIYNNNEAFKVE 20
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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SEQUENCE 95, APPLICATION

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GENERAL INFORMATION:
APPLICANT: Pollock, Joanne:
APPLICANT: Pollock, Joanne:
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Johlan E.)
APPLICANT: Wow, Mel-Chang:
APPLICANT: Mollon E.)
APPLICANT: Mel-Chang:
APPLICANT: Mel-Chang:
APPLICANT: Mel-Chang:
APPLICANT: Mel-Chang:
APPLICANT: Powers. Steven
TITLE OF INVENTION: Japanese Cedar Pollen.
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSES: Immulogic Platimaceutical Corporation, Inc.
STATE: MA
COUNTRY: Waltham
COUNTRY: Waltham
CONNUTER READABLE FORM:
MEDIVE TREADABLE FORM:
MEDIVE TREADABLE FORM:
MEDIVE TREADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/OOCKET NUMBER: 025.6 USD2 (IMT-528CFD2)
INTECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7403
INFORMATION FOR SEQ ID NO: 95.
SECUENCE CHARACIER:STICS:
LENGTH 367 amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  Length 367
                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 86.4%: Score 108; DB 10: Length 36' Best Local Similarity 85.0%: Pred. No. 3.54e-05; Matches 1; Mismatches 2: Indels Matches 1; Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: December 6, 1994
ATTCRNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRAILON NUMBER: 38,872
REFERENCE/CDOCKET NUMBER: 025.6 USD6 (IMI-028CPD6)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,006
FILING DATE: June 6, 1995
CLASSIFCATION 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                          MOLEGULE TYPE: protein
JENCE 367 AA: 39846 MW: 695078 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 SSGKIEETNIYNSNEAFKVE 351
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US-08-467-006-95
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APPLICANT: Griffeth, Irwin 3.

APPLICANT: Bond, Julian F.

CC APPLICANT: Garman, Richard 3.

C APPLICANT: Garman, Richard 3.

C APPLICANT: Wenny, Sulmei H. APPLICANT: Brauer Andrew:

APPLICANT: Brauer Andrew:

APPLICANT: Powers, Steven P.

TILE OF INVENTION: Albergenic Proteins And Peptides From TILE OF INVENTION: Apparent Calar Poilen

NUMBER OF SCHOKOES: 261

CORRESPONDENCE ADDRESS: 261

CORRESPONDENCE ADDRESS: 261

CORRESPONDENCE ADDRESS: 261

CORRESPONDENCE ADDRESS: Abermaceutical Corner Calar Waltham

STREET: 610 Lincoln St.

CITY: Waltham
                                                                                                                                              Sdpt
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MEDIUM TYPELS.

COMPUTER: Floppy disk

COMPUTER: BW PC compatible

OPERATING SYSTEM: PC-DOS/MS-ECS

SOFFWARE: Patestin Release #i.0, Version: #1.25

CURRENT APPLICATION DATA: US/08/467.697

FILING DATE: June 6, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

ATIORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 78,872

REFERENCE/DOCKET NUMBER: 78,872

REFERENCE/DOCKET NUMBER: 78,7594;
TELEPHONE: (617) 227-74;
TELEPHONE: (617) 227-594;
INFORMATION FOR SEC ID NO: 9::
                                                                               Query Match

86.4%; Section 10: Length 367.

Best Local Similarity 85.0%; tel No. 3.54e-05;

Matches 17: Conservative i Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                             367 AA
                                                                                                                                                                                                                                                                                                                                                             PPT
MOLECULE TYPE: Protein
SEQUENCE 367 AA: 39846 MW; 645078 CN;
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SEQUENCE
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APPLICANT: Yeung. Siu-mei H.;
APPLICANT: Yeung. Siu-mei H.;
APPLICANT: Brauer. Andrew:
APPLICANT: Brauer. Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Alleroemic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Poilen
NUMBER OF SEQUENCES: 26.
CORRESPONDENCE ADDRESS:
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: imm.logic Pharmaceutical Corporation, Inc 610 Linceln St
                                    Score 108; DB 10; Length 367;
Pred No. 3.54e-05;
1: Mismatches 2: Indels
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AEDION TYPE: FLORM:

AEDION TYPE: FLORM:

COMPUTER: IN PC COMPATIBLE

COMPATIN: SYSTEM: PC-505/NS-unS

SOFTWARE: PALCO IN ROLOSP #1.0. VETSION #1.25

SOFTWARE: PALCO IN NOMBON: US/CC/SC1.25

FILING DATE: Leventon 6. 1994

CLASSIFICATION NUMBER: 08/25,248

FILING DATE: APPLILS #1094

APPLICATION NUMBER: 08/25,248

FILING DATE: September 1, 1994

APPLICATION NUMBER: 07/938-996

FILING DATE: September 1, 1992

APPLICATION NUMBER: CT/US93/00139

STILING DATE: SEPTEMBER: CT/US93/00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Carlene A. Vanstone
RECISTRATION NUMBER: 35,729
REPERENCE/DOCKET NUMBER: 025.6 US (IMI-028CP2)
IELECOMMONICATION INFORMATION:
FELEPHONE: (617),466_6000
                                                                                                                                                                                                                                           367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 367 AA; 39846 MW; 695078 CN;
357 AA: 39846 MM: 695078 CN:
                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08350225
                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffeth, Irwin C.;
Pollock, Joanne:
Bond, Julian E.;
Garman, Richard D;
Kuo, Mei-Chang:
Yeung, Siu-aet H.;
Brauer, Andrew:
Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEC ID NO: 95: SEQUENCE CHARACTERISICS: LENGTH: 367 anino acids TOPOLGY: linear
                                                                                                                                                                                                                                                                                                                                                                     Sequence 95, Application US/08350225
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                        332 SSGKTEETNIYNSNEAFKVE 351
                                                                                                                                               1 SSGKNEGINIYNNEAFKVE 20
                                      Cuery Match
Hest Local Similarity 85.0%:
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waltham
                                                                                                                                                                                                                        RESULT 7 15 US-08-350-225-95 XX
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  SECUENCE
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86.4%; Score 108; DB 8; Length 367;

Query Match

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Sans
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APPLICANT: Braiser, Andres.
APPLICANT: Braiser, Andres.
APPLICANT: Powers, Stever H.
TILLE OF INVENTION: Alleise to Proteins And Peptides From TILLE OF INVENTION: Japaness : wdar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108; DB 10; Length 367; Pred. No. 3.54e-05;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Immulogic Pha Liventical Corporation.
1: 610 Lincoin St
Walthan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCMPUTER READBALE FORM:
MDDIJM TYPE: Froppy disk
MDDIJM TYPE: ISM PC compatible
OCMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/WE DUS
SOFTWARE: Patentin Release #1.5. Version #1.25
GURRENT APPLICATION DAIN:
PILLING TAIE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Darlene A. Vansione
REGISTRATION VUMBER: 35.729
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-G28CP2)
TELECOMMUNICATION INFORMATION:
Best Local Similarity 85.0%; Pred. No. 3.546-05:
Matches 17: Conservative 1: Mismatches 2:
                                                                                                                                                                         367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U8/246.24
FILING DATE: April 3, 1994
APPLICATION NUMBER: 07/93.99U
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/00139
FILING DATE: January 15, 1993
ATIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
IENCE 367 AA: 39846 MW; 695078 CN;
                                                                                                                                                                           , Y.
                                                                                                                                                                                                                                                                                                                                 Sequence 95. Application US/38468740
                                                                                                                                                                                                                                                                                          Sequence 95, Application US/08468940
                                                                                                                                                                                                                                                                                                                                                                                                            Bond, Julian F.
Garman, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 456-6600
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids TOPOLOGY: 14-10
                                                                                                                                                                                                                                                                                                                                                                   Griffeth, Irwin
Pollock, Joanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHASSIFICATION: 424
PRICE APPLICATION CATAL
APPLICATION NUMBER: PK/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuc, Mei-Chang
                                                                                                                                                                           STANDARD
                                                          332 SSGKTEETNIYNSNEAFKVE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%;
85.0%;
                                                                                1 SSGKNEGINIYNNNEAFKVE
                                                                                                                                                                                                                                                                                                                                                   INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: C2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                           US-08-468-940-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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RESULT 10
ID US-07-938-990A-57
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US-08-468-940-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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   Gaps
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CORRESPONDENCE ADDRESS: ADDRESSE: Immulogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St. CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC COMPALIBLE
COMPATION: PC-DCS/MS-DCS
CORRATING SYSTEM: PC-DCS/MS-DCS
CORRATING SYSTEM: PC-DCS/MS-DCS
CURRENT ASPLICATION DATA:
APPLICATION NUMBER: US/08/467,697
FILING DATE: June 6. 1995
CLASSIFICATION NUMBER: US/08/467,697
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: Decomber 6, 1994
ANTONEY/ASPN IND/ARATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 025.6 USD4 (IMI-028CPD4)
FILECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.4%: Score 93: DB 10: Length 20: Best Local Similarity 70.6%: Pred. No. 4.09e-03: Matches 3: Indels Anatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
   Indels
   5
                                                                                                                                                                                                                           20 AA.
   Mismatche
                                                                                                                                                                                                                           PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08467697
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/38467697
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FRAGMENT FYPE: internal
SEQUENCE 20 AA; 2221 MM: 2174 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFURMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICALT: Pollock, Joanne:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHCNE: (617) 227-7400
TELERAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 57:
SEQUENCE CHARACTERISTICS:
LENGIH: 20 amino acids
                                                                                                                                                                                                                           STANDARD:
                                                         332 SSGKTEETWIYNSNEAFKVE 351
                                                                                                               1 SSCKNEGINIYNNNEAFKVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSGKYEGGNIYTKKEAFNVE 20
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   17: Conservative
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DE SEQUENCE 57, APPLIAN

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                                                                                                 Sequence 57, Application US/079*8940A
GENRAL INFORMATION:
APPLICANT: Griffith, Irwin ...
APPLICANT: Bond Julian
IITLE OF INVENTION: Allerenno Proteins And Peptides From TITLE OF INVENTION: Japanese Grdar Follen
NUMBER OF SEUGENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 74.4%: Score 93: DB 4: Length 20: Best Local Similarity 75.0%: Pred. No. 4.09e-03; Antches 14; Conservative 3: Mismatches 3; Indels
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7.
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                                                                          Sequence 57, Application US/07338990A
                                                                                                                                                                                                                     ADDRESSEE: Lahive & Cockfleid
STREET: Sixty State Struct
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/08468940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEBETAN: (617) 227-7400 INFORMATION: (617) 227-7400 INFORMATION FUR SEC. ID. N. SECCENDE CHARACTERISTICS. LENGTH: 20 aminority.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGENI TYPE: internal
JENCE 20 AA; 2221 RW: 2174 CN:
STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGKNEGINIYNNEAFKVE 20
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                   02109
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OFFICANT OFFICANT CONTROL OFFICANT OFFICANT POLICEK, JOAGNE, APPLICANT POLICEK, JOAGNE, APPLICANT BOND, Julian F., APPLICANT BOND, Julian F., APPLICANT KAO, Mel-Chang. APPLICANT KAO, Mel-Chang. APPLICANT Extery, Slutmei H., APPLICANT Extery, Mark A., APPLICANT Extery, Mark A., APPLICANT Extery, Mark A., TITLE OF INVENTION: Aleraent: Proteins And Peptides From TITLE OF INVENTION: Aleraent: Proteins And Peptides From NUMBER OF SEQUENCES: 26: CORRESPONDER: ADDRESSEE: Immulogic Pharmacellinal Corporation, Inc., STREET: 610 Lincoln St.
                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

21F 02184

COMPULA READABLE FORM:
MEDICUL TYPE: Floppy disk
COMPUTER: 18M PC compatalle
OPERATING SYSTEM: PC-DS/MS DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/55.225
FILING DATE: December 6, 1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Darlene A, Vanston
REGISTRATION NUMBER: 35, 29
REFERENCE/DOCKET NUMBER: .25 6 US (IMI-628CP2)
TELECOMMUNICATION INFORMATE: N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 8; D6 Pred, No. 4.09e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA.

APPLICATION NUMBER: 08/226.24#

FILIN DATE: APPLI 8. 1594

APPLICATION NUMBER: 07/98.95;

FILIN: DATE: September: 1:992

APPLI ATION NUMBER: PCI/0594/00139

FILIN: DATE: January: 15, 1993

ATIONEXYAGEN: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
              Application US/08350225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/08226248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEMPHONE: (617) 466-6000
INFORMATION FOR SHOULD SEQUENCE CHARACTERY (517) 466-6040
SEQUENCE CHARACTERY STICS:
LENGTH: 20 aminor: Type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA: 2221 MW; 2174 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSGKYEGGNIYIKKEAFNVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 70.0%:
Matches 14; Conservative
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            Sequence 57,
                              GENERAL
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                                                                                                                                                                             APPLICANT: Powers, Steven P.
TILLE CF INVENTION: Albergenic Froteins And Peptides From TITLE OF INVENTION: Abanese Cedar Pollen NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ġ
                                                                                                                                                                                                                                                        ADDRESSE: Immulcaic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St CITY: Waltham STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guery Match 74.4%; Score 93; DB 10; Length 20; Best Local Similarity 76.0%; Pred. No. 4.09e-03; Matches 3; Indels Matches 3; Indels
                                                                                                                                                                                                                                                                                                                                           ZIP: 22154
COMPUTER REACABLE FORM:
MEDIUM TYPE: Fioppy disk
GOMPUTER: IBM PC compatible
JPERAIIN: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-028CP2)
TELEOWININTALIEN INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6000
INFORMATION INS SCO.
SEQUENCE GRANACTERESSIONS
LENGTH: 20 amino solds
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CLASSIFICATION, 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING LATE: December 6, 1994
APPLICATION NUMBER: 08/256,249
FILING LATE: APPLI 8, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/00139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
        Sequence 57. Application US/38468940
GENERAL INFORMATION:
APPLICANT: Griffett, Irwin J.:
APPLICANT: Policet, Joanne:
APPLICANT: Bond, Unlian F.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57, Application US/08350225
                                                                                          Garman, Richard D.
Kuo, Mol Chang:
Young, Siu-mel B.;
Brauer, Andrew:
Exley, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORDING TIMES TO THE WAS THE TABLE TYPE: peptide FRAGMENT TYPE: internal TYPE: Internal TYPE: 22.2 MW: 2174 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
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AC XXXXX
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US-08-467-697-91
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GENERAL INFCRMATION:

APPLICANT: Griffeth, Irwin J.;

APPLICANT: Bollock, Joanne;

APPLICANT: Bollock, Joanne;

APPLICANT: Garman, Julian F.;

APPLICANT: Weing, Julian F.;

APPLICANT: Yeing, Siu-mei H.;

APPLICANT: Yeing, Siu-mei H.;

APPLICANT: Weing, Siu-mei H.;

APPLICANT: Siu-mei H.;

APPLICANT: Siu-mei H.;

APPLICANT: Weing, Siu-mei H
                                                                                                                                                                                                                                                                                                                                                        CIP: C2154
COMPUTER READABLE FORM:
MEDIJU TYPE: Floppy disk
COMPUTER: Elbopy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRIESS #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/226,248A
FILING DATE: APPLI #1.1994
PROCK APPLICATION NUMBER: 07/938,990
FILING DATE: SEPTEMBER: 1,1992
APPLICATION NUMBER: PCT/USS3/00139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70.0%: Pred. No. 4.09e-03:
Matches 14: Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Darlene A. Vanstone
REJSTRAIICN NUMBER: 35.729
REFERENCE/DOCKET NUMBER: 35.729
RELEPHONE: CALTON INFORMATION:
TELEPHONE: (617) 466-6000
TELEPHONE: (617) 466-6040
INFORMATION FOR SEQ. ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 A.A.
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APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 91, Application US/08225248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: incernal
SEQUENCE 20 Ast: 2221 MH: 2174 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
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CIIY: Waltham
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APPLICANT: Garman, Richard D:
APPLICANT: Year, Mai-chang:
C APPLICANT: Year, Stu-mei H.;
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
TILE OF INVENTION: Aleryenic Proteins And Peptides Fion TILE OF INVENTION: Japanese Cedar Polle:
NUMBER OF SEQUENCES:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation: Inc.
STREET: 610 Lincoin STATE: MA
COUNTRY: Waltham
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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74,4% Sonally 18.7, Lebati 26:
Best Coral Similarity 70.0% Pred No. 4 Jan-03.
Matches 14: Conservative 3. Mistatches 5: Indexs
Matches 14: Conservative 3. Mistatches 5: Indexs
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CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA: 990
FILING DATE: September: 1992
APPLICATION NUMBER: 07/93#,990
FILING DATE: September: 1992
APPLICATION NUMBER: 07/93#,993
ATONNEY AGENT INFORMATION: MAME: DATIENE A' VANSCO: ERGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 35,729
FELECOMMUNICATION INFORMATION: TELEPONE: (617) 466-5000
TELEFAX: (617) 466-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC "D'NS/MS-DNS
SOFTWARE: Patentin Re-ware" #1.0. Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 AA.
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FILING DATE: April 8, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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APPLICANT: Griffeet, Irwin J.:
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D:
APPLICANT: Kuo, Mei-Chang:
APPLICANT: Yeung, Siu.:mei H.;
APPLICANT: Brauer, Andrew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91, Application US/38467697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST TYPE: amino acids IYPE: amino acids ICPCLOGY: 1:-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEG ID NC:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 SSGKYEGGNIYTKKEAFNVE 26
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FRAGMENT TYPE: internal
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AFPLICANT: Exiety, Mark A.;

AFFLICANT: Powers, Steven P.

IIILE OF: INVENTION: Allergenic Proteins And Peptides From
IIILE OF: INVENTION: Jepanese Cedar Polican
IIILE OF: INVENTION: Jepanese Cedar 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release *1.0, Version *1.25
COMPUTER: Patentin Relaase *1.0, Ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGNEUT TYPE: internal
UENCE 26 AA: 2873 MM: 3776 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Search completed: Non Jun 19 16:28.51 2000 Job time : 17 secs.

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MEstch_pp protein protein database search, using Smith-Waterman algorithm

Mon Jun 19 16:15:28 2000; MasPar time 5.59 Seconds 168.815 Million cell updates/sec Fun on:

Tabular output not deserated.

>US-09-142-524A-12 (1-20) from US09142524A.pep 125 1 SSGKNEGINIYNNNEAFKVE 20 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Minimum Match O% Listing first 45 summaries Post-processing: Searched:

142080 seqs, 47172406 residues

Database:

Mean 25.871; Variance 38.428; scale 0.599 pir62 1:pirl 2:pir2 3:pir3 4:pir4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.75e-37	.75e-		8.72e-01	3.C8e+00	4.64e+00	4.54e+00		6.97e+30	6.97e+30	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	†	1.04e+01	1.04e-01	1.04e-01	1.55e+01	S	1.55e+01	2.29e-01
Description	major allergen Cry j	major allergen Cry j	ketolase (EC 2	probable membrane pro	regulatory protein SW	probable fiagellar ba	hypothetical protein	peroxisomal membrane	hypothetical protein	finger protein tramtr	hypothetical protein	flagellar basal body	abortive phage resist	abiC protein - Lactoc	glycine hydroxymethyl	late cyc	yegH protein precurso	tentoxylysin (EC 3.4.	hypothetical protein		hypothetical protein	killer toxin resistan	flagellar basal body
91	JC2124	7	A45050	S66700	ന	C71259	T15906		G64030	S35017	T03992	E70196	A47025	27	T05258	A34896	F64839	BICLIN	G71511	B39415	T13539	BVBYKS	XMEBEG
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A42851	S15748	5 7 7	C71158	C247 5	T084.0	A385 9	2 E727 1	F72651	B32905	304650	F69875	B5552	D72084	5	S35092	5	563453	\sim	S551 3	E716.2	
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295	485	491	514	668	872	888	1039	161	215	292	298	331	337	4.81	621	732	737	744	274	1308	28:5
44.0	44.0		44.0	44.0		2. C	44.C	43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.2	
22	S	55	55	55	35	5.5	55	54	24	54	₹	7	Š	54	54	54	54	24	54	2	54
4	25	26	27	28	53	0	31	32	33	34	35	36	37	38	35	40	41	2,4	43	44	45

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RESULT ITTLE DATE DATE TOTALE SATE ACCESSIONS STOCESSIONS STOC	DUIT 1 JUG2124 *type con lete RN
TITLE	major allergen Cry j I precursor (clone pCCI-2-2) - Japanese cedar
ORGANISM DATE	cedal second name Cryptomeria japonica #common_name Japanese cedar 14-Jul-1964 #secuence revision 14-Jul-1964 #text change
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**experimental_source strain S288C
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KEYWORDS transmembrane protein
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                                                                                                                                **experimental_source brain
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Best Local Similarity 50.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        *domain signal sequence *status predicted *label 513\
*product major allergen Cry j I (clone pCCI-2-2) *status
predicted *label MAT\
54 ** *binding_site carbohydrate (Asn) (covalent) *status
predicted
predicted
*length 374 ** *nolocular-weight 40645 ** checksim 2920
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**note sequence extracted from NCBI backbone (NCBIP:122C84)

SYNCE S29657

Thors McCool B.A.: Plonk. S.G.: Martin, P.R.: Singleton, C.K.

Jahors Submitted to the EMBL Data Library, August 1992

escription cloning of human transketolase CDNA and comparison of the mickedide sequence of the coding region in Mernicke-Korsakoff and non-Wernicke-Korsakoff individuals.
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A45050
A45050 A45050
A45050 BACOOL BALL PLONK, S.G.: Matth. P.R.: Singleton, C.K.
Aauthors McCool, E.C. (1993) 2681397-1404
#fille cloning of human transketolase CDNAs and cumparison of the ruckeotide sequence of the coding region in Wernicke-Korsakoff and non-Wernicke-Korsakoff individuals.
#accession A45050 Individuals.
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                                                                                                                                                                                                                                                                                                  ##molecule_type protein
##residues 22-53:58-81:219-232:236-258:299-307:346-372 ##label SO2
                 UC2123: PC2065
UC2123
SOCE, T.: Komiyama, N.: Shimizu, K.: Kusakabe, T.: Morikubo,
K.: Kino, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status preliminary; not compared with conceptual translation ##molecule_type mRNA ##residues 1-623 ##label MCC ##stross-references GB:X87688; GB:S52775; NID:937266: PIDN:CAA47919.1; PIDS:937267
                                                                                                                                                                        the authors described carbohydrate binding site for residue 279
*Superfamily pectate lyase LAT59
dlycoprotein: pollen
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transketolase (EC 2.2.1.1) - human
#formal_name Homo sapiens #common_name man
[0-0.n.1944 #sequence_revision 18-Nov-1994 #fext_change
18-0nn-1999
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                                                                                                                     ū
                                                                                   #journal Blochem Blophys. Res. Commun. (1994) 199:619-625 atilite Cloning and sequencing of CDNA coding for Cry j 1. allergen of Japanese cedar pollen.
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26-Aug-1999
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#submission
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WIE
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                                        REFERENCE
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FEATURE
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AESULT ENTRY

<u>0</u> 20

SUMMARY

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*journal Biochem. Biophys. Res. Commun. (1992) 193:1159-1166
*Litle Nucleotide and predivited amino acid sequence of a cDNA cloud encoding part of human transketolase.
*Cross-references.WUID:92231878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##CFOSS-Teferences EMBC:274760; NID:@1419794; PID:@252261: PID:@1419795
MIPS:YOLO18e
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                                                                                                                                                                                          the sequence differences at both ends are affilt fally
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                                                                                                                   **FEGlecule_type protein 284-291:439-454:457-470 **;abel ABEL 284-291:439-454:457-470 **;abel ABEL XH.1914 catalyzes the transfer of a two-carbon ketol in xhis enzyme catalyzes to an aldose acceptor, either fibuse 5-phosphate or erythrose 5-phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 02317
#formal_name Sacciarumyces cerevisiae
12-301-1996 #sequentelrevision 12-301-1996
846706
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Fraser, C.M.: Norris, S.J.: Weinstock, G.M.; White, O.: Sutton, G.G.: Dodson, R.: Gwinn, M.: Hickey, E.K.: Clayton, R.: Ketchum, K.A.: Sodesgren, E.: Hardham, J.M.: Wolked, M.P.: Saizberg, S.: Peterson, J.: Khalak, H.: Richardson, D.: Howell, J.K.: Chidambaram, M.: Utterback, T.: McDonald, L.: Artiach, P.: Bowman, C.: Cotton, M.D.: Fujii, C.: Garland, S.: Hatch, B.: Horst, K.: Roberts, K.: Watthey, L.: Weidman, S.: Smith, H.O.: Venter, J.C.
Science (1998) 281:375-388
Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c71259 *type complete
probable lladellar basal body rod protein (flgG:) / sypbilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ssuperfamily regulatory protein SW16; ankyrin repeat homology DNA binding; transcription regulation
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                                                                                                                                                             #authors Breeden, I.; Nasmyth, K.
#journal Nature (1987) 329:651-654
#title Similarity Detween cell-cycle genes of budding yeast and
#cross-references MUID:88014241
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24.Jul-1998 #sequence_revision 24-Jul-1998 #text_change
protein 19470.8: protein YLR182w
*rormal_name Sarcharomyces cerevisiae
31-Dec-1991 *sequence_revision 31-Dec-1991 *text_change
18-Jun-1999
$C3161; $51427
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*domain ankyrin repeat homology *label AN2
*length 803 *molecular-weight 90559 *checksum 7241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-803 ##label WOH
##cross-references EMBL:017246: NID:9577192: PIDN:AAB67450.1:
PID:9577200: MIPS:YLR182#
                                                                                                                                                                                                                                                                                                                                                                                                                *authors Wohldmann, P. *submission submitted to the EMBL Data Library, November 1994 *description The sequence of S. cerevisiae cosmid 9476. *accession S51427
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PIDN:AAC65915.1; PID:93323281
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Pred. No. 3.28e+00:
6. William
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##residues 1-803 ##label BRE
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#accession C71259
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Best Local Similarity 45.0%;
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**residues 1-25
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Hoehfeld, J.; Veenhuis, M.; Kunau, W.H.
J. Cell Biol. (1991) 114:1167-1178
PAS3, a Saccharcmyces corevisiae gene encoding a percxisomal
integrai membrane protein essential for percxisome
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PAS3 protein; protein YDR329c
*formal_name Saccharomyces cerevisiae
17-Jul-1992 *sequence_revision 17-Jul-1992 *text_change
05-Dec-1997
                                                                                                                                                                                                                                                                                                             hypothetical protein EV4F6.3 - Caenorhabditis eledans *formal_name Caenorhabditis eledans 20-Sepi1999 *text_chlanse 20-Sepi1999 *text_chlanse 115906
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30/1: 77/2: 236/3
*length 298 *mclerular-weight 32721 *checksum
                                                    *superfamily rod protein flag
*length 254 *molecular-weight 28597 *checksum
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##molecule_type DNA
##residues 1-298 ##labe! PAU
##cross-references EMBL:U28043: NIP:Q861333: PID:q861336;
##experimental_source strain Bristc! Nz
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                                                                                             Query Match 47.2%; Schre 59; UB 2: Length 298. Best Local Similarity 36.8%; Pr d. No. 4.64e+00: Matches 7: Conservative 7 Mismatches 5: Indels
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**experimental_source strain Nichols
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*accession A40550
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Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Jomb, J.F.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Jomb, J.F.; Korkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Jomb, J.F.; Filds, G., Godgyfer, C.J.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weldman, B.F.; Phillips, C.A.; Sprages, T.; Hedbley, J.M.; Weldman, M.D.; Utterlack, T.R.; Hanna, M.C.; Nguyen, D.J.; Saudek, D.M.; Brandon, R.C.; File, L.D.; Fritchman, J.L.; Fibrmann, Small, K.V.; Fosser, C.M.; Smith, H.D.; Venter, J.C.; Science (1995) 269:496-512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      064030 *type complete
hypothetical protein HI1458 - Haemophilus influenzae (strain
Rd KW20;
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##rcsidues 1-441 ##label DJZ
##cross-reterences EMEL:U32517: NID:q914989; PID:d.15034; MIPS:YUR329c
##experimental_source strain S288C (A8972)
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13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
24-Sep-1998
838017, 810881
838017
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18-Aug-1995 *sequence_revision 18-Aug-1995 *text_change
30-Jun-1998
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Best Local Similarity 42.1%; Pred. No. 6.97e-00;
Matches 8; Conservative 7; Mismatches 4; Indels
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Pred. No. 4.64e+30:
6: Mismatches 2:
                                                                                                           ##cross-references MIPS:YDR329c: SGD:S0002737
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Sest Local Similarity 46.7%:
Matches 7: Conservative
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                                                                                                                                                                              *authors Harrison, S.D.: Travers, A.A.
#journal EMBO J. (1990) 9:207-216
#title The transfack gene encodes a frosophila tinger profess flat, interacts with the fix transcriptional regulatory region and shows a novel embryonic expression pattern.
#cross-references MUID:99107945
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**seross-references FlyBase,FBan0003870
CLASSIFICATION *superfamily POZ domain inmojogy
KEYWORDS DNA binding: nucleus: transcription :equiation
Montell, C.
Submitted to the EMBL Data Library, April 1993
836017
                                                                                         ##experimental_source cultivar Columbia: BAC clone ISL19
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Best Local Similarity 54.5%: Pred. No. 6.97e+00:
Matches 6: Conservative 5: Mismatches (; Indeis Matches
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##residues 1-185 ##jabcl HEV
##cross-references EMBL:AL049481
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*note I:
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J. Barteriol. (1992) 174:4643-7469
Molecular characterization of a second abortive phage
resistance gene present in Lactococcus lactis subsp. lactis
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*Cormal_name_cortococcus_lactis_subsp._lactis

$3.May-1994 *sequence_revision 33.May-1994 *text_change
                    spirochete
*formal_name Borrelia burgdorferi #conmon_name Lyme disease
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PIDN:AAC67132.1; PID:g2688724; TIGR:BB0774
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Bancroft, I.: Means, H.W.: Mayer, K.E.X.: Schueller, G.
submitted to the Profest Septembe Database, Pethoday 1999
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*type trudment abid protein - Lactococcus lactis (fragment)
*formal_name Lactococcus lactis
06.Jan=1995 *sequence_revision 06.Jan=1995 *text_change
$27587
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F18A5_280
*superfamily glycine hydroxymethyltransferase
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

protein - protein database search, using Smith-Waterman algorithm Mon Jun 19 16:14:36 2020; MasPar time 3.71 Seconds 164.264 Million cell updates/sec MPsrch_pp First On:

Tabular output not generated.

>US-09-142-524A-12 (1-20) from US09142524A.pep 125 I SSGKNEGINIYNNNEAFKVE 20 Title: Description: Perfect Score: Sequence:

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83857 segs, 30454973 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Mean 27,434; Variance 35,186; scale 0,780 Statistics: Pred. No. is the number of results prodicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	.35e-08	٠	.57e-01	.57e-01		.94e-01	. 55	٠,	.43e-00	.75e+00		.76e+00	.76e+00	.76e+00		.76e+00	.79e+00	.79e+00	.87e+00	.87e+00	.87e+00	.87e+00	.87e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCool B.A., Plonk S.G., Martin P.R., Singleton G.K.; 
"Cloning of fouran transketodase cDMs and compariso: of the 
nucleotide sequence of the coding region in Wernicke-Korsakoff and 
non-Wernicke-Korsakoff individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schenk G., Layfield R., Candy J.M., Duggleby R.G., Nixon P.F., Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S > 7 (1N CNU J 1-8).

C > 8 (1N CNU J 1-8).

C > 4 (1N CNU J 1-8).

K > 9 (1N CNU J 1-8).

POTENTIAL.

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NJ 74825950248F56F CRC64:
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Submitted (SEP-1993) to the EMPL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 224-623 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: D26544: FAA05542.1; -..
EMBL: D26545: BAA05543.1; -..
EMBL: D34645: BAA07020.1; -..
PIR: 444773: A44773.
PRAM: PF00544: Pec_lyase: 1..
PRINTS: PR00867: AMBALLERGEN.
SIGNAL.
SIGNAL.
SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93: DB 1: L
Pred. No. 4.05e-08:
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0EC-1992 (Rel. 24, Created)
01-001-1996 (Rel. 34, Last sequence ipdate)
TRANSKETOLASE (EC 2.2.1.1) (TK).
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AMB A IZAMB A IIZORY C : SUBFAMILY
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[2]
SEQUENCE FROM N.A.
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les 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
374 AA;
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MEDLINE: 92231878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-LIVER:
MEDLINE: 93123263.
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MEDLINE: 96214928.
Schimmer B.P., Tsac J., Czerwinski W.;
Schimmer B.P., Tsac J., Czerwinski W.;
"Amplification of the transketolase gene in desensitization-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-129/SV;
Salamon C., Chervedak M., Platigorsky J., Sax C.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
                                       Solve
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Mus.
Abedinia M., Layfield R., Jones S.M., Nixon P.F., Mattick J.S. Nucleotide and predicted amino acid sequence of a CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                           *! SIMILARITY: BELONGS TO THE TRANSKETCLASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68: DB 1; Ed Pred. No. 2.3le-02: 4: Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-FEB-1200 (Rel. 39, Last annotation update)
TRANSKETOLASE (EC 2.2.1.1) (TK) (P68).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.25 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X67688; CAA47919.2; -. EMBL; L12711; AAA61222.1; -. EMBL; U55017; AAA98961.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.4%; 50.0%; E
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PIR; PH0845; PH0845.
MIM; 277730;
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585
608
623 AA;
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472 TSRPENALIYSNNEDFQV 489
                                                                                                                                SWI6_YEAST
P09959;
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DOMAIN
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Sec http://www.isb-sib.ch/announce/or sond an email to license@isb-sib.ch).
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O
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Submitted (APR-1994) to the EMB-/Gerank/DDBJ databases.
-!-CATALYIC ALTIVITY: SEDCHEDIUCSE 7-FHCSPHATE - C-GLYCERALDEHYDE
-!-CRACTOR; THIANIR PYROPHATE - D-XYJULGSE 5-PHOSPHATE.
-!-CCRACTOR; THIANIR PYROPHASPHATE.
-!-SUBGNIT: HOMODYKER (BY SIMILARITY).
-!-SUBGNIT: HOMODYKER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eutheria, Rodentia, Schurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64: DB 1: Length 623:
Pred. No. 1.57e-01:
5: Mismatches 5: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 1; Length 623; Pred. No. 1.57e-01;
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MGD: MG2:105992: TTT.
PROSITE: PS00801: TRANKETOLASE_1: 1.
PROSITE: PS00802; TRANKETOLASE_2: 1.
PROSITE: PS00802; TRANKETOLASE_2: 1.
PFMM: PF00456: Lransketolase: 1.
Transferase: Thiamine pyrophosphate.
Transferase: Thiamine pyrophosphate.
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623 AA; 67643 MW; A198AB56A73C23CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-007-1996 (Rel. 34, Created)
01-00T-1996 (Rel. 34, Last sequence update)
01-00T-1996 (Rel. 34, Last annotation update)
TRANSKETOLASE (EC 2.2.1.1) (TX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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PROSITE; PS00802: TRANKETOLASE_2: 1.
PFAM. PF00456: transketolase: 1.
Transferase: Thiamine pyrophosphate.
SEQUENCE 623 AA; 67643 WW; A198AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY: TISSUE-LIVER:
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                                                                                                                                                                                                                                                                                        EMBL; U05809; AAC52443.1; -. EMBL; U90889; AAC53570.1; -. SWISS-2DPAGE; P40142; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 TSRPENALIYSNNEDFQV 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guery Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sucry Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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ID TKT_RAT
AC P50137;
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-1: SIMILARITY: STRONG, TO S.P.MBE CUALL.
-1: SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-027-1994 (Rel. 34, Last annotation update)
REGULATORY PROTEIN SWIS (CELL-CYCLE BOX FACTOR, CHAIN SWIS) (TRANS-SCTING ACTIVATOR DE HO ENCONCOLEASE GENE) (MRF SUBUNIT P90).
SWIS OR YLR182W OR L9470.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breeden L., Nasmyth K., "Similarity between cell-cycle genes of bidding yeast and fission yeast and the Notch gene of Droscphila.":
Nature 329:551-554(1967).
                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota: Saccharomycetes; Saccharomycetales.
Saccharomycetaceae: Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dirick L., Moll T., Auer H., Nasmyth K.).
"A central role for SW16 in modulating cell cycle Start-specific transcription in yeast.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SIRAIN-S288C / AB972:
Johnston M., Andrews S., Brickman R., Cooper J., Ding H., Durienston M., Andrews S., Brickman R., Cooper J., Bing H., Duriender D., Fulton L., Gattung S., Greco T., Kirsten J., Roucha T., Hallsworth K., Hawkins J., Hilliot J., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Fellson Riften L., Riles L., Talch A., Trevaskis E., Vignati D., Wilcox L., Wohlden P., Vandish M., Wilson R., Vignati D., Submitted (NOV-1994) to the TMBL/SenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ranscription regulation; DNA-binding; ANK repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9B317FCACEEC493C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 X ANK MOTIF REPEATS ANK MOTIF 1.
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2 SGKNEGINIYNNEAFKV 19
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR. S03161: RGBYW6.
TRANSFAC: T00096: --
TRANSFAC: T01013: --
SGD: L0002254: SWIF.
PFAM: PF00023: ank: 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92301535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A. MEDLINE: 88014241.
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                                       Gaps
                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADENVLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                            Troic: P., Sismetro C., Vivars C., Glaser P., Roy A., Danchin A.; Submitted (FEB-1966) to the EMB-/Genbank/DBJJ databases.

-:- GATAINTIC ACTIVITY: AIP = 3'.5'-CYCLIC AMP + PYROPHOSPHATE.

-:- BNZYME REGULATION: THE REGULATORY DOMAIN IS IS INVOLVED IN THE REGULATION OF CYCLARE ACTIVITY BY THE CARBON SOURCE.

-:- SUBCELLUIAR LOCATION: CYTOPLASMIC.

-:- SIMILARITY: BELONGS IO ADENVLYL CYCLASE CLASS-: FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycetes: Saccharomycetales:
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Ö
                                                                                                                                                                                                                                                                                                              Aeromonas hydrophila.
Bacteria: Proteobacteria: gamma subdivision: Aeromonas group:
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Pred. No. 9.94e-01:
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   Length 803;
                                    5; indels
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Locry Match
Rest Local Similarity 45.0%: Pred. No. 9.94e-01:
Matches 9: Conservative 6: Mismatches 5
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01-DEC-1992 (Rc). 24. Last sequence update)
01-NCV-1997 (Rc). 35. Last annotation update)
PEROXISOMAL MEMBRANE PROTEIN PASS (PEROX:N-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4: Mismatches
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                                                                                                                                                                           843 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PSC1092: ADENYLATE_CYCLASE_11: 1.
PROSITE: PSC1093: ADENYLATE_CYCLASE_12: 1.
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MEDLINE: 91373453.
Hochfeld J., Veenhuis M., Kunau W.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALATIC
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                                                                                                                                                                           PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM: PF31295; Adenylate_cvcla:
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                                                                        651 SSGIDWDSSEYDADEPFKVE 670
                                                                                               1 SSGKNEGINIYNNNEAFKVE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: X95881; CAA65130.1; -
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Hest Local Similarity 52.9%;
Matches 9; Conservative
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Domain 537
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P28795;
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                                                                                                                                                                             CYAA_AERHY
                                                                                                                                                                                                                                                                                                                                                 Aeromonas.
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                                                                                                                                                                                                    STRIN-$2286C NO. N.A.

A FOLDON M., Andrews S., Brinkman R., Cooper J., Ding B., C. Z., Johnston M., Andrews S., Brinkman R., Cooper J., Since T., Kissten J., Katello A., Folion L., Gattung S., Greeo T., Kissten J., Mardis E., Mandrews J., Hillier E., Jier M., Johnson D., Johnston L., Langston Y., Catrellie P., Le F., Mardis E., Mandress S., Mile M., Naan M., Pauley A., Peluso D., Mardis E., Wondati D., Mardox L., Taich, Tevokasis E., Vignati D., Mikoo L., Wohldman P., Vaud M., Wilson R., Waterston R., Submitted (JUL-1995) to the EMBL/GenBank/DBS databases.

I Submitted (JUL-1995) to the EMBL/GenBank/DBS databases.

I FUNCTION: INVOLVED IN PERCAISOME BIOSYNTHESIS. MAY FUNCTION AS A RECEPTOR PROTEIN. LACK OF THIS PROTEIN CAUSES THE CYTOSOL OF PERCAISOMAL MATRIX PROTEINS.

C. TOSOL OF PERCAISOMAL MATRIX PROTEINS.

C. TOSOL OF PERCAISOMAL MATRIX PROTEINS.

C. TINUCTION: BY OLEIC ACID.
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*PAS3, a Saccharomyces cerevisiae gene encoding a peroxiscmal
integral membrane protein essential for peroxisome blogenesis.
J. Cell Biol. 114:1167-1178(1991).
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Bacteria: Proteobacteria: gamma subdivision: Pasteurellaceae:
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3CDC110336DF0D0F9 CRC64:
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POTENTIAL.
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Ol-NOV-1995 (Rel. 32, Last sequence update)
Ol-NOV-1995 (Rel. 32, Last annotation update)
HYPCTHETICAL PROTEIN HI.458.
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Local Similarity 46.78;
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MEDLINE; 95350630.
                                                                                                                                                                                     SEQUENCE FROM N.A.
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P44204;
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Fairal L., Schabbe J.W.R., Chapman L., Finch J.T., Rhodes D., Fairal L., Schabbe J., and L. Schabbe J., sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptora, Brachycera, Musconorpha,
Ephydroidea, Drosophilidae, Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE, 90107945.
Harrison S.D., Travers A.A.;
Harrison S.D., Travers A.A.;
The tramtrack gene encodes a Drosophila finger protein that interacts with the fiz transcriptional regulatory region and shows a movel embryonic expression pattern.*;
EMBO J. 9:207-216(1950).
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"Trantrack is a transcriptional repressor required for ceil fate
determination in the Drosophila eye.";
Genes Dev. 7:1085-1096(1993).
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01-AC3-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRAMIRACK PROJEIN, BETA ISOFORM (IRAMIRA ' P69) (FUSHI IARAZU
REPRESSOR PROJEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58: UB 1; Length 80;
Pred: No. 2.43e+00:
7: Mismatches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown J.L., Sonoda S., Ueda H., Scott M.P., Wu C.;
Submitted (XXX-1991) to the EMBL/Genbank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                       E43DD2FC77114CDD CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 499-561.
MEDLINE: 94067350.
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                                                                                                                                                                                                                                                                                                                                                                                          i protein.
80 AA: 9400 MW:
                                                                                                                                                                                                                                                                                                                       EMBL: 032824: AAC23113.1; -. IIGR: H11458: -.
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Local Similarity 42.1%;
es 8: Conservative
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                   Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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P17789:
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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MFDLIED: 98065943.
Fraser C.W., Casjens S., Hua: W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchu. K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fle.schmann R.D., Richardson D.,
Peterson J., Kerlavage A., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Jtterback T., Kathrey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch R.,
Smith H.O., Venter J.C.,
Genomic sequence of a Lyme disease spirochaete, Borrelia
SEGMENTATION GENE TRANSC! TION DURING EMBRYOGENESIS. P69 IS REQUIRED TO REPRESS THE L. RESSION OF GENES THAT ARE INCOMPATIBLE WITH THE DEVELOPMENT OF PRIVIORECEPTOR CELL FATES. MAY BING TO
                                                                  -:- SUBGELLULAR LOGATION: NUCLEAR.
-:- SUBGELLULAR LOGATION: NUCLEAR.
-:- ALTERNATIVE PRODUCTS: TWO ISOFORMS, ALPHA AND BETA, AME FRIUNCED:
BY ALTERNATIVE SPLICING OF THE C-TERMINAL DOMAIN.
-:- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT EMBRYGGENESIS. LORING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation: Zinc-finger: Metal-binding: DNA-binding:
                                                                                                                                                              THE FAST PHASE OF GERM AND ELONGATION, THIS FORM IS PRESENT
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15-DEC-1998 (Rel. 37, Last sey-ence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FLAGELLAR BASAL-BODY ROD PROTEIN FLGG (DISTAL ROD PROTEIN).
FLGG OR BB0774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1: Length 641:
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279 H -> Q (IN REF. 2).
4-5 I (IN REF. 2).
69511 MM. B5EB0541281716B8 CRC64;
                                                                                                                                                                                                  SIMILARITY: CONTAINS A N UBMINAL BR-C/TTK DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; 3D-structure; Alternative splicing.
DOMAIN 1 114 BR-C/TIK D-MAIN.
1 20 CBL-TYPE.
ZN_FING 536 559 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrella burgdorferi (Lyme disease spirochete)
Bacterla: Spirochaetales: Spirochaetaceae: Borrella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLYBASE; FBqn0003870; ttk.
PROSITE; PS00028; ZINC_FINGER_C2H2;
PFAM: PF00096; zf-C2H2; 2.
PFAM: PF00651; BIB: 1.
                                                                                                                                                                                                                                                                                                                                                                           EMBL: X17121; CAA3498113; -
EM51: M62856; AAA285441; -
EM51: X71627; CAA56634 1; AUL_INIT.
PTR: S10881; S16881.
PDB: 2DRP: 31-AGG-94.
TRANSFAC; 100943; --
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                                                       THE REGION 5' -GGICCIGC-3'
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Matches 6; Conservative
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536
253
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499
641 AA:
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CONFLICT
CONFLICT
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Local Similarity
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P17555:
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   Best Loc
Matches
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Richinormhius and the EMBL outstation the European Bloinformatics Institute. Insteare no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ္ပ
                                                                        OF
TC
Durgdorferi.";
Nature 390:80-586(1997).

-i- Subunit THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FASBULLAR GRANDLE AND CONSISTS OF FOUR RINGS (L.P.S. AND M.)

ROBELLAR GRANDLE AND CONSISTS OF ABOUT 26 SUBURITS (MOINTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBURITS (MOINTED UP THE PROXIMEL PORTION, AND FIGH, PIGC AND FIGE ARE THOUGHT BUILD UP THE PROXIMEL PORTION OF THE ROD WITH ABOUT 6 SUBURITS FACH (RY SIMILARITY).

-- SIMILARITY: BELONDS 10 THE FLAGELLA SASAL BOUT 30 PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Durmaz E., Historia D.L., Kiaenhammer 1.R.;
Molecular characterization of a second abortive phage resistance among ene present in Lactococcus lactis subsp. lactis ME2.";
J. Bacteriol. 174:746-7469(1992).
-:- FUNCTION: PROVIDES RESISTANCE TO BACTERIOPHAGE BY ABORTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .:
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Plasmid pIN2..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 265;
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Pred. No. 3.75e+00:
5: Mismatches 5:
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01-0CT-1993 (Rel. 27, Last Sequence update)
10-0CT-1993 (Rel. 27, Last annotation update)
ABCRTIVE PHASE RESISTANCE PROTEIN ARIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                    PS00588; FLAGELLA_BB_ROD: 1.
                                                                                                                                                                                                                                                                                                                                                 EMBL: AE001177: AA067132.1: -.
TIGR: BB0774: -.
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Pest Local Similarity 33.3%:
Matches 5: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 DGTYAYTRDGSEKID 123
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PIR; A47025; A47025.
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Q01457:
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MEDLINE: 90235281.
Field J., Voltok A., Ballester R., Bolger G., Colicelli J.,
Field J., Voltok A., Ballester R., Michaell T., Powers S., Micus M.,
Rodgers L., Wieland J., Whelan B., Wigler M.,
"Cloning and characterization : CAP, the S. cerevisiae usine encodin;
"the 70 kd adeny;"J. cyclase-ess clated protein.";
cell 61:319-327(1990).
                             Saro
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                                                                                                                                                                                                                                                                     01-A0G-1990 (Rel. 15, Created)
01-A0G-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ADENVIXL CYCLASE-ASSOCIATED PROTEIN
SRVZ OR CAPI OR YNL130W OR NIZIG OR NI895.
SACCHAROMYCES CEREVISIAG (Bakor's yeast)
Eukarycta: Fungi: Ascomycota saccharomynetes: Saccharomycetaedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fedor-Chaiken M., Doschenes B.J., Broach J.R.;
"SRV2, a gene required for RAS activation of adenylate cypluse
waser ".
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OEB4D41205E2D454 CRC64;
No. 3.75e+00:
Mismatches 3:
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POLY-PRO.
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     Pred.
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277 282 P
526 AA: 57521 MW:
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PROSITE; PS01089; CAP_2;
                                                                          271 GINLFGDEKDFKID 284
                                                                                                                            7 GINIYNNNEAFKVE 20
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SGD: L0002068; SRV2
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MEDLINE: 90235282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
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MEDLINE: 7 Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inda T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Maxino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomira K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Soki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horluchi T., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horluchi T., Saito N., Paris M., Sequence of the Escherichia coli K-12 genome corresponding to the 12 7-28 0 min region on the linkage map.":
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STRAIN-KIZ / MG155:
MEDLINE: 97426517.
MEDLINE: 9742657.
MEDLINE: PALUNKett G. III. Bloch C.A., Perna N.T., Burland V., Blattior F.R., Plunkett G. III. Bloch C.A., Rose C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria: Protecbacteria: gamma subdivision: Enterobacteriaceae:
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                (1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FE5-2000 (Rel. 35, Last annotation update)
HYPOTHETICAL 78-7 XD LIPEPROTEIN IN APPA-CSPH INTERGENIC REGION
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SIGNAL
CHAIN 19 698 HYPOTHETICAL LIPOPROTEIN YMCA.
LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
SECUENCE 698 AA: 78687 MW: 37771D2DC57FA4E7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
Length 526:
                                                                     5; Indels
Score 57; DB 1; L
Pred. No. 3.75e-00;
                                                              7; Mismatches
                                                                                                                                                                                                                                                                                                                                     698 AA
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EMBL: D90735: BAA35749.1: -.
EMBL: D90736: BAA36124.1; -.
ECOGEL: D60736: BAA36124.1; -.
PROSITE: EG13729; YMCA.
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-!- SIMILARITY: STRONG, TO E.CHI YJBH.
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Local Similarity 72.7%:
Ouery Match
Best Local Similarity 40.0%:
Matches 8: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12;
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P75882:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thouring Company of the EMBL/Genback/UCBJ databases.
Submitted (NOV-1997) to the EMBL/Genback/UCBJ databases.
FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CA:ALYZINS THE FIRST REACTION IN THE BIOSYNTHESIS FROM L'PHENYLALANINE OF A WICE VAREETY OF NATURAL PRODUCTS BASED ON THE PHENYLHOPANE SKELETON:
CATALYZIO ACTIVITY L'PHENYLALANINE - TRANS-CINNAMATE - NH(3).
CATALYZIO ACTIVITY L'PHENYLARANINE - TRANS-CINNAMATE - NH(3).
COFACTOR: HAS A DEHYNDRACALNINE (DHA) IN THE ACTIVE SITE
COFACTOR: HAS A DEHYNDRACALNINE (PROBBLE).
SUBCELLULAR LOCATION: CYTOPLASMIC (PROBBLE).
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                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8126.5
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Eukaryota: Fungi; Ascomycota: Schizosaccharomycetales;
Schizosaccharomycetaceae: Schizosaccharomyces.
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ACT_SITE 199 199 BY SIMILARITY
SECUENCE 713 AA: 77732 WW: 7470E6400006A GROGG.
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01-001-1996 (Rel. 34, Last sequence update)
15-FEB-0000 (Rel. 34, Last annotation update)
RENING/THREDMINE-PROTEIN XIX: E MHKI (RC 2.7,-MHKI OR PMKI OR SPACIF3.02C)
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PROSITE: PS00488; PAL_HISTIDASE: 1.
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## SEQUENCE FROM N.A

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Search completed: Mon Jun 19 16:14:43 2000 Joh time : 7 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 15:14:59 2000; MasFar time 9.10 Seconds 152 449 Million cell updates/sec Run on:

Tabular output not generated.

>95-39-142-524A-12 (1-20) from 9S9142524A.pep 125 1 SSGKNEGINIYNNNEAFKVE 20

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Minimum Match Ow Listing first 45 summaries Post-processing:

225878 seqs. 69334122 residues

Sourched:

sptrembl12 Satabase:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_anvertebrate 6:sp_pmammai 7:sp_mhc 8:sp_organelle 5:sp_hage 10:sp_plant 11::sp_rodent 12:sp_unciassified 13:sp_vertebrate 14:sp_v1rus

Variance 35.964; scale 0.738 Mean 26.555; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Cuery	Query Match Length	53	ID	Description	Pred. No.
	125	100.0	375	2	095385	CHAO1 PRECURSOR.	2.25e-15
7	108	86.4	357	10	7UN 260	POLLEN MAJOR ALLERGEN	4.376-11
٣	69	55.2	1198	10	092557	DYNEIN HEAVY CHAIN ISO	4.01e-02
4	63	50.4	397	٣	C08144	CHROMOSOME XV READING	6.52e-01
S	r1 9	48.8	420	7	Q92HI7	NADH OXIDASE (FRAGMENT	1.60e+00
Θ	9	48.0	126	33	073615	TRANSKETOLASE (FRAGMEN	2.48e+00
7	59	47.2	146	~	045841	17 KD HEMAGGLUTININ CO	3.84e+00
œ	93	47.2	346	7	045878	HA17.	3.84e+00
σ.	53	47.2	264	~	083926	FLAGELLAR BASAL-BODY R	3.84e+00
10	59	47.2	298	'n	019058	SIMILAR TO HYDRATASE-D	3.84e+00
Ξ	58	46.4	290	7	Q59078	BETA-AGARASE I PRECURS	5.92e+00
12	58	46.4	379	14	Q9YW42	ORF MSV050 HYPOTHETICA	5.92e+00
13	58	46.4	432	7	087980	HYPOTHETICAL 50.7 KD P	5.92e+00
14	57	45.5	2206	Ŋ	096205	HYPOTHETICAL 264.1 KD	9.07e+00
15	57	45.6	4550	Ŋ	077336	PFC0425W PROTEIN.	9.07e+00
15	57	45.6	4981	S	077372	PFC0820W PROTEIN.	9.07e+00
1.7	56	44.8	163	7	00100	SMFE PROTEIN PRECURSOR	1.38e+01
80	56	44.8	321	σ	Q92XD3	ORF50.	1.38e+01
19	5.6	44.8	334	~	092168	1, 2-DIHYDROXYBENZYLPY	1.38e+01
20	r)	44.8	383	7	09ZNI1	LYIN.	1 386+01

1.386-01	1.38⇔-01	1.386-01	1.386-01		2.100-01	2 10e-01	2.10e-01	2.10e+31	2.10e+01		2.10e+01		2.100-01	2.10e+01	e-4	3.16e+01	3.150-01	3.16e+61	3.16e-01	3.16e+01	3.16e+01	3.160+01	3.164-01	3.16e-01
NADH OXIDASE (FRAGMENT	NADH OXIDASE (FRAGMENT	SE	١.	CTHETICAL	BK150C2.3 (PUTATIVE NO	ENVELOPE GLYCOPROTEIN	MAPK-RELATED KINASE.	HYPOTHETIC	IME MOLD (D	HYPOTHETICAL 70.4 KD P	101 KDA PROTEIN PRECUR	9AA LO	PECO105W PROTEIN.	VARIANT-SPECIFIC SURFA	AARPI PROTEIN (FRAGMEN	HYDRATASE/ALDOLASE PHN	HOLLIDAY JUNCTION HELL	LYSINE-KETOGLUTARATE R	LYSINE-KETOGLUTARATE R	MAL3P4.27 PROTEIN.	PFC0860W PROTEIN.	PREDICTED MEMBRANE ASS	z	STRAIN HB3 CG2 (CG2).
ECH260	C92HJ2	618265	C42GP2	C9X:X2	09Y555	041627	C5XXV2	058209	096849	23898	. 9554	SYF27	C77306	025031	Q9464F	94н260	Q528F3	004884	004 55	9	227:50	096129	•	015792
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5.6	55	55	26	26	55	55	52	55	55	5.5	55	52	55	55	55	V		54	ν •		54	iv 4	54	54
21	22	23	24	25	26	27	28	58	30	31		33	34	35	36	37	38	38	0.4	41	4.2	4 3	44	4.5

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ILSSUE-POLICEN.

MEDINE: 96265194.

SUCHIA N.:

CHIA N.:

CHIA N.:

Parification characterization and molecular clonics of the O.: a major allerges of Chamacyparis obtusa (lapances oppies) pollen.":

MOI. Immunol. 33:451-460(1996).

MANDEL: 7626: Chaobise8:7626.

PRINI: PRO544; pec_lysse: 1.

PRINI: PRO0697; AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Gaps
Ouery Match
100.0%: Score 125; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.25e-15;
Matches 20; Conservative 6; Mismatches 3; Indels
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ID 092NU7

O92NU7:

D 01-NAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-NAY-1999 (TrEMBLrel. 12, Last senotation update)
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: A0981492 CRC32;
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    SEQUENCE
    375 AA;
    40258 MW;

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SIGNAL
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Match 50.4%; Cocal Similarity 53.3%; Res 8; Conservative
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Best Local Similarity 35.38;
Matches 6; Conservative
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                                                                                                                                                                                                                                       342 SGGRNNGSNKYNNDD 356
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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092HI7:
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073616;
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Matches
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                                                                                                                                                                                  "Molecular closing of mountain cedar (Juniperus ashei) pollen major allequen, Jun all.";
substitution all.";
substitution all.";
substitution allegue, to the EMBL/GenBank/DDBJ databases.
EMBL: AF106662: AAC33608.1: -
EMBL: AF106662: AAC33608.1: -
EMBLE: AF106652: AAC33608.1: -
EMBLE: AF106653: AAC33608.1: -
EMBLE: 36544: Juneas.1268.39544.
EMENDEL: 36545: Juneas.1268.39544.
EGUENCE: 367 AA: 39824 WW: 4C209630 CRC32.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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POLLEN MAJOR ALLERGEN 1-2.
Juniperus ashei (Ozark white cedar).
Bukaryotay Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Conlferopsida: Conlferales:
Taxod:aceae: Juniperus.
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Eukaryota: Virdiplantae: Chlorophyta: Chlorophyceae: Volvocaies:
Chlamydomoradaceae: Chlamydomonas.
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Submitted (OCT 1998) to the EMBL/Genhank/DDSJ Gatulases.
EMBL: AFG96277; AAG99457.];
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59: DB 10; Length 1198: Pred. No. 4.01e-02: 10: Mismatches 1: indels
                                                                                                                          SEQUENCE FROM N.A.
MIDORC-HORIUTI T.M., GOLDBEUM R.M., KUROSKY A., WOID T.G.,
BROOKS E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
HUGHES B., POHL T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0928S7 PPELLIMINARY: PRT: 1198 AA.
0128S7-
01-MAY-1999 (ILEMBLEE: 10, Created)
01-MAY-1999 (TEMBLEE: 10, Last sequence update)
01-MAY-1999 (TEMBLEE: 10, Last sequence update)
DYNEIN HEAVY CHAIN ISOFORM DHCIB (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 SSGKIEEINIYNSNEAFKVE 351
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Best Local Similarity 35,3%:
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 REESAKLYKEAEAFKID 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KNEGINIYNNEAFKVE 20
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Xenopus laevis (African clawed frog).
Eukaryota: Metazoa; Chordata: Craniata: Vertebrata: Amphibia:
Batrachia: Anura: Mesobatrachia: Pipoldea: Pipidae: Xenopodinae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ت
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                                                                                                                                      Score 63: DB 3: Length 397,
Pred. No. 6.52e-01:
6: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61: Da 2: Length 420:
No. 1.600+30:
Mismatches 6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN P280/:
STRAIN P280/:
STRAIN P280/:
SUBDITION R. S. STANTON T. B., HAMPSON D.J.;
SUBDITION (APR-1988) to the EM5L/Gombank/DDBJ databases.
EMBL: AFF060815; AAC78824.1: -...
HSSP: P3762: 1JOA. 1
NON_TER 1
NON_TER 420 420
SEQUENCE 420 AA, 46594 MW; TE88D66 CRC12;
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TISSUE=KIDNEY;
SUBMITTED (FEB-1998) to the "BL/GenBank/DDBJ databases.
Submitted (FEB-1998) to the "BL/GenBank/DDBJ databases.
EMBL: AJ24484: CAA11971.1: -..
NON_TER 126 126
  the EMF: /GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-MAY-1999 (TrEMBLrel. 1C, Created)
Ol-MAY-1999 (TrEMBLrel. 1C, Last sequence update)
Ol-MAY-1999 (TrEMBLrel. 1C, Last sequence update)
Ol-MOY-1999 (TrEMBLrel. 12, Lust annotation update)
Setpullina sp. P280/A.
Bacteria: Spirochaetales: Spirochaetaceae: Scrpulina.
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01-A0G-1998 (TrEMBLiel. 07. Last sequence update)
01-A0G-1998 (TrEMBLiel. 07. Last annotation update)
IRANSKETOLASE (FRAGMENT).
Submitted (JUL-1996) to the EMF /GenBank/DDBJ (EMBL: 274766) - 26A990171.1. Submit PF000304; Syntaxin: 1 SEQUENCE 397 AA: 45875 MA: 79FBIA99 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 AA; 13539 MW; B740600F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                     420 AA
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420 AA; 46594 MW;
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SCKNEGINIYNNEAFKV 19

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SEQUENCE FROM N.A.
STRAIN-CC 3.28: (ATCC 43757);
MEDIJEN 98440323.
SANTOS-BUELGA J., COLLINS M.E., EAST A.K.;
Characterization of the genes encoding the botulinum neurotoxin complex in a strain of Clostridium botulinum producing type B and F neurotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saps
                                                                                                                                                                                                                                                                                                                  Gaps
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Clostridium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
       04584] PRELIMINARY: PRT: 145 AA.
045841:
045841:
01.NOV-1996 (ITEMBLEE]: 01. Created;
01.NOV-1996 (ITEMBLEE]: 02. Last sequence update;
01.AUG-1998 (ITEMBLEE]: 07. Last annotation update)
01.AUG-1998 (ITEMBLEE]: 07. Last annotation update)
HEMIZ/B: COMPONENT:
Closticidium botulinum.
Bacteria; Firmicutes; Bacillus/Clostridi m group; Glostridiaceae;
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MEDLINE: 96291660.
MEDERSON I., WHELAN S.M., DAVIS T.U., MINION N.F.:
"Genetic characterisation of the bottlingm toxin complex of clostridium betulinum strain NGTC 2916.";
FEMS Microbiol. Lett. 140:151-158(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB 2; Length 146; Pred. No. 3.84e+00; 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                 Score 59: DB 2: Length 146: Pred. No. 3.84e+00; 4; Mismatches 1: Indels
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-LAMANNA;
YANG G., RHEE S., JUNG H., YANS K.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U2443: AAA99056.1; -.
SEQUENCE 146 AA: 16908 MW: 6150A4C9 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequenc update;
Last annotation update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17034 MW; C1990B1B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AA
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAY-1999 (TrEMBLrel. 10, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT:
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EMBL: 142537; AAB42188.1; -.
EMBL: Y13630; CAA73964.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.3%;
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                  Clostridium.
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045878
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ID 083926
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STRAIN-BRISTOL N2:

MEDLINE; 94150718

A MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., CONBELL M., COPSEY T., COOPER J., COULSON A.,

RA CRATTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

A DONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,

A LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGRAN M.,

A PARSONS J. PERCY C., RIFKEN L., SAUNDERS D., SHOWNKEEN R.,

A MALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

A HIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

A WISSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,

T.2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                  FRASER C. M., NORIS S.J., LEINSTOCK G.M., WHITE G., SUITON G.G., DODSON R., GWINN M., HICKEL E. K., CLAYION R., KETCHUK K.A., SODERGREN E., HARDHAM J.M., E. LEOD M.P., SALZBERG S., PETERSON J., KHALAK H., RICHARDSON D., HOWILL J.K., CHIDMARARAM M., CITERRACK T., MCDONALD L., ARTIACH P., BGWKNN C., COITON M.D., FUJII C., GARLAND S. VENTER J.C.,
                                                                                                                                                                                                       FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUITON G.G., DODGON R., GWINN M., HICKEY E.K., CLATION R., KEICHMM K.A., SODERGEN E., HARDHAM J.M., MOLECO M.P., SALZBEKG S., TETERSON G., KHALMK H., RICHREDSON D., HOWELL J.K., CHIDAMBARAM M., UITERREAUX I., MODONALD L., ARZIACH P., BOWMAN G., COITON M.O., FUJI C., GARLAND S. HAICH B., HORSI K., ROBERTS K., WAITHEY L., MEIDMAN J., SMITH H.).
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Rhabditina: Rhabditoidea: Rhabditidae; Peloderinae: Caenor:atditis
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                                                                                                                                                                                                                                                                                                                                          Complete genomé sequence of Freponema pallidum, the syphilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1998) to the 'MBL/Genbank/DDBJ databases.
EMBL: AEC01264: AAC65915.1;
TIGR: TP0956;
PFAM: PF00450; t1g_bb_rod: 1
                                                                                                            Treponema pallidum.
Bacteria, Spirochaetales: Spirochaetaceae: Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (IrEMBLrel. 01, Greated)
01-NOV-1996 (IREMBLrel. 01, Last sequence update)
01-NOV-1999 (IREMBLrel. 12, Last annotation update)
SIMILAR TO HYDRATASE-DEHYDROGENASE-EPIMERASE.
              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, 13st sequence update)
01-NAY-1999 (TrEMBLrel. 10, 1st annotation update)
FLAGELIAR BASAL-BODY ROD PK: EIN (FLGG-1).
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Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Science 281:375-388(1998).
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                                                                                                                                                                                           MEDLINE; 98332770
                                                                                                                                                                                                                                                                                                                                                                    spirochete."
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Virol. 73:533-552(1999).
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                                                                    STRAIN-TUCSON:
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GUAN C., RIGGS P.D., BENNER J.S., ZBOU P. CHOU D., HALL I.S.,
GUAN C.P.,
SLAMITHOG C.P.,
SLAMITHOG C.P.,
- CATALYTIC ACTIVITY: HYDROLYSIS OF 1.'-BETA-D-SALACTOSIDIC LINKAGES
IN AGAROSE, GIVING THE TETRAMER AS THE PREDOMINANT PRODUCT.
BMBL: M73783: AAA918891...,
SIGMAL
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Entomopoxvirus B.
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MEDLINE: 99102612.
AFDLINE: 99102612.
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
The genome of Melanoplus sanguinipes entomopoxvirus.":
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01-NCV-1996 (TERMELTEL CL. Created)
01-NCV-1996 (TERMELTEL CL. Created)
01-NCV-1996 (TERMELTEL CL. Last sequence update)
01-NCV-1996 (TERMELTEL CL. Last annotation update)
BETA-AGARASE : PRECURSOR (EC 3.2.1.81)
Altercomonas allantica (Pseudomonas atlantica).
Bacteria: Proteobacteria: gamma subdivision: Alteromonadaceae:
Pseudoalteromonas.
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                                                                                                                                                                                                                                                                                                                                      Cuery Match
47.2%; Score 59; UB 5: Length 298;
Best Local Similarity 36.8%; Pred. No. 3.84e-00;
Matches 7; Conservative 7; Mismatches 5: Indels
                                                                                                                                                                                                                           Submitted (JUN-1995) to the EMBL/Genbank/JDBJ databases EMBL, 1028943; AAA683581; PFAM: PFO1575; MAGC-11ke; SEQUENCE 298 Ab; 32721 MW: F564B8FE CRC32;
                                                                                                                 Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
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Orwar-1999 (IrEMBLrel. 10, Created)

Ol-MAY-1999 (IrEMBLrel. 10, Last sequence update)

Ol-MAY-1999 (IrEMBLrel. 10, Last annotation update)

OR MSV050 HYPOTHETICAL PROTEIN.

MSV050

Melanoplus sanquinières entomopoxvirus
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Nature 368:32-38(1994).
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                                                                                                                                                              SECUENCE FROM N.A. STRAIN-BRISTOL N2: WATERSTON R.;
                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2:
PAULEY A.:
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MEDLINE: 99021743.
GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L.,
GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., PEDERSON J.,
SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,
SALZBERG S., ZHOU L., SUTTON G.G., CLAYTON R., WHITE C., SMITH H.G.,
FRASER C.M., ADAMS M.D., VENIER J.C., HOFFMAN S.L.;
FChicomosome 2 sequence of the human malaria parasite Plasmodium.
falciparum.";
                                                                                                                                                                                                                                   Sing
                                              AFONSO C.L. TULMAN E.B., LU , OWA E., KUTISH G.F., ROCK L.L. SUBmitted (MAY-1998) to the E.BL/GenBank/CDBJ databdases.
EMBL: AF063866: AAC97519.1; - SEQUENCE 379 Aa: 43956 MW: 70041767 GRC32.
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Eukaryota: Alveolata: Apicomplexa: Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Proteobacteria: beta subdivision: Alcaligenaceae:
Bordetelia:
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                                                                                                                                                                                                                                   2: Indels
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SIEVENS K., CHURCHER C.M., BADGCCK K.L.;
Submitted (AUG-1998) to the EMPL/Genbarx/filb; databases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARKHILL J., PRESTON A., MASKELL D J., FARRELL B G.,
Submitted (AUG-1998) to the EMBL/SenBank/CDBJ databases
EMBL, AJO07747; CAA07646.1;
                                                                                                                                                                          Query Match
Best Local Similarity 62.5%; Pred. No. 5.920-00:
Matches 8: Conservative 3: Mismatches 2: Inde
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01-NCV-1996 (TEMBLrel. 08. Last sequence update)
01-NCV-1998 (TEMBLrel. 08. Last annutation update)
HP2CHESICAL 50.7 XD PROTEIN.
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01-MAY-1999 (TEMBLEEL: 10, Created)
01-MAY-1999 (TEMBLEEL: 10, Last sequence update)
01-MAY-1999 (TEMBLEEL: 10, Last sequence update)
HYPOTHETICAL 264:1 KD PROTEIN.
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SEQUENCE 432 AA: 5074+ MW: 4789EB34 7PGYZ:
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Best Local Sicilarity 40 0%.
Matches 6: Cousestative
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Pred. No. 9:07e+00;
6: Mismatches 3; Indels 0;
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O77336 O77336 O77336
O77336 O77336
O77336 (TEMBLE) 08, Created)
O1-NOV-1998 (TEMBLE) 08, Last sequence update)
O1-NOV-1999 (TEMBLE) 12, Last annotation update)
PPCG4258 PROTEIN.
Plasmodium falciparum.
Exaryota: Alveolata: Apicomplexa; Haemosporida: Plasmodium.
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Pred. No. 9.07e+00;
9: Mismatches 4: Indels
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EMBE: AE001403; AAC71901.1; -. Hypothetical protein. SEQUENCE 2206 AA: 254100 MM: AEE13480 CRC32:
                                                                                                                                                                                                 Query Match
Best Local Similarity 35,7%;
Matches 5: Conservative
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Best Local Similarity 18.6%;
Matches 3: Conservative
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Search completed: Mon Jun 19 16:15:11 2000 Jcb time : 12 secs.

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Release 3.1A John F. Collins. Biocomputing Research Unit. Copyright (c) 1993-1998. University of Edinburgh. U.K. Distribution rights by Oxfort Molecular Ltd.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:17:34 2000; MasPar time 3.82 Seconds 80.637 Million cell updates/sec Sam on:

Tabular output not generated.

>US-69-142-524A-13 (1-13) from US09142524A.pep 94

Description: Perfect Score: Sequence:

: VFIKRVSNVIIHG 13

PAM 150 Gap 15 Sporing table:

188963 seys, 23686106 residues

Searched:

Minimum Match 3% Listing first 45 summaries Post-processing:

a-deneseq35 ligeneseqp Satabase:

scale 0.322 Variance 56.950; Mean 18.336: Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Pred. No.	2.88e-03	2.88e-03 2.88e-03 3.88e-03		2.86e-03			7.22e-02 2.12e+00	2.12e+00 3.51e+00	7.46e+00	7.46e+00	1.57e+01 1.57e+01
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SUMMARIES	R89291 R45552	~ ~	1 EU EU	CO LC	R31937 R82490	R45541 R60166	W57750 R45553	R82502 R45578	W57751 W27372	W27373	
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paris ob inase-in talls gl talls gl	Babesia microti antige Hepatitis C virus isol Hepatitis C virus enve Spider venom FIL-376 M Mycobacterium tubercul	Mycobacterium tubercul Mycobacterium tubercul M. tuberculosis imeuno Staphylococcus aureus PSDF (WDPP) protein in Omega-cyclobexane fatt	Staphylococcus aureus Staphylococcus aureus E. coli heat shock pro Photorhabdus luminesce Toxin IccB, encoded by
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ALIGNMENTS

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Japanese cedar pollen allergen Cryj I derived T-cell epitope peptide.

Japanese cedar pollen allergen: Cryj I: T-cell epitope; peptides:

Wevention; treatment: cryptomeria pollenosis.

Cryptomeria japonica.

JOT18295-A.

JOT18
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13-JUL-1994 (first entry)
Cry J. pollen allergen pepti je CJI-11.
Japanese cedar: detection: a.ergy: treatment: diagnosis:
I cell epitope: sensitivity.
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15-JAN-1993: U00139.
10-JUL-1992: WG-U05661.
01-SEP-1992: U9-388990.
(IMMU-) IMMULOGIC PHARM CORP.
Bond JF, Garman RD, Griffith IJ, Kuo M, Pollock J:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94: DB 1: D
Pred. No. 2.88e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
I
R89291 standard: peptide: 15 AA
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O
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R45552 standard; Protein; 20 AA.
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Local Similarity 100.0%;
Res 13: Conservative
                                                      R89291;
12-MAR-1995 (first entry)
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WO9401560-A.
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from different allergens
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10-MAR-1997: J00740.
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                                                                                                                                                                                                                                                         8 VFIKRVSNVIIHG
                                                                                                                                                                       30 AA:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified Cryptomoria japonica (Cry j) I peptide(s) - useful for treuting altergy to japonese cedar pollon illergen of the folloning altergen of the folloning section of the folloning section is a section of the folloning section scheme to develop an optimized and into the preference to section scheme to develop an optimized section action scheme to develop an optimized drue product for the rapecular treatment of humans suffering from allergy to Japanese cedar pollen altergen or an altergen which is imminologically cross freative with Japanese cedar pollen altergen. Such modified peptides possess certain characteristics which render them particularly suitable for drug product formulation. Prepride frauments of Cry J. modified and unreditied are given in Re2491 Re2518. This peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                            allergy claim. In 13: 137pp; Enailsh.
The sequence is that of an isolated peptide of the Japanese cedar. The sequence is that of an isolated peptide of the peptide, CJI-11. can be used for the freatment and diagnosis of allergies associated with Japanese cedar polien. It has enhanced therapeitic properties but reduced side effects compared to naturally occurring allergens. Sequence
                                                                                                                                                                                                                                                                                                                                                 Cry j I Japanese Cedar pollen allergen peptide fradment (CJI-11).
Cry j I: japanese Cedar pollen allergen: modified: drug production:
allergy: Cryptomeria japonica.
Crytpomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment corresponds to amino acids 191-126 of the allergen mature
WPI; 94-035066/24.
Antigens derived from Japanese cedar pollen allergen Cry j I -
contain at least two I cell epitope(s), used to treat or diagnose
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Pred. No. 2.88e-03;
                                                                                                                                                                     Score 94: DB 1/ Length 20: Pred. No. 2.88e-03: C: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-M/Y-1998 (first entry)
Theel epitope peptide #2 of sugi pollen antigen.
Theeli epitope: sugi pollen antigen: sigi pollinosis.
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POWers SP.
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W44683:
                                                                                                                                                                                                                                                                                                      I 3
R82501 standard: Protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             66-APR-1995; U04249;
08-APR-1994; US-226248;
06-DEC-1994; US-35C225
(IMMU-) IMMULONIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    udery Match
Hest Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                          CLERY Match 100.0%, Hest Local Similarity 100.0%; Matches 13: Conservative
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                                                                                                                                                                                                                                               1 VFIKRVSNVIIHG 13
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J10001700-A.
13-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 95-366391/47
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24-JUN 1996; JP-163287.

24-JUN 1996; JP-163287.

(MELJ ) DATCEL CHEM IND LTD.

(MELJ ) BATCEL CHEM IND LTD.

(MELJ ) BATCEL CHEM AISHA LTD.

(MELJ ) 8-133630/13.

T cell epticope peptide of sugi polien antiaen - useful in the ireatment of sugi pollinosis.

T cell epticope peptides (44682-88 and their derivatives react with sugi pollinosis patient peripheral blood T lymphocytes. A composition prepared by combining at least 2 of the above peptides and/or their derivatives, is used for the prevention and ireatment of sumi pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be used to prevent and treat a wide variety of alieraic diseases, e.g. by desensitisation. Side effects, e.g. those rediated by Tab. are induced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6. Page 31. 58pp. Jepan. c.
The present sequence represents a multi-epitope peptide which is used as new immunotherapeutic agent. It comprises T cell epitope requois from 2 or more different allergens (preferably) linked via archinne of ysine dimers), where the T cell epitope regions: have a positivity index allergen. To cell epitope regions: have a positivity index allergen. have at least T 08 eventivity with ymphosytes from patients responding to the responding to the allergen. But and are not reactive with immunoal billin E (192) antibodies from patients responsive to the allergen. The Jernin can
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Multi-epitope peptide used as immunotherapeutic agent #1.
Multi-epitope peptide; immunotherapeutic agent; allergic disease:
T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
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Multi-epitope peptide used as immunotherapeutic agent #2.
Multi-epitope peptide immunotherapeutic agent; allergic disease;
T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
Syntheric.
W99732600-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI: 97-477495/43.
Peptide is unostherapeutic acent to freat alloraic diseases contains multi-epitope peptide containing is cell epitope fedious
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Pred, No. 2.886-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 1; Le
Pred. No. 2.89e-03;
0: Mismatches 0:
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(MEIP ) MELCI MICK PROD CO LTD.
Dairiki K, Iwama A, Kino K, Kume A. Sone T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 6
W27376 standard; peptide: 105 AA.
W27370;
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Local Similarity 100.0%:
nes 13: Conservative
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Local Similarity 100.0%;
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12-MAR-1996 (first entry Japanese cedar polien alletan Cryl I. Japanese cedar polien alletann. Cryl I. Ticell epitope: peptides: prevention: treatment: cryptomeria pollinosis. Cryptomeria Japonica.
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/note= "I-cuil epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -cell epitope
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08-SEP-1995: 306295.

10-SEP-1994: JF-220137.

14-JUL-1995: JP-20021.

14-JUL-1995: JP-200204.

(HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                 Location/Qualiters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R81587;
R61587;
24-MAY-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEIP.) MEIJI MILK PROD CO LT. WPI; 95-203834/27.
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Best Local Similarity 100.0%;
Matches 13; Conservative
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/note= "I-...
211.
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106. .120
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20-CCT-1993: 262625.
20-CCT-1993: JP-2626
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WPI: 96-140976/15.
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            NO COCCOCCO SERVICE SE
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                                                                                                                                                                                                                                                                                                              The present sequence represents a multi-epitope peptide which is used as a new lammachterapeutic agent. It comprises I cell epitope regions from 2 or move different allergents (I comprises I cell epitope regions from 2 or move different allergens (Preferably linked via arginine or lysine dimers), where the I cell epitope regions; have a positivity index director have at least 70% reactivity with lymphocytes from patients responding to the allergen; and are not reactive with immunoquobulin E (IGE) antibodies from patients responsive to the allergen. The agent can describe the patients responsive to prevent and treat a wide variety of allergic diseases, e.g. by desensitisation. Side effects, e.g. those mediated by IGE, are reduced. Sequence 105 AA:
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2(MEIP) MEIJI MILK PROD CO LTD.

Dairiki K. Iwama A. Kino K. Kume A. Sone I:
WPI: 97-470495743.

Peptide immuno:therapeutic agent to treat allergic diseases -
contains multi-epitope peptide containing I cell epitope regions
from different allergens.
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Hest Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1997.
10-MAR-1997; J0074G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09732600-A1.
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G G Š

n. 8 R75388 standard: protein: 353 AA. R75388:

RESULI ID R7 AC R7

Matches

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5
                                                                                                                                                                                                                                                                                                                                                                                                         prevention, treatment and investigation of Japanese cedar pollenosiss Disclosure: Figs 1-2: Bpp: Japanese. R75388 is the Japanese cedar rollen allergen Cryj I, from which the T-cell epitope peptides R892. R89255 were derived. The peptides Can be used for the preventics and treatment of cryptomeria pollenosis, and also for the investigation of pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide(s) derived from cedar pollen allergens - activate allergen-specific T-cells, but not allergen-specific IgE antibodies, used for treating cedar pollinosis.

Claim 5: Page 31-32: 36pp; English.

Synthetic peptides based on portions of cedar pollen allergens A (R81586) and B (R81587) were tested for their ability to activate cedar allergen-specific T-cells, but not allergen-specific IgE antibodies. 6 Peptides (R81580-R81585) were identified as T-cell epitopes. These peptides, plus subsequences (R81573-79) essential for T-cell recognition, and homologous peptides (R81588-95) can be used as immunotherapeutic agents to treat or prevent cedar pollinosis, avoiding side-effects such as anaphylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sars
                                                                                                                                                                                                                                                                                                                                                                                    New cryptomeria pollen allergen T-cell epitope peptide - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cedar pollen allergen B. Cedar pollen allergen B. Cedar pollen. allergen: Immunosiokolin B. 1985 Theeli epitope: antibody: pollinosis: therapy: Ambanocherapy. Cryptomeria japonica. EP-700929-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                  /note="T-cell epitope peptide"
146, .160
                                                                                                                                                       /note="T-cell epitope peptide" 335, 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1red. No. 2.88e-53;
                                                                                                                                  11 epitope peptide
                                                                                                                                                                                                                       /note= "I-cell epitope peptide"
"I-cell epitope peptide"
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W09401550-A
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ID R6
AC R6
DT 24
DE J6
KW J6
CS C:
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Fresh pollen and staminate cone samples were collected from a single Cryptocorial approvice (Japanese cedar) tree. RNA was prepd. and used to synthesise cENA. The subjected to successive rounds of PCR to yield a full length Cry 3 I alone. Cry 3 I or an antiqenic fragment of it may be used for detecting, treating and preventing an aileror response to Japanese sedar pollen allargen. It is capable of modifying both the B and I cell response to a Cry 3 I and 7 cell response to a Cry 3 I and 7 cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-Apk-1996 (first entry)
Cry ] Japanese Cedar pollen allergen.
Cry ] I 'spacese Cedar pollen allergen: modified: drug production:
allergy. Cryppmeria japonica.
Cryppmeria japonica.
19-cor-1995.
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                            pollon; allergen; antigen; allergy: B cell; I cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN 1993.

21-JAN 1993.

10-JUL 1991: US-729134.

12-JUL 1991: US-730452.

15-JUL 1991: US-730452.

15-JUL 1991: US-730452.

BOND US- CTIFITL IC. POLLOCK J:

WPI; 93-045434405.

N-PSDB: Q35304.

N-PSDB: Q35304.

10-The diagnosis treatment and prevention of allergen reactions to Japanese codar pollen
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                     Score 94: DB 1: Lenath 50:,
Pred. No. 2.98e 03:
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                                                                                                                                                                                                                                                                                                                                                                                                         /sote~ "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                "mature Cry j I"
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                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R82490 standard; Protein: 374 AA.
R82490
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R31937 standard: Protein: 374
R31937:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 190.0%; todal Similarity 100.0%; test 13; Conservative
                                    Cuery Match
Best Local Similarity 100:0%;
Matches 13: Conservative
                                                                                                                                                                                                                                                                                     03-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            174
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08-APR-1994; US-226248;
06-DEC-1994; US-350225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
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                                                                                                                      108 VFIKRVSNVIHG 120
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                                                                                                                                                            1 VEIKRVSNVIJHG 13
                                                                                                                                                                                                                                                                                                                                               japonica.
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N-PSDB: T04248.
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6.00
                                                                                                                                                                                                                                                                                                        Cry ) :
Japanese cedar
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Sequence
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Modified Cryptomeria japonica (Gry j) I peptido(s) - useful for treating allergy to japanese cedar pollen allergen or immunologisally cross reactive allergens
Disclosure: Flgure 1: 60pp: English.
Novel peptides of cry j I have been modified as a part of a preformulation scheme to develop an optimised drug product for therapeutic treatment of human suffering from allergy to Japanese cedar pollen allergen on an ai ergen which is immunologically cross reactive with Japanese cedar pollen allergen. Such modified peptides possess certain characteristics which render them particularly modified and unmodified, are given in R82491-R82525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saps
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Japanese cedar pollen antigen Gryjl.
Japanese cedar: pollen antigen: allergen: Cryjl: sugi: polinnosis.
Cryptomeria japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigens derived from Japanise cedar pollen alleraed fry ) in contain at least two T cell Pytope(s), used to treat or distances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The segmence is that of the Japanese codar polled allergon crys 1 with contains at last two left periopses. Perhiduantians drived from the used for the treatment and diagnosis of allergates associated with Japanese cedar polled. The populdes have enhanced therapeutic properties but reduced
                                                                                                                                                                                                                                                                                                                                                                                                               Length 374;
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Pred. No. 2.88e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alleray: treatment: diagnosis:
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 94: DB 1: 1A
Pred. No. 2:88e-03;
0: Mismatches C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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The segmente is that of the Japane
Cry J I which contains at the Japane
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R45541 standard; Protein; 374 AA.
R45541;
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R60166;
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Bond JF, Garman RD, Griffith
WPI: 94-035066/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cry 3 I pollen allergen."
Japanese cedar, detection: a
T cell epitope, sensitivity.
Cryptomerla japonica.
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Best Local Similarity 100.0%;
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Local Similarity 100.0%;
les 13; Conservative
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01-SEP-1992; US-938990.
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15-JAN-1993; U00139.
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MODELLY 1998.

This MELLI MICK PRODUCTOR.

This MELLI MICK PRODUCTOR.

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                                                                                                                                                                                                                                                                                             Sign (Japanese cedar) police antique Cryll 'is useful for diagness. Tredement and prevention of sugi pollinosis claim. I part 5-7, ppp: Japanese.

Cryll was sequence for the Japanese cedar (Sugil) pollen alleraen Cryll was isolated from a cENA library propared from polyA mRNA. All or pert of the Cryll protein can be used for diagnosis, treatment sequence. (3 sugi pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saps
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Residurs 165-120 of Cry 3 a.
Cry 3 l. Japanese cedar pollen antiden: allergy: immunotherapy:
HLA class II molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94: 03 is Length 374: Pred. No. 2.88e-03: 0: Mismatches 0: Indels
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Pred. No. 7.22e-02;
0; Mismatches 1;
                  1. .21
//abel-signal_peptide
22. .374
                                                                                                /label- mature_Cry);
Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; peptide: 15 AA
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larity 52.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Juery Match
Best Local Similarity 10%,0%;
Matches 13; Posservative
                                                                                                                                                                                                                                SEIKA KAISHA
                                                                                                                                                                                                07-CAN-1993; UP-001116.
(MEIC ) MEICE SEEKA KAE
WPE: 94-268687/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 VETKRVSNVT18G 141
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Rest Local Similarity
These 12, Conserv
                                                                                                                                                                                                                                                     WPI: 94-268687
N-PSDB: Q71601
                                                                                                                                                        19-JUL-1994
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W57750...
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Gaps

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1: Indels

.I :: R45553 standard: Protein: 20 AA. R4555+;

RESULT IC R4 AC R4

T VFTKRVSNVIIHG 13 3 VETKRVSNVTHHG 15

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allergy Claim 1: Fig 13: 137pp; English.

Allergy Claim 1: Fig 13: 137pp; English.

The sequence is that of an isolated peptide of the dayness redain poller allerge in the readence of the peptide. (23:12:13), the peptide. (23:12:13), the peptide. (23:12:13), the peptide of the readence; and disansis of allergies associative with Japanese sedar poller. (3: has enhanced therapeutic proportions but reduced side effects our read to naturally occurring allergency sequence 20 AA:
                                                                                                                                                                                                                                                                  Antiques derived from Japanese reda: politen allerges (19.5) decenais at least two 1 cell epitope(s), used to freat of discuss-
13-JUL-1994 (first entry)
Cry ] I pollen allergen peptide CJI-12.
Japonese cedar: detection: allergy: treatment: diagnosis:
I cell epitops: sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match 73.4%, the 69, 08-1, Lebath 20, Best Local Similarity 100.0%, Pred. No. 2 12e-60, Matches 10, Conservative 1, Mismutches 0, Indois Matches
                                                                                                                    20-JAN-1994.
15-JAN-1993: UG0139.
31-SEP-1992: WO-095661.
31-SEP-1992. US-946990.
(IMMN3-1 IMMULOGIC PHARM CORE
Bond UF, Garman RD, Griffith, IX. Kuo M. Followk J. WPI: 94-035066/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Mon Jun 19 10:17 40 _{\rm 2000} Job time : 6 secs.
                                                                               Cryptomeria japonica
W09401560-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I KRVSNVIIHG 10
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4 KRVSNVIIBG 13
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein protein database search, using Smith-Waterman algorithm

Tue Jun 20 13:37:24 2000; MasPar time 2.28 Seconds 82.449 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-13 (1-13) from US09142524A.pep 94 1 VFIKRVSNVIHG 13 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

145341 seqs, 14437480 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_CCMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Mean 17.285; Variance 56.805; scale 0.304 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or egual to the score of the result being printed, and is derived by analysis of the total score do tribution.

STIMVARIES

		ø			SUMMARIES			
Result		Suery						
C	Score	Watch	Length:	e a	CI	Description		Pred. No.
-	, w		255		US-08-459-	Seguence 4.	Applicatio	3.666-01
~	56	Ġ,	255	٠.	US-08-459-	₹,	Applicatio	3.556-01
œ	56	er.	408	~	US-09-120-	6.4	Applicatio	3.56e-01
77	55	59.6	408	~	US-08-926-	7		3.66e+01
S	52	'n	192	•3*	PCI-1895-1	80	, Applicati	
9	52	55.3	192	٠,٠	US-08-086-	80	. Applicati	9.20e+01
7	25	S.	192	~	.08	80	, Applicati	9.20e+01
œ	32	Š	192	7	US-08-458-	Seguence 80,		
Q,	51		295	7	US-08-504-		, Applicati	. 16
10	5.	54.3	297	~	US-08-504-			1.16e+02
11	51		625	۲,	80			1.16e+02
12	20		316	7	US-08-846-	Seguence 9,	Applicatio	1.45e-02
13	90	53.2	317	٣	US-08-951-	Sequence 2,	Applicatio	1.45e-02
14	20	₩.	317	7	ns-06-066-	Seguence 2,	Applicatio	1.45e+02
15	50		317	~	US-08-518-	Sequence 2,	Applicatio	1.45e+02
16	50		806	7	US-08-249-	Sequence 2,	Applicatio	1.45e+02
17	67	ζ.	299	7	US-09-504-	Sequence 10,	, Applicati	1.81e-02
18	48	51.1	85	~	US-08-659-	Sequence 3,	Applicatio	2.27e+02
19	87	ä	85	7	US-08-480-	Sequence 3,	Applicatio	
20	8 7	51.1	111	-	US-08-111-	Sequence 23,	٠.	2.27e+02
21	8 7	51.1	160	~	-08-16	7		_
22	87		218	~	-03	Sequence 4,	Applicatio	2.27e+02
23	φ 37	51.1	218	-	US-01-601-	Sequence 4,	Applicatio	2.27e+02

Sequence 2, Applicatio 2.27e-02 Sequence 14, Applicatio 2.27e-02 Sequence 14, Applicati 2.27e-02 Sequence 14, Applicati 2.27e-02 Sequence 14, Applicati 2.27e-02 Sequence 2, Applicati 2.27e-02 Sequence 2, Applicatio 2.27e-02 Sequence 4, Applicatio 2.27e-02 Sequence 4, Applicatio 2.27e-02 Sequence 4, Applicatio 2.27e-02 Sequence 40, Applicatio 2.27e-02 Sequence 40, Applicatio 2.27e-02 Sequence 40, Applicati 2.83e-02 Sequence 40, Applicati 2.83e-02 Sequence 40, Applicati 2.83e-02 Sequence 40, Applicati 2.83e-02 Sequence 2, Applicati 2.83e-02	; 255 AA.	S AND AMING ACID SEQUENCES ETA-LACTAMASE ENZYMES FROM BACTEMOIDES	S 0, Version #1.30 264 18026-US3
		ACID S SE ENZY	1.3
	د س	AND AMENO A-LACTAMA	Version
357 1 US 08 356 400 2 US 08 474 400 1 US 08 474 400 1 US 08 488 400 1 US 08 486 407 2 US 08 986 432 2 US 08 986 432 2 US 08 986 432 2 US 08 986 432 2 US 08 986 430 2 US 08 8471 410 2 US 08 471 410 2 US 08 471 449 2 US 08 471 449 2 US 08 471 449 2 US 08 471 462 2 US 08 471 463 US 08 471	ENTS PKT 554	JENCES S B BE'S S C C C C C C C C C C C C C C C C C C	6.5.005 8.1.0 459,2 459,2
24		Patent No. 570534 GENERAL INPORMA APPR JANT: TI APPL JANT:	CCAPUTER REACABLE FCRM: MEDIUM TYPE: Floppy disk OMEDIUM TYPE: Floppy disk OMEDIUM TYPE: Floppy disk OMEDIUM TYPE: Propertib: OPERATING SYSTEM: PC-DOS/N SOFTWARE: PATCHIA REPLEATION DATA: APPLICATION NUMBER: US/CB, FILING DATE: QS-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: MAME: RODAISON: JOSEPH R REFERENCE/DOCKET NUMBER: 33,44 REFERENCE/DOCKET NUMBER: GTLECOMMUNICATION INFORMATION TELEPHONE: 212-527-770 TELEFAX: 216697 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTER:STIGS: LENGTH: 255 amino acids TYPE: amino acid
นี้พี่พี่พี่พี่พักกักกักกักกับสุดสุดสุด	70.8	888888888888888	888888888888888888888888888888888888888

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OPERATING SYSTEM: COSPATILLE OPERATING SYSTEM: COSPUSSOR SOFTWARE PATENTIA FASE #1.0.

CURRENT APPLICATION DA APPLICATION NUMBER: 05/09/120.05/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
FENCE 468 AA: 43042 MW: 779745 CN:
                                                                                                                                                                                                                                                   1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926,256
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09120053
Patent No. 5932464
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/0912905*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 46285
CCMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEGISTANTION NOMBER - 4. P. HERERENELY STATE NORMER - P. HELECOMMUNICATION INFORMATION TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION NAME: Webster, Thomas L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 408 amino acids
amino acid
                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 317-276-333
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8%;
Matches 7: Conservative
                       Query Match 59.5%;
Best Local Similarity 70.3%;
Matches 7; Conservative
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                                                                                                           103 FOKRVTDVII 112
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                                                                                                                                          2 FIKRVSNVII 13
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ID US-08-926-258-2
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                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                 Patent No. 579262

SENERAL INFORMATION:
APPLICANT FASMUSSEN, Beth A
APPLICANT FALLY, Francis P
APPLICANT TALLY, Francis P
APPLICANT TALLY, Francis P
APPLICANT TALLY, Francis P
TITLE OF INVENTION: OF CLASS B BETA-LACTAMASE ENZYMES FROM BACTEROIDES
TITLE OF INVENTION: OF CLASS B BETA-LACTAMASE ENZYMES FROM BACTEROIDES
TITLE OF INVENTION: OF CLASS B BETA-LACTAMASE ENZYMES FROM BACTEROIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE: 9
CORRESPONDENCE: 9
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COMPUTER READABLE FORM:

MUDIUM TYPE: FIGEPY disk

CONFUTER: INP COMPUTED:

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IMMEDIATE SOURCE:
CLONE: B-LGATAMASE
JENCE 255 AA: 27847 MW: 349604 CN:
                                                                                    ORGANISM: Bacillus cereus
IMMEDIATE SOURCE:
CLONE: B-LACIAMASE
SECUENTE 255 AR: 27647 WW: 349604 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08459263
Patent No. 5792642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4. Application US/08459263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Darby & Darby PC : 805 Third Avenue New York
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
  STRANDEDNESS: Single
TOPOLOGY: linear
MCLECULE TYPE: peptide
ORIGINAL SCURCE:
                                                                                                                                                                                                Cuery Match
Hest Local Similarity 70.0%;
Matches 7: Conservative
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                                                                                                                                                                                                                                                                                                                            2 FIKRVSNVII II
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STREET: 80
                                                                                                                                                                                                                                                                                                                                                                                                         LT 2
US-08-459-263-4
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SEQUENCE 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Richard H.
APPLICANT: Teadway, Parti J.
ITLE OF INVENTION: Glucosylltansferuse Sene utfE From IIILE OF INVENTION: Amycolatopsis urientalis NUMBER OF SEQUENCES: 3 NUMBER OF SEQUENCES: A SECRESSONDENCE ADDRESS: ADDRESSEE: Lilitilly and Company STREE: Lility Corporate Gener STATE: Indianapolis STATE: Lidanapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
O
Length 255:
Score 56; DB 1; Length 255;
Pred. No. 3.66e+01;
2: Mismatches 1; Indels
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Pase #1.0, Version #1.50
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Px d. No. 3.66e+01;
4: Mismatches 2;
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TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSE: ADBRESSE: APRGAN & FINNEGAN
SIREET: 345 PARK AVENUE
CITY: NEW YORK
SIATE: NEW YORK
COUNTRY: USA
ZIP: 10:154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANCLEOTIDE AND DEDUCED
ANION ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ore 52: DB 4: Length 192; ed. No. 9.20e+01; 5: Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 80, Application US/08086428B
PATENT NO. 5514539
GENERAL NO. 5514539
GENERAL BUKH, J., MILLER, R.H. AND
APPLICANT: BUKELL, P.H.
ITLE OF INVENTION: WJCLEOTIDE AND DEDUC
TILE OF INVENTION: AMINO ACID SEQUENCES
ITLE OF INVENTION: OF 51 ISOLATES OF HE
ITLE OF INVENTION: OF 51 ISOLATES OF HE
ITLE OF INVENTION: DIAGNOSTIC METHODS AND MUMBER OF SEQUENCES: 159
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DAIE: 15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
00760 CN;
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NOWBER: 68/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUG.S. 1994
ATTCRNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8C, Application US/08085428B
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NC: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homosapiens
INDIVIDUAL ISOLATE:
NCE 192 AA: 20855 MK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unknow:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPCLOGY: unknown ORIGINAL SOURCE:
                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 YVMRVPEVII 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FIKRVSNVII 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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NUCLEOTIDE AND DEDUCED
AMINO ACID SECUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                             Patent No. 5871993
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Soleoberg, Patricia J.
APPLICANT: Treadway, Patri J.
TITLE OF INVENTION: Glucosyltransferase Gene qifE From III.E OF INVENTION: Arycolatopsis orientalis NUMBER OF SEQUENCES: 3
CORRESPONDENCE AUGUSTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 2; Length 408;
Pred; No. 3.66e+01;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              COMPUTER REALPREE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CPERAINS SYSTEM: PC DCS/MS-DCS
SOFTWARE: Patentin Release #1.0. Version #1.3C
CURRENT APPLICATION DATA:
EXPLICATION NUMBER: US/08/926,258
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80. Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH. J., MILLER, R.H. AND
APPLICANT: BUKH. J., MILLER, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCTION OF ANY ORDIO SEQUENCES
TITLE OF INVENTION: AND THE USE OF ISOLATION: AND THE USE OF REAGE
                                                                                                                                                                                                                                   ADDRESSEE: Ell Lilly and Company STREEL: Lilly Corporate Center Ciry: Indianapolis STATE: Indiana COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-10430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCLEGULE TYPE: protein
SEQUENCE 408 AA: 43042 MW: 779745 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application PC/TUS9510398
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MEDSCET, THOMBS D.
REGISTRATICN NUMBER: 39.872
REFERENCE/DOCKET NUMBER: P-10.
FELECOMIUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-3861
                                                                                                Sequence 2, Application US/08926258 patent No. 5871983
                                                                      Sequence 2, Application US/08925258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 amino acids amino acids
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Best Local Similarity 53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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PCT-US95-10398-80
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145 YVMRVPEVII 154
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Sequence 90, Application US/08290665A

SEREMAL INFORMATION:
APPLICANT: BUKH, J. MILLER, R.H. AND
APPLICANT: BUKH, J. MILLER, R.H. AND
APPLICANT: BUKH, J. MILLER, R.H. AND
TITLE OF INVENTION: NOCIECTIDE AND DEDUCED
TITLE OF INVENTION: AND THE USE OF ISCLAIES OF HEPATITIS OF VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCRCAN & FINNEGAN
SIRRET: NEW YORX
SIRRET: NEW YORX
SIRRET: NEW YORX
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                                                       CURPUTER TEACHER DESK
CUMPUTER THE PECOPPY DISK
CUMPUTER THE PECOPPY DISK
CUMPUTER THE PECOPPY DISK
CUMPUTER THE PECOPPY DISK
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/C86.428B
FILLING DATE: 29-JUN.1993
CLASSIFICATION: 435
ATPRINGPYAGENT INFORMATION:
NAME: RIGHAR WASTER WASTER TOWNER: 26459
HEFRENCE/DOSKET NUMBER: 2026-4070
TELEPHENE (212) 758-4890
TELEPHENE: (212) 751-6849
                                                                                                                                                                                                                                                       ORGANISM: homosaplens
INDIVIDUAL ISCLATE: USIO
NCE 192 AA: 20855 MW: 200760 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NEW YGRK
COUNTRY: USA
2.1P: 10154
COMPOTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: ISM PC COMPATIBLE
                                                                                                                                                                          TELEFAX: (212) 751-6849
TELEX: 421792
INPORMATION FOR SEQ 1D NO: 80: SECUENCE CHARACTERISTICS: LENGTH: 192 amino acids TYPE: amino acid STRANDENNESS: unknown
E: MCRGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                          STANDARD:
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                     unknown
ADDRESSEE: MCRGAN
STREET: 345 PARK
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                              CRICINAL SOURCE:
                                  SA
                                                                                                                                                                                                                                                                                                                        145 YVMRVPEVII 154
                                                                                                                                                                                                                                                                                                                                         2 FIKRVSNVII 11
                       STATE: NEW COUNTRY: US ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                          CS-08:290-665A-80
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Sequence 80, Application US/ 8458570

Patent No. 5871962

GENERAL INFORMATION:
APPLICANT: BUCKL, A., M. UER. R.H. AND
APPLICANT: BUCKLL, R.;
ITILE OF INVENTION: WO COTTE AND DUDDED:
ITILE OF INVENTION: APPLICANT: BUCKLL, R.;
ITILE OF INVENTION: APPRAINTS CANTESTED OF THE ENVELOPE IN TITLE OF INVENTION: APPRAINTS CANTESTED ON THESE SEADENCES IN NUMBER OF SECUENCES: 15,
CORRESPONDENCE ADDRESS: 15,
CORRESPONDENCE ADDRESS: 15,
CORRESPONDENCE ADDRESS: APPRAINTS CANTESTED OF THE CONTROL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -;
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                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 84.459
REFERENCE/DOCKET NUMBER: 226-4116
ILECOMMUNICATION INFORMATION:
TELERAX: (212) 758-4800
TELERAX: (212) 758-4800
TELERAX: (212) 758-649
TELEX: 421792
INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS
LENGTH: 192 action act
TYPE: action act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: US10
JENCE 192 AA: 20855 MW: 20076C CN:
OPERATING SYSTEM: PC-56.8/MS-DOS
SOFTWARE: WORDPERFECT *.1
CURRENT APPLICATION DATA
APPLICATION NUMBER: 18/290,60
FILING DATE: 15-AUG-1: 1
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 3 68/468,5 FILING DATE: 6-JUN-19 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: 06/286,428 FILING DATE: 29-JUN-1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U. 27FF: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
ANNUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/19468570
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Gaps
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IIILE OF INVENTION: Adhesin Genes and Proteins Involved in IIILE OF INVENTION: Trichomonas Vaginalis Cytoadherence CRRESPONDENCE: 30 CCRRESPONDENCE ADDRESS: ADDRESSE: ANDLESE: ANDLE
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                                                                                                                            Score 51; DB 2; Length 295; Pred. No. 1.156+02; 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.3%; Score 51; DB 2; Length 297; Best Local Similarity 38.5%; Pred. No. 1.16e+02; Matches 5; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lenath 297:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/C8/504,459 FILING DATE: COOCULTE: tip herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           297 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5
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ENCE 297 AA: 31082 MW; 429472 CN;
         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 295 AA: 30887 MH; 423730 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/U8504459
Patent No. 5922563
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08504459
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TELECOMMUNICALION INFORMATION:
TELEPHONE: SIZ/418-3900
IELEFAX: S1Z/44-7577
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGIH: 297 amino acids
IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 17.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                            Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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! VFIKRVSNVIIHG 13
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| VFIKRVSNVIIHG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Texas
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LI 11
US-08-365-981-13
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Patent No. 592253
GENERAL INFORMATION:
Alderee, John F.
IITLE OF INVENTION: Adhesin Genes a: i Proteins Involved in ITLE OF INVENTION: Tithomonas Vag :alis Cytoadherence NUMBER OF ESCUENCES: 30
CORRESPONDENCE ADDRESS: 30
CORRESPONDENCE ADDRESS: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 AA
AIORNEYAGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
RECISTRATION NUMBER: 36,459
REFERENCE/COOKET NUMBER: 2026-407CUSI
TELECHANICATION INFORMATION:
TELEFAX: (212) 751-6849
TELEFX 421792
INFORMATION FOR SED ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homosapiens
INDIVIDUAL ISOLATE: US10
CE 192 AA; 20855 MW; 202760 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08504459
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SEQUENCE CHARACTERISTICS:
LENGTH: 295 maino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 YVMRVPEVII 154
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S FINRVARVLV 14
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ID US
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TILLE OF INVENTION: METHOD FOR CHINING
TILLE OF INVENTION: ANTIFUNGAL AND HERBICIDAL COMPOUNDS THAT TARGET THE
TILLE OF INVENTION: FIRST COMMITTED S.PP IN SPHINGOLIPID LONG-CHAIN
TILLE OF INVENTION: BASE BIOSYNTHESIS
UNGREEN OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: LONE, PRICE, LEBLANC & PECKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 AA
                                                                                                                                                                           E: LOWE, PRICE, LEBLANC & PECKER
STE. 300, 99 CANAL GENTER : AZA
                                                                                                                                                                                                                                                                                                                                                                                        NAME: D.J. MILLS
REGISTRATION NUMBER: 34506
RECISTRATION NUMBER: 434-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: Single
TOPOLGGY: Linear
MCLECULE TYPE: Polypeptide
SEQUENCE 625 AA: 69612 MM: 2352240 CN.
                                                                                                                                                                                                                                                                                        SOFTWARE: DOS TEXT FILE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365.961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIT: TYPE: FIOPPY disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DCS
                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 06/30/92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08846762A Patent No. 5994072 GENERAL INFORMATION:
APPLICANT: Lam. Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
                                                             Sequence 13, Application US/08365981
Patent No. 558336
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08846762A
                                            Sequence 13, Application US/U8365981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                       STREET: STE. 300,
CITY: Alexandria
STATE: Virginia
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CC TILLE DE INVENTIONS OF 99497261 Processis Involved in the Synthesis & Bird Assemble CC TILLE DE INVENTIONS OF 99497261 Processis Involved in the Synthesis & Bird Assemble CC TILLE DE INVENTIONS OF 99497261 Processis Involved in the Synthesis & Bird Assemble CC CONTRACT & STRIP 974940 (CC CONTRACT & STRIP 9
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STRANDEDNESS:
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CORRESPONDENCE ADDRESS:
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              Score 50: DB 3: Length 317;
Pred. No. 1.45e+02;
2; Mismatches i: Indels
                                                                                                                                                                                                                                              ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSFLAND CITY: ROSFLAND STATE: NEW JERSEY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 AA.
                                                                                                          3:7 AA
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REFERENCE/JOCKET NUMBER: 331400+20
TELECOMMUN'CATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/518,615
FILING DATE: AUGUSE 23, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
CUSTUARE: WORD PERFECT 5.1
CUSTRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: LINEAR
MOLEGULE TYPE: PROTEIN
SEQUENCE 317 AA; 37355 MW; 525334 CN:
317 AA; 37355 MW; 525334 CN;
                                                                                                          PRT:
                                                                                                                                                                                                                                                                                                   2.PP: 0758
C.MUTER READABLE FORM:
MEDIUM TYPE: 35 INCH DISKETTE
DOMBUTER: IBM PS/2
OPERATING SYSTEM: MS-DGS
                                                                                                                                                                                Sequence 2. Application US/09066075 Patent No. 5925749 GENERAL INFORMATION:
                                                                                                                                                                 Sequence 2. Application US/09056075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 317 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                           STANDARD;
                Query Match
Best Local Similarity 66.7%:
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FIKRVSNVI 10
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ID US-08-518-615A-2
                                                                                                   US-09-066-075-2
SEQUENCE
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Sequence 2. Application US/09518615A

Sequence 2. Application US/09518615A

Sequence 3. Application US/09518615A

Sequence 3. Application US/09518615A

CONTROL MATURE OF INVENTION:

CONTROL MATURE OF INVENTION:

CONTROL MATURE OF CECCHI, STEWAR 6 OLSTEIN

CONTROL MATURE FORM

CONTROL MATURE FORM

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CONTROL MATURE FORM

CONTROL MATURE IS 15 INCH DISKETTE

CONTROL MATURE
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Pelease 3.1A John F. Collins, Biccomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp | protein - protein database search, using Smith-Waterman aigorithm

Mon Jun 19 16:28:19 2000; MasPar time 14.74 Seconds 88.845 Million cell updates/sec Rud on:

Tabular output not generated.

>US-09-142-524A-13 (1-13) from USO9142524A.pep 94 1 VFIKRVSNVIIHG 13 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

721208 segs, 100765575 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Dalabase:

a-pending 1:PCT 2:U6 3:U60 4:U7 5:U8C 6:U81 7:U82 8:U83 9:U84A 10:U84H 11:U8S 12:U8C 13:U87 14:U88 15:U89 16:U90 17:U91 18:U92 19:U93 20:U94 21:U95 22:NEMP 23:NEMUGO 24:NEMUB 25:NEMU9

Mean 20.556; Variance 54.758; scale 0.375 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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94 100.0 374 10 US-08-467- Sequence 2, Applicatio	19	46	100.0		4	US-07-938-	Sequence	~	Applicatio	3.51e-03
	50	94	100.0	374	0	US-08-467-	Sequence	2	Applicatio	3.51e-03

21 94 100.0 374 7 0£-08-226- Sequence 2, Applicatio 3.51e-03 22 94 100.0 374 10 05-08-467- Sequence 2, Applicatio 3.51e-03 24 94 100.0 374 4 07-729- Sequence 2, Applicatio 3.61e-03 25 94 100.0 374 10 08-458- Sequence 2, Applicatio 3.61e-03 26 94 100.0 374 10 08-458- Sequence 2, Applicatio 3.61e-03 27 94 100.0 374 10 08-457- Sequence 3, Applicatio 3.61e-03 28 69 73.4 20 10 05-08-457- Sequence 37, Applicatio 5.84e-06 39 69 73.4 20 10 05-08-457- Sequence 37, Applicatio 5.84e-06 31 69 73.4 20 10 05-08-457- Sequence 37, Applicatio 5.84e-06 38 69 73.4 20 10 05-08-457- Sequence 37, Applicatio 5.84e-06 39 69 73.4 20 10 05-08-457- Sequence 37, Applicatio 5.84e-06 39 67 71.3 370 10 05-08-457- Sequence 37, Applicatio 5.84e-06 39 67 71.3 370 10 05-08-457- Sequence 97, Applicatio 1.02e-01 39 67 71.3 370 10 08-457- Sequence 97, Applicatio 1.02e-01 40 68.1 31.7 05-08-457- Sequence 97, Applicatio 1.02e-01 41 64 68.1 31.7 05-08-457- Sequence 97, Applicatio 2.36e-01 42 68.1 31.7 05-08-457- Sequence 97, Applicatio 2.36e-01 43 69 367 8 05-08-350- Sequence 97, Applicatio 2.36e-01 44 68.1 31.7 05-08-350- Sequence 97, Applicatio 2.36e-01 45 61 64.9 367 8 05-08-350- Sequence 95, Applicatio 2.36e-01 46 61.3 370 10 05-08-457- Sequence 95, Applicatio 2.36e-01 47 64.5 64.7 05-08-350- Sequence 95, Applicatio 2.36e-01 48 66.7 05-08-350- Sequence 95, Applicatio 2.36e-01 49 66.7 05-08-350- Sequence 95, Applicatio 2.36e-01 41 64.9 367 8 05-08-350- Sequence 95, Applicatio 2.36e-01 42 64.9 367 10 05-08-467- Sequence 95, Applicatio 2.36e-01	ALIGNMENTS SULT US-08-150-225-36 STANDARD: PRT; 20 AA. XXXXXX Sequence 36. Application US/0835C225 Sequence 36. Application US/0835C225 Sequence 36. Application US/0835C225 Sequence 36. Application US/0835C225 SEQUENCE 1
	#AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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Sequence 35, Application USZA 46700*
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FRAGMENT TYPE: internal
UENCE 20 AA: 2080 MW: 2:04 ON:
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SENERAL LAWARDATION:
APPLICANT Griffell, Irwin 3.1
APPLICANT Boilock, Joannel
APPLICANT Boilock, Joannel
APPLICANT Garden Milan F.;
APPLICANT Kow Mea-Chang
APPLICANT Wenny, Starrel H.;
APPLICANT Brayer Mark A.;
APPLICANT BRAYER ALIGNORY FOR PROPERTY BRAYER BRAYER ALIGNORY FOR PROPERTY BRAYER BRA
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COMPUTER READABLE FORM:
COMPUTER IN FROME FORM:
COMPUTER IS FOR COMPATIBLE
COMPUTER IS FOR COMPATIBLE
COMPUTER IS FOR COMPATIBLE
SUSTEMNE: PATENTIN REJOS/WS-DOS
SUSTWARE: PATENTIN REJOS/WS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/26,246A
FILING DATE: April 8, 1994
CLLASSIFICATION: 424
FRICK APPLICATION DATA:
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: COT/US93/00139
FILING DATE: January 15, 1993
ALIDNE FOR COMPATION:
APPLICATION NUMBER: DET/US93/00139
FILING DATE: January 15, 1993
ALIDNE FOR COMPATION:
APPLICATION NUMBER: PCT/US93/20139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Datione A. Varietone
ATGISTRALION NUMBER: 35,729
BEFERENTE/COKET NUMBER: 35,729
TELEPHONE: (617) 466-6600
TELEPHONE: 30 withou acids
TYPE: amition acids
TYPE: amitio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36. Application US/08226248A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%.
Nest Local Similarity 100.0%.
Matches is: Conservative
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SIREET: 610 Lin
CITY: Waltham
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-226-248A-36
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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GENERAL INFORMATION:
APPLICANT STIFFE, ITALE 3
APPLICANT STIFFE, John W.
APPLICANT STREAM, Michael M.
APPLICANT Sarman, Michael M.
APPLICANT Sarman, Michael M.
APPLICANT Years, Surmer H.
APPLICANT Years, Surmer H.
APPLICANT Exley Surmer H.
APPLICANT Exley Mark M.
APPLICANT Exley Mark M.
APPLICANT Exley Mark M.
APPLICANT DOWNER, Steven P.
ITILE OF INVENTION Alleraence Froteins and Meptides Flow MIMBER OF SECUENCES.
AND MIMBER OF SECUENCES.
CONDECTION AND ADDRESS AND ADD
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Terralogic Frameworking, Composation, SIRERI, Cl. Clarelin St. Vincelin 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jane E. Remillard
REGISTRAILON NUMBER: 38.872
REGISTRAILON NUMBER: 025.6 USD5 (IMI-028GPD5)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100:0%, Pred. No. 1.51e:03.
Matches lö: Conservative or Mismatches or reduce
REGISTRATION NUMBER: 35.729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-600
TELEFAX: (617) 466-5040
INFORMATION FOR SED ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA
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US-09-142-524A-13.rap

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Best Local Similarity 100.0%:
Matches 13; Conservative
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                                                                                  Gaps
                                                                                                                                                                                                               Sequence 36. Application US/07938990A
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Boilock, Joanne
APPLICANT: Bood Julian
ITLE OF INVENTION: Allergenic Proteins And Peptides From
ITLE OF INVENTION: Japanese Cedar Pollon
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                  .;
0
                                                                  Sength 20;
                                                                Score 94: DB 10; Length 20;
Pred. No. 3.61e-03;
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBL
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DAIA:
CURRENT APPLICATION DAIA:
FILING DAIE: 19920931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: IPC-625CC (IMI-628) TELECOMMUNICATION INFORMATION:
                                                                                                                                                  20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           PAPELCATION NUMBER: C7/730,452 FILING DATE: July 15, 1991 APPLICATION NAME O/729,134 FILING DATE: July 10, 1991 ATTONEY/AGENT INCRMATION: NAME: Amy E. Mandragouras REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                   Sequence 56, Application US/0793899CA
                                                                                                                                                                                                                                                                                            ADDRESSEE: Lahive & Cockfield STREET: Sixty State Street
                              MOLECULE INFELLIGE
FRAGMENI TYPE: Internal
SEQUENCE 20 AA; 2080 MW; 2304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4T TYPE: internal
20 AA: 2080 MW: 2304 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFCRMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   STANDARD:
         20 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
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PRIOR APPLICATION DATA:
                                                                Query Match
Best Local Similarity 160.0%;
Matches 13; Conservative
               amino acid
XX: linear
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                                                                                                  8 VFIKRVSNVIIHG 20
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                TYPE: ami
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DB 4: Length 20;

100.0%: Score 94;

Ouery Match

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                      Gaps
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APPLICANT: Yeung, Siu-mei H.,
APPLICANT: Yeung, Siu-mei H.,
APPLICANT: Brauer, And Applicant: Exley, Mark A.,
APPLICANT: BOWETS, Steven
APPLICANT: POWETS, Steven
TITLE OF INVENTION: Japanese Cedar Poilen
NUMBER OF SEQUENCES;
ADDRESSEE: ImmuLogic Pharmaceutical Corporation: Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
Pred. No. 3.51e-03;
0; Mismatches 0; Indels
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610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy ..isk
COMPUTER: IBM PC comjatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOPTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 025.6 US (IMI-028CP2) TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         2C AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
PREDICATION NUMBER: 06/350.225
FILING DATE: December 6: 1994
APPLICATION NUMBER: 05/25.249
FILING DATE: APRIS 8: 1994
APPLICATION NUMBER: 07/984.990
FILING DATE: September 1: 1952
APPLICATION NUMBER: 07/984.990
FILING DATE: 3404715; 1993
ATTORNEY/AGENT INFORMATION: 1993
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                                                                                                                                                                                           PRT:
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                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/08468940
                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/08468940
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gliffeth, Irwin J.:
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richard D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 20 AA; 2080 MW; 2304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IELEFAX: (617) 466-6640
INF AMAIION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (617) 466-6000
                                                                                                                                                                                           STANDARD
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GY: linear
                                                             8 VFIKRVSNVIIHG 20
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CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSA
                                                                                      1 VFIKRVSNVIIHG
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US-08-468-940-35
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APPLICANT: Kuc, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew,
APPLICANT: Brauer, Mark A.;
APPLICANT: Powers, Steven P.
ITLE OF INVENTION: Albergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Polien
CO-FESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic marmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                    CONTUTER: NEADER LEFORM.

MEDIUM INTEL FLORMY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-70S/MS-DS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
APPLICATION DAIA:
F. ING DAIE: June 6, 1995
C. ASSIFICATION: 4.24
PRIOR APPLICATION DAIA:
APPLICATION DAIA:
APPLICATION NUMBER: 08/350,225
FILING DAIE: December: 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remiliard
REGISTRATION NUMBER: 38.872
RECECHMUNICATION NUMBER: 38.872
RECECHMUNICATION INFORMATION:
TELEPHONE: (617) 227-74:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%: Score 94: DB 10; Length 20; Best Local Similarity 100.0%: Pred. No. 3.61e-63: Matches 13; Conservative 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   E: ImmuLogic harmaceutical Corporation,
610 Lincoln S.
                                          20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6C AA.
                                         PRT:
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                                                                                                                                            Sequence 36, Application US/08467023 GENERAL INFORMATION:
                                                                                                                   Sequence 36, Application US/08467023
                                                                                                                                                                   APPLICANT: Griffeth, Irwin J.:
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.:
APPLICANT: Garman, Richar F.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AA: 2080 MW: 2304 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02154
COMPUTER READABLE FURM:
MEDIUM IYPE: Floppy
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SIREET: biv.
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ID US-08-350-225-62
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AC XXXXXX
                                         US-08-467-023-36
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                 Gaps
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                                                                                                                                                                                        Sequence 36, Application US/09467697
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne)
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Garman, Richard D;
APPLICANT: Young, Siurmel H.;
APPLICANT: Braucr, Andrew:
APPLICANT: Braucr, Andrew:
APPLICANT: Braucr, Andrew:
APPLICANT: Braucr, Andrew:
APPLICANT: Braucr, Alergenic Proteins And Peptides From TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen
CHARSPECNDERCES: 261
COMPRESSEE: Immirral: 1
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                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jane E. Korillard
REGISTRATION NUMBER: 38.872
REGISTRATION NUMBER: 025.6 0.04 (IMI-0.46CFD4)
RECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7490
INFORMATION FOR FG 017) 227-7941
INFORMATION FOR SEQ 017 036:
Pred, No. 3.61e-C3;
0: Mismatches 0;
                                                                                                                   ZO AA.
                                                                                                                   PRI,
                                                                                                                                                                                          Sequence 36, Application US/08457697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 20 AA; 2060 MM: 2304 CN;
                                                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immuscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 20 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
    Rest Local Similarity 100.0%;
Matches 13; Conservative
                                         8 VEIKRVSNVIIHG 20
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                                                      : VETKRVSNVITHG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                 US-08-457-597-35
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Sequence 62. Application US/98226246A
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin 3.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Corresponder Price Control of the Communication of the Corresponder Price Corresponder ADDRESS.
AUDRESSEE: Immulogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoin St.
                                                                                                                                                                                                                                                                                                                      COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PREMEITIN REPEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US 08/226,248A
FILING DATE: April 8. 994
PRIOR APPLICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94; DB 7; Length 60;
Pred. No. 3.51e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028GP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICAR APPLICATION DATA:
APPLICATION NUMBER: 07/938.99C
FIZING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/C0139
FILING DATE: January 15, 1993
ATIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
           708225248A
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FRAGMENT TYPE: Internal
JENCE 60 As; 6644 MW: 19454 CN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6240
INSCRMATION FOR SEQ ID NO: 62: 62: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%;
Local Similarity 100.0%;
les 13; Conservative
           Sequence 62, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arino acid
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                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .T 10
US-08-468-940-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT
SEQUENCE 60
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                                                             Sequence 62, Application US/0835025
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Bond, Julian F.:
APPLICANT: Garran, Richard D;
APPLICANT: Wou, Mei Chard D;
APPLICANT: Reung, Sir-mei H.;
APPLICANT: Reare, Andrew:
APPLICANT: Relay, Mark A.;
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Bray, Mark A.;
APPLICANTION: Allergenic Cedar Poilen
NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                       E: Immulogic Pharmaceutical Corporation, Inc
610 Lincols St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 100.0%; Score 94; DB 8; Length 60; Local Similarity 100.0%; Pred. No. 3.61e-03; nes 13; Conservative C; Mismatches O: Indele
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-005/MS-70S
SOFTANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/350,225
FILING DATE: December 6, 1994
CLASSIFICATION: 424
PRICR APPLICATION: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jariene A. Vanstone
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-0280F2)
TELEOMNUN.CATION INFORMATION:
TELEPHONE: (617) 466-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: (8/226,248 FILING DATE: APPLI 8, 1994 APPLICATION NUMBER: (07/938,990 FILING DATE: September 1, 1992 APPLICATION NUMBER: PCI/US93/00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: January 15, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal
SENCE 60 AA: 6644 MW; 19464 CN;
                                      Sequence 62, Application US/08350225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEFAX: (617) 466-6040 INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACIERISTICS:
LENGIH: 60 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 VFIKRVSNVIIHG 60
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                                                                                                                                                                                                                                                                                              SIREET: 610 Li
CITY: Woltham
                                                                                                                                                                                                                                                                                                                                        USA
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ZIP: 02154
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     APPLICANT Griffeth, Irwin J.;
APPLICANT Pollock, Joanne:
APPLICANT Bond, Julian F.;
APPLICANT Bond, Julian F.;
APPLICANT Kuo, Rei-Chang:
APPLICANT Fung, Slimel H.;
APPLICANT Fung, Slimel H.;
APPLICANT Exley, Mark A.;
APPLICANT Dowers, Sleven P.
IIIL OF INVENTION: Allergenic Proteins And Peptides From NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
AUGUSTSTELL OF LINCOLN St.
ALEREIT F. LINCOLN ST.
                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                               Length 60
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                            NAME: Sarlone A. Varstone
REGISFRATION NUMBER: 35,729
REFENCE/COCKET NUMBER: 025.6 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
TELEPRINE: (617) 466-6000
TELEPRINE: (617) 466-6000
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  Score 94; DB 10; 1
Pred. No. 3.61e-03;
0; Misratches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6C AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 52, Application US/08467306
                                                                                                                                                                                                                                                                                                                                                         MCLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 60 As: 6644 MW: 19464 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 62, Application US/08467006
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                    60 amino acids
                                                                                                       STREET: (10 Lincoln St
CITY: Waltham
STATE: NA
COMMEN: USA
CLP: (2.1%
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match 100.0%:
Best Local Similarity 100.0%;
Matches 13: Conservative
                                                                                                                                                                                                                                                                                                                                   LENGTH: 50 amino
TYPE: amino acid
TOPOLCGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                48 VFIKRVSNVIIHG 6C
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SENERAL INFURMATION:
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                     APPLICANT SOLITOR, JOHN S. APPLICANT Bond Julian F. APPLICANT Bond Julian F. APPLICANT Bond Julian F. APPLICANT Kuo, Melichard D. APPLICANT Kuo, Melichard B. APPLICANT Young, Sig-mel H.; APPLICANT STAVET, Actiew. AAPPLICANT EXIEW. Mark A. APPLICANT EXIEW. Mark A. APPLICANT STAVET, STEVEN P. TITLE OF INVENTION: Japanese Gedar Follen NUMBER OF SECUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORK:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILED FOR COMPAILED FOR COMPAILED FOR COMPAILED FOR COMPAILED FOR COMPAILED FOR CHARGE PALENTION DATA:
CURRENT APPLICATION NUMBER: US/06/467.056
FILING DATE: June 6, 1995
CLESSIFICATION NUMBER: 08/350,225
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATCENTATION NUMBER: 38,872
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 38,872
RECECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 60:
                                                                                                                                                                                                                                                                   ADDRESSE: Immuloqic Pharmaceutical Corporation
STREET: 610 Lincoln St
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94: DB 10: Le
Fred. No. 151e-03.
O: Mismatches 0:
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GENERAL INFORMATION:
APPLICANT: Griffeeth, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Ullan F.;
APPLICANT: Garman, Richard D;
Garman, Richard D. Bond, Julian F.;
Bond, Julian F.;
Garman, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/C8467597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 227-594.
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACIERISTICS:
LENGTH: 60 amino acid
TYPE: amino acid
TYPE: Jinear
MOLECULE TYPE: peptide
FRAGMENT TYPE: interna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
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Best Local Similarity 100.0%:
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
COUNTRY: USA
ZIP: 02154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 12
US-08-467-697-62
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PRT:
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FRAGMENT TYPE: interra.
SEQUENCE 60 AA; 6644 MW: 1:464 CN:
                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227 7400
TELEFAX: (617) 227 7400
INFORMATION FOR SEQ ID N: 62:
SEQUENCE CHARACTERISTIC:
LENGTH: 60 amino acids
IYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ImmuLogic Pl
STREET: 610 Lincoln St
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
Local Similarity 106.0%;
nes 13; Conservative
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ZIP: 02154
COMPUTER READABLE FORM:
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02109
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US-08-467-023-62
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         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Pollock, Joanne
APPLICANT: Pollock, Joanne
TILLE OF INVENTION: Allergenic Proteins And Peptides From
TILLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Allergenic Cedar Pollen
NUMBER OF SEQUENCE: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive 6 Cockfield
SIRRET: Sixty state Street
CITY: Boston
     APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark M.;
AFPLICANT: Exley, Mark M.;
AFPLICANT: Powers, Steven P.
IITLE OF :NVENTION: Allergenic Proteins And Peptides From IITLE OF :NVENTION: Japanese Gedar Poilen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IRM FC COMPATIBLE
COMPUTER: IRM FC COMPATIBLE
CUERRAINUS SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PATEMENT Release #1.0, Version #1.25
CUERRAIN AFPLICATION DATA:
APPLICATION NUMBER: US/08/467,697
FILING (AIE: Jace 6, 1945
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: 08/350,225
FILING AFPLICATION NUMBER: 08/350,225
FILING CATE: December 6, 1944
ATCORREY FACENT INFORMATION:
NAME: COMPATIBLE TO COMPATION:
AND COMPATION COMPATION:
AND COMPATION 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jace E. Remillard
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET WURBER: 025.6 USD4 (IMI-029CPD4)
TELECOMMICATION INFORMATION:
TELEPHONE: (617) 227-7430
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CRARACTERISISS:
LENGTH: 60 amino acids
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FRAGMENT TYPE: internal
SEQUENCE 60 AA; 5644 MW; 19464 CN;
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                                                                                                                                                                                                                COUNTRY: USA
ZIR: 20154
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compa
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Best Local Similarity 100.0%,
Matches 13: Conservative
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GY: linear
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GENERAL INFORMATION
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RUG, Mei-Chang,
APPLICANT
RUG, Mei-Chang,
APPLICANT
Brauer, Andrew,
APPLICANT
Brauer, Andrew,
APPLICANT
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TILLE OF INVENTION
TITLE OF INVENTION
Albergenic Proteins And Peptides From
TITLE OF INVENTION
CORRESPONDENCE
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                      ImmuLogic Pharmaceutical Corporation, Inc
COMPUTER TABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: ISM PC COMMENTALE
COMPUTER: PROFILE FORM:
COMPUTER: PROFILES/MS-DOS
SOFIWARE: PATENT: PC-DCS/MS-DOS
SOFIWARE: PATENT: PC-DCS/MS-DOS
CURSING SYSTEM: PC-DCS/MS-DOS
CLASJFICATION NOMBER: S/27/938.990A
FILING DATE: 192-29c
FILING DATE: 192-29c
FILING DATE: JUJ 193: FILING DATE: JUJ 193: FILING DATE: JUJ 193: FILING DATE: JUJ 194: JUJ 194: FILING DATE: JUJ 194: JUJ
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APPLICANT: Since Toshio
APPLICANT: Kine A KKINO I
APPLICANT: Kine A KKINO I
APPLICANT: Mine A MINE A KKINO I
ATILE OF INVENTION: Allergic Diseases
FILE REFERENCE: Docket NO. SPO-103
CURRENT APPLICATION NUMBER: US/09/142,524
CURRENT FILING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: PCT/JP97/0074C
EARLIER FILING DATE: 1997-03-10
NUMBER OF SEO, ID NOS: 5
SOFTWARE: PALENTIN Ver. 2.0
SEO ID NO 1
EENSTH: 80
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MEDIUM TYPE: Floppy disk
CEMPUIER: IBM FC compatible
OFERAINS SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Re-bease #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/G8/467,023
FILING DATE: Use 6, 1995
CLASSIFICATION 1424
PLOOR APPLICATION DBARE: 08/350.225
FILING DATE: December 6, 1994
ATTORNEY/AUGHT INFORMATION:
NAME: Lane E. Remilland
REGISTRATION NUMBER: 38,872
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 94: DB 16: Length 60:
Pred. No. 3.61e-03:
0: Mismatches 0: Indels
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 055.6 USU2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ 1D NO: 62:
SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE: internal
SEQUENCE 60 An: 6644 MM: 19464 CN:
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Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 VFIKRVSNVIIHG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Unknown
FEATURE:
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Ouery Match 100.0%: Score 94: DB 17: Length 80: Best Local Similarity 100.0%: Pred. No. 3.51e-03;

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Jun 19 15:17:09 2000; MasPar time 5.14 Seconds 119:270 Million cell updates/sec R.::: on:

Tabular output not generated.

>US-09-142-524A-13 (1-13) from US09142524A.pep 94 1 VFIKRVSNVI:HG 13 Title: Description: Perfect Score: Sequence:

2AM 150 Cap 15 Scoring table:

142080 seqs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 l:pir1 2:pir2 3:pir3 4:pir4 Database:

Nean 26.420; Variance 35.957; scale C.735 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES		
Result No.	Score	Query Match	Length	ä	QI.	Description	Pred. No.
	75	100.0	374	2	JC2124	major allergen Cry j	6.70e-08
ſ		000	117	:			'
7	4	0.001	9/0	7	621200		ė
'n	9	6.49	326	7	857509	pectase lyase - Asper	20
4	57	9°39	256	N	A32017	9	
S	57	9.09	300	7	F69719		S.
9	56	59.6	257	-	PNBS2S	beta-lactamase (EC 3.	œ
7	56	9.65	257	-	PNBSU2	beta-lactamase (EC 3.	8.33e+00
α	55	58.5	317	~	305696		1.26e+01
σ	55	58.5	452	•	WZBE4	gene 4 protein - huma	1.26e+01
7.0	55	58.5	550	7	T15858	hypothetical protein	1.26e+01
I	55	58.5	1894		T02155		1.26e+01
12	54	57.4	303		F70716	probable succinyl-coa	1.90e+01
13	53	56.4	7.5	٦	574973	virulence associated	2.85e+01
14	53	56.4	190	7	B72330	transcription regulat	2.85e+01
5.5	53	56.4	317	7	G70356	thymidylate synthase	2.85e+01
16	53	56.4	375	-	A28630	muconate cycloisomera	2.85e+01
17	53	56.4	475		JN0327	sulfate adenylyltrans	2.85e+01
18	ເນ	56.4	835		JC6140	cell surface associat	2.85e+01
19	ς C	56.4	985		S 59330	Na+/H+-exchanging pro	2.85e+01
20	52	55.3	365		575167	hypothetical protein	4.25e+01
21	52	55.3	404		S12209	pectate lyase (EC 4.2	4.25e+01
22	52	55.3	552		S4 6809	hypothetical protein	4.25e+01
23	51	54.3	111	~	A72079		6.30e+01

51 54.3 238 2 716640 51 54.3 254 2 571225 51 54.3 379 2 546187 51 54.3 379 2 546187 51 54.3 379 2 546187 51 54.3 379 2 546187 51 54.3 379 2 546187 51 54.3 378 2 2546187 51 54.3 785 2 946187 51 54.3 785 2 946187 51 54.3 785 2 946187 51 54.3 810 1 140088 51 54.3 1006 2 770445 51 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770445 52 54.3 1006 2 770446 52 55.2 270 2 H64248 52 55.3 2 66.2 2 F71258 52 53.2 67.2 1708079 52 57.2 170807 52 57.2 1	hypothetical protein 6.330+01 hypothetical protein 84 6.30+01 probable membrane pro 6.30+01 probable membrane pro 6.30+01 probable membrane pro 6.30+01 probable membrane pro 6.30+01 hypothetical protein 6.30+01 DS protein vaccinia 6.30+01 DN polymerase 111, 5 6.30+01 DN polymerase 111, 5 6.30+01 DN prothetical protein 6.30+01 probable healt short 9.27+01 endopolymerase 111, 5 6.30+01 endopolymerase 111, 5 6.30+01 probable healt short 9.27+01 endopolymerase 111, 5 6.30+01 endopolymerase 111, 5 6.30+01 probable healt short 9.27+01	precursor (clone pCC:-15) - Japanese ia Japonica #common_name Japanese cedar evision 14-Jui-1994 #fext_change	Shimizu, K.; Kusakate, T.; Morikubo, Commun. (1994) 199:619-625 of CDNA coding for Cry j i, a rajor cedar pollen. 19493633; PID:dl006087; PID:q493634 ibed carbohydrate binding site for wase LAT59	unce status predicted tabel SiGN predicted tabel SiGN predicted tabel SiGN war. MAIN hydrate (Asn) (covalent) *status weight 40702 *checksum 3692 1: DB 2: Length 374; 3: 6.70e-08;	recursor (clone pCCI-2-2) - Japanes japonica *common_name Japanese Cer
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51 54.3 51 54.	44444444444444444444444444444444444444	#ty gen ie 0 #8	K S S S S S S S S S S S S S S S S S S S	De lict	* # # # # # # # # # # # # # # # # # # #
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*domain signal sequence *status predicted *label SIG\ *product major allergen Cry j I (clone pCCI-2-2) *status predicted *label MAT\
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the authors described carbohydrate binding site for
residue 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERENCE Silsoy M.C.: Whitehead, M.P.; Cleveland, T.E.; Dean, R.A. Ho, M.C.: Whitehead, M.P.; Cleveland, T.E.; Dean, R.A. Hournai Curr. Genet. (1995) 27:142-149

*Journal Sequence analysis of the Aspergillus cidulans pectate lyase per A sequence and evidence for binding of promoter regions to PREA, a receiptor of carbon catabolity repression.
                                                           N.; Shimizu, K.; Kusakabe, T.; Mcrikubo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A320;7 *type complete
beta-lactamase (EC 3.5.2.6) II precursor - Bacillus cereus
(strain 5/B/6)
*formal_name Bacillus cereus
07.Jun-1990 *sequence_revision 07.Jun-1990 *text_change
                                                                                                                                                                         *pinding_site carbohydrate (Asn) (covalent) *status
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                                                       #authors Sone, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; IX.; K.; Kino, X.; Kitchen, Blochen, Blochen, Res. Commun. (1994) 199:619-625 #title Cloning and sequencing of cDNA coding for Cry j I.; Albarose cedar pollen.
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##residuer
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26-Aug-1999
JC2123: PC2065
JC2123
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Natches 7; Conservative
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**residues 22-53:5
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**molecule_type mRNA
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KEYWORDS
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Autoni, G.; Reevedo, V.; Bertero, M.S.; Bossieres, P.;
Alloni, G.; Reevedo, V.; Bertero, M.S.; Bossieres, P.;
Bolotin, A.; Stevedo, V.; Bertero, M.S.; Bossieres, P.;
Bolotin, A.; Stevedo, V.; Bosse, R.; Hourser, D.; Braun, S.;
Bruschi, C.; Caidwell, H.; Capuano, V.; Carter, N.;
Choi, S. K.; Codan, J.J.; Connerton, F.; Carminsts, N. J.;
Daniel, R.A.; Debract, F.; Devine, K.M.; Fritz, C.; Fullmaton, J.;
Fabret, C.; Ferrari, E.; Fouger, D.; Fritz, C.; Fullmaton, J.;
Fabret, C.; Ferrari, E.; Fouger, D.; Fritz, C.; Fullmaton, J.;
Gusseppi, G.; Y.; B.J.; Hada, K.; Hatz, C.; Fullmaton, J.;
Gusseppi, G.; Y.; B.J.; Hada, K.; Hatzeri, G.; Farwood, C.; K.; Herrari, A.; B.; Hatzeri, A.; Galdero, M.; Gofteau, A.; Goliqhtly, E.J.; Garadi, G.;
Gusseppi, G.; Y.; B.J.; Hada, K.; Hatzeri, G.; Rarano, M.;
Kasalira, Y.; Kadei, F.; Lardino, S.; Rareno, M.;
Kasalira, Y.; Kadei, F.; Lardino, S.; Rareno, M.;
Kasalira, Y.; Lapidis, A.; Lardino, S.; Lauber, J.;
M.; Gogwa, K.; Coftwara, A.; Cudega, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
Schowska, A.; S.; Chrosto, P.; Shin, B.S.; Soldo,
B.; Scokin, A.; Takeuli, M.; Tamakoshi, A.; Yaria, A.;
Wandent, R.; Wedler, E.; Wedler, T.; Wander, T.;
Winters, P.; Wipat, A.; Yoshikawa, H.F.; Zumstein, E.;
Voshikawa, H.; Danchin, A.; Yoshikawa, H.F.; Zumstein, E.;
Voshikawa, H.; Danchin, A.;
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- Bacillus subrilis
#formal_name Bacillus subtilis
05-bec-1997 # sequence_revision 05-bec-1997 # text_change
            FERNCE A32017
Fauthors Lim, H.M.; Pene, J.J.; Shaw, R.W.
Fournal J. Bacteriol. (1949) 170.2873.2878
Fittle Cloning, nucleotide sequence, and expression of the Familius cereus S/B/B/ Eela-lactamase II structural dene
                                                                                                                                                                                                                                                               ##residues 1-256 ##label LIM ##crossreferences GB=N9530: NIL; #10143127; PIEN:AAA22542.1; Pil:3147)28 CLASSIFICATION #superfamily besistance if Revivence antibiotic resistance hydrolase
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Best Local Similarity 70.0%; Pred. No. 5.47e-60;
Matches 7; Conservative 2; Mismatches 1: Indels
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Nature (1997) 390:249-256
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C.: Waley, S.G.
#journal FEBS Lett. (1985) 189:207-211
#title The amino acid sequence of the zinc-requirion tela-lactamase
#cross-references MUID:86505446
#accession A91344
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##residues 1-257 ##label HUS
##cross-references GB:MI:189: NID:q142603: PIDN:AAAZ2276 i: PID:0142604
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    beta-lactamase (EC 3.5.2.6) II precursor - Bacillus cure.scephaloporinase II: penicallinase II
*formal_name Bacillus cereus
04.pec-1985 *sequence_revision 04-Dec-1985 *text_crange
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prolyl aminopeptidase (EC 3.4.11.5) - Serratia marcescems
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Prolyi aminopeptidase from Serratia marcescens: Cloning
the enzyme gene and crystallization of the expressed
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                                                                                                                                                                                                                                                                                   Hussain, M.; Carlino, A.; Madonna, M.J.; Lampen, J. Bacteriol, (19.5) 164-223-229
Cloning and sequencing of the metallothic protein
beta-lactamase II gene of Bacilius cereus 569/H
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A91806; A91344; A01006
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#cross-references MUD:86C08056
#accession A91806
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*product beta-lactamase II *status predicted *label BL2\
*active_site 3iu *status predicted\
10 *linding_site 2inc, high affirity (His, His, Cys, His)
*status predicted
#length 257 *molecular-weight 28:53 *checksum 2375
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#s.perfamily succinate--CoA ligase (ADP-forming) alpha chain
acid-thiol ligase: ATP: phosphohistidine: phosphoprotein;
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#fittle The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. #cross-references MCID:98044033
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##residues 11-48 ##labe, KAT2
CLASSIFICATION #superfamily beta*iactamase II
KEYWORDS antiblotic resistance; hydrolase; metailoprotein; zinc
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beta-lactamase (EC 3.5.2.6) II precursor - Bacillus sp.
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#length 366 #molecular-weight 31382 #checksum 2503
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#journal J. Gen. Microbiol. (1985) 131:337-3324
#title Nuclectide sequence of the beta-lactamase gene of alkalophilic Bacilius sp. strain 176.
#cross:references MujD:86170399
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Pred. No. 5.47e-00;
"...marnhes 2: Indels
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31-Dec-1988 #sequence_revision 31-Dec-1988
18-Jun-1999
                                                                                                                                                                    nucleic acid sequence
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##cross-references EMBL:X04370: NID:u59989: PIDN:TAAZ7887.1; PID:q59993
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                                                                                               This enzyme catalyzes the removal of amino-terminal proline from
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#formal_name Ceenorhabditis elegans
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alpha-amincacylpeptide hydroiase
#length 317 #molecular-weight 36083 #checksum 7818
#authors Davison A.J.: Scott. J.E. #ioural J. Gen. Virol. (1986) 67:1759-1816 #ittle The complete DNA segmence of varicellarzester virus. #cross-references MCID:86306657
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Pred. No. 1.26e+Ci:
6: Mismatches 2: Indels
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Pred. No. 1.26e-01;
6: Mismatches 1: Indels
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##fresidues | 1-1894 ##label VYS | ##cross-references EMEL:AC004393; NIP:q3:C8024: PID:j3:176661; | ##cross-references EMEL:AC004393; NIP:q3:C8024: PID:j3:176661;
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Best Local Similarity 50.0%; Pred. No. 1.26e+31;
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S
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##mocecute_type DNA
##colous
##cross-references EMBL:D90902; GB:AB001339; NID:q1652027;
##cross-references EMBL:D90902; GB:AB001339; NID:q1652027;
##note the nucleotide sequence was submitted to the EMBL Data
##note Library, June 1996
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*title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
**Recoss-references MUD:98295987**
**accession F70716
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ENA binding: transcription regulation
#length 75 *molecular-weight 8539 *checksum 9185
                                                                                                                                                       **molecute_type DNA
**residues
1-303 **label CCL
**cross-references GB:279700, GB:A1123456; NID:93261628;
PICN:CABG1998.1: PID:e264228; PID:91224210
**experimental_source strain H37Rv
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                                                                                                           preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 1.90e+01:
6: Mismatches 2: Indels
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Pred. No. 2.85e+01;
5; Mismatches 1; Indels
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Sest Local Similarity 38.5%;
Matches 5; Conservative
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*type complete

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RESULT

ENTRY

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*authors Nelson K.E.: Clayton, R.A.: Gill, S.R.: Gwinn, M.L.: Dodson, R.J.: Haft, D.Y.: Hickey E.K.: Pererson, C.D.: Nelson, R.J.: Haft, D.Y.: Hickey E.K.: Pererson, C.D.: Nelson, W.C.: Ketchum, K.A.: McDonald, L.: Utterback, T.H.: Milek, W.C.: Ketchum, K.A.: McDonald, L.: Utterback, T.H.: Milek, W.D.: Pratt, M.M.: Stewart, A.M.: Coffor, M.D.: Pratt, M.S.: Phillips, C.A.: Richardson, D.: Heldelberg, J.: Suitton, G.D.: Fleischmann, R.U.: Wilter, O.: Salzberg, S.L.: Smith, H.D.: Venter, J.C.: Fraser, C.M.: *title Evidence (S.L.: Smith, H.D.: Venter, J.C.: Fraser, C.M.: *title Evidence for lateral Jene transfer between Archaea and Bacteria from genome sequence of Thermotoga mailtima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thymidylate synthase complementing protein - Aquifex aeclicus *formal_name Aquifex aeclicus 08-May-1998 *text_chande 08-May-1998 *text_chande
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transcription regulator, TetR family - Thermotoga maritima (strain MSB8)
#formal_name Thermotoga maritima
1.Jun-1999 #sequence_revision 11-Jun-1999 *text_chanse 20-Aug-1959
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The complete genome of the Ayperthermophilic bacterium
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56.4%: Score 53: DB 2: Length 317;
Best Local Similarity 60.0%: Pred. No. 2.85e+01;
Matches 6: Conservative 3: Mismatches 1; Indels
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*accession G70356
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Search completed: Mon Jun 19 16:17:16 2000 Job time : 7 secs.

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procein - protein database search, using Smith-Waterman algorithm MFsrch_pp

Mon Jun 19 16:16:17 2000: MasPar time 3.50 Seconds 112.990 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-13 (1-13) from US39142524A.pep 94 Description: Perfect Score: Sequence:

VEIKKVSNVIIHG 13

PAM 150 Gap 15

Scoring table:

93857 seqs, 30454973 residues Serreted:

Summaries Minimum Match 0% Listing first 45 Post-processing:

swiss-prot38 1:swissprot Jatabase:

Mean 27.045; Variance 31.177; scale 0.867 Statistics: Pred. No. is the number of results predicted by whence to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	01-856	1.620-01	4.45e-01	1.196+50	1.39e+0C	1.93e+00	1.93e-00	1.936-00	3.11e+00	3.11e-00	4.986+00	7.9.e+00	7.91e+00	7.91e+00	1.25e-01	1.25e+01	1.25e+01	1.95e+01	1.95e+01	1.95e+01	1.95e+01	1.95e-01	1.95e+01
Description	SUGI BASIC PROTEIN PRE	PECIAIE LYASE PRECURSO	LET-756 PROTEIN.	BETA-LACIAMASE, TYPE I		BETA-LACTAMASE, TYPE I	BETA-LACTAMASE, TYPE I	7.	TRANSCRIPTIONAL REGULA	HYPOTHETICAL 59.4 KD P	SUCCINYL-COA SYNTHETAS	MUCCNATE CYCLOISCMERAS	SULFATE ADENYLATE TRAN	NA(+)/H(+) ANTIPORTER.	SIYLE DEVELOPMENT - SPEC	CYTOCHROME P450 109 (E	HYPOTHETICAL 63.3 KD P	40S RIBOSOMAL PROTEIN	LIGASE (SUCCINYL-COA LIGASE [G	HYPOTHETICAL 45.2 KD P		HYPOTHETICAL 45.3 KD P
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S Query Match	100.0	64.8	: N	60.6	9.39	59.6	59.6	59.6	В В	58.5	57.4	55.4	56.4	56.4	55.3	55.3	v.	54.3	54.3	54.3	54.3	54.3	54.3
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HYPOTHETICAL 58.8 KD P HYPOTHETICAL 92.1 KD P		PROTEIN D5.	PROTEIN DS.	NEGATIVE REGULATOR OF	HYPOTHETICAL 91.1 KD P	-	DNA POLYMERASE III, AL	PUTATIVE SNRNP SM-LIKE	CYSTATIN PRECURSOR (OV	40S RIBOSOMAL PROTEIN	HYPOTHETICAL PROTEIN M	PROBABLE G PROTEIN-COU	CHREE PROTO-CACOGENE P	PROBABLE SULFATE ADENY	HEAT SHOCK PROTEIN HIP	GLUCAN 1, 3-BEIA-GLUCOS	PROT	TRANSPORT REG	PROLINE IMINOPERTIDASE	SIUTAMATE-AMMONIA-LIGA
YE06_SCHPO YM52_YEAST	VD05_VACCC	VD05_VACCV	VD05_VARV	MECB_BACSU	YOR3 NPVOP	CLPB_ECOL:	DP3A_BCRBU	RCXX_ARCFU		RS4_CANAL	Y442_MYCGE	KICLRAT	REL_MOUSE	WCCO_RHISB	HTPG_TREPA	EXG1_COCCA	H104_YEAST	MIRA_YEAST	PIP_NEIGO	GENE_HAEIN
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24 25	52	27	28	58	30	3.7	32	33	34	35	36	37	38	36	0 *	4.1	43	4 3	44	45

ALIGNMENTS

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01-NOV-1950 (Rel. 15, Created)
01-NOV-1955 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
17-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last annotation upd
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MEDLINE: 89031257,
Taniai M., Ando S., Usui M., Kurimoto M., Sakaguchi M., Inouye S.,
Matuhasi T.,
Matuhasi T.,
Neterminal amino acid sequence of a major allergen of Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequencing of cDNA coding for Cry ) 1, a major alterned of Japanese cedar pollen.":
Biochem. Biophys. Res. Commun 199:519-625(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM M.A.
TISSUE-POLLEN,
Namba M., Kurose M., Torland K., Fokuda S., Kurimoto M.;
Submitted (JUL-1994) to the EMBL/Forthank/Nobl-Catabases.
                               374 AA.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                               PRI;
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 22-41.
                                                                                                                                                                                                                                                                                                                                                                        TISSUE-POLLEN;
MEDLINE: 94183234.
LI 1
SBP_CRYJA
Ple532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kino K.;
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L756_CAEEL
Q11184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLAB_BACCE
P14488;
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                                                                                                                                                           STINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioliformatics and the EMBL outstailon the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not recoved. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenselisb-sib.ch).
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :
:
                                                                                                                                                                                                                                                                               Score 94: DB 1: Length 374: Pred. No. 7.99e-10:
                                                                                                                                                                                                                                                                                                  0: Indels
                                                                                                                                                                 SUGI BASIC PROTEIN.

L -> F (IN CRY J 1-B).

K -> Y (IN ORY J 1-B).

S -> T (IN ORY J 1-B).

L -> S (IN ORY J 1-B).

L -> S (IN ORY J 1-B).

K -> C (IN CRY J 1-B).

POTENTIAL.

POTENTIAL.

POTENTIAL.

W: 74825950248F56F CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans).
Eukaryota: Fundi: Ascomycota: Plectomycotes: Eurotiales:
Trickocomaceae: Emericella.
                                                                                                                                                family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                            15-0EC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PECTATE LYASE PRECURSOR (EC 4.2.2.2).
                                                                                                                                                                                                                                                                                                   0; Mismatches
AMB A I/AMB A II/CRY J : SUBFAMILY.
                                                                                                                                              Allergen: Glycoprotein: Multigene SIGNAL
                                                                                                                                                                                                                                                               M.
                                                                                        EMBL, D26544; BAR05542.1;
EMBL; D26549; BAR05543.1;
EMBL; D34639; BAR07020.1;
PIR; A44773; A44773.
                                                                                                                               PFAM: PF00544; ped_lyase: l.
PRINTS: PR00807; AMBALLERGEN.
                                                                                                                                                                                                                                                                                Junery Match
Rest Local Similarity 100.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                               40645
                                                                                                                                                                                                                                                                                                                      129 VFIKRVSNVIIHG 141
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIRAIN-FGSC
                                                                                                                                                                                                                                                                                                                                                                    PEL_EMENI
Q00645:
                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                             CARBCHYD
                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                    CHAIN
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Du 2.;
Submitted (MAY-1996) to the L/GenBank/DDBJ databases.
-;- SIMILARITY: BELONGS TO 7:: HEPARIN-BINDING GROWTH FACTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caps
                                                                                                                                                                                                                               Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Nematoda, Geornentea, Rhabditia, Rhabditida,
Rhabditina, Rhabditoidea, Rhabditidae, Pelodorinae, Caenorhabditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
BETA-LACTAMASE, TYPE II PRECURSOR (EC 3.5.2.6) (PENICILLINASE)
                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screens 19. 18.1. Length 113. cred No. 4.45e-01.
5. Mismatches 1: Indels
                                                                                                                                                                       Score 61: DB 1: Length 326:
Pred. No. 1.62e-01:
4. Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48118 MW 7800702ADA005B6F CRC64:
                                                                             POTENTIAL.
PECTATE LYASE.
F6445A4A6D615D49 CRC64:
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Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 413 AA
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PROSKIE; PS02247: HBGE_FGF: FALSE_NEG.
PFEM: PF00167: FGF: 1
SEQUENCE 413 AA: 48118 Mn 78007D2
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT:
                                                             15
326
34580 MW:
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HSSP: P05230: ZAXM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Maich
Rest Local Similarity 50.0%;
Matches 6: Conservative
EMBL: U05592: AAA80568.1; -
PFAM: PF00544: pec_lyase:
Lyase: Signal. 15
SIGNAL 16
CHAIN 16 326
                                                                                                                                                                            Query Match 64.9%;
Best Local Similarity 63.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LET-756 PROTEIN.
LET-756 OR C05D11.4.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 VEVKKNSDVVIN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VFIKRVSNVIIH 12
                                                                                                                                                                                                                                                                            110 YIRRVSNVIMR 120
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                                                                                                                                                                                                                                                                                                         SEQUENCE 325 AA:
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MEDLINE: 88227879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus cereus
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BLA2_BACSP
PlC425;
                                               STRAIN-168;
                                                                                                                                                    STRAIN-IS58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
ACT_SITE
                                                                                                                                                                                                                      Hecker M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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    SOUTH THE REAL PROPERTY OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \ddot{c}
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                                                                                                                                                                                                                                                                                                    Lim H.M., Iyer R.K., Pene 3.3.:
"Site-directed mutabenesis of dicarboxylic acids near the active site of Bacillus cereus 5/8/6 beta-lactamase II.":
Biochem. J. 276:401-404(1991).
-!- FOURTION: CAN HYDROLYZE CARRAFENEM COMPOUNDS.
-!- FOURTION: ACIVITY: A RETA-LACTAM + H(2)0 - A SUBSTITUTED BETA-AMINO ACID.
                                                                                                      MUTAGENESIS.
MEDLING: 89308559.
Lim H.M., Pene J.J.;
"Mutations affecting the catalytic activity of Bacillus cereus 5/B/6
"Mutations affecting the catalytic activity of Bacillus cereus 5/B/6
Lim. H.M., Pene J.J., Shaw R.W.; and expression of the Bacillus cereus "Cloning, nucleotide sequence, and expression of the Bacillus cereus 5/78/6 beta-lactamase II structural gene."; J. Bacteriol. 170:2873-2878(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA-LACTAWASE, TYPE II.
ZINC 1 (BY IMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 3 (BY SIMILARITY).
ZINC 5 (BY SIMILARITY).
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ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: BINDS TWO ZINC LONS PER MCLECULE.
SIMICARITY: SELONGS TO THE CLASS-B BETA-LACTAMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JT 5
SUCD_BACSU STANDARD: PRT: 299 AA.
980865:
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5) (SCS-ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillus/Clostridium group,
Bacillus/Staphylococcus group, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; DB 1; L4
No. 1.19e-00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR: A32017; A32017.

HSSP: P0419C; 19MC.

PROSITE: PS00743; BETA_LACTAWASE_B_1: 1.

PROSITE: PS00744; BETA_LACTAWASE_B_2: 1.

PROSITE: PS00753; 1accamase_B; 1.

Hydrolase: Zinc; Antibiotic resistance; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (VEGETATIVE PROTEIN 239) (VEG239)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: M19530: AAA22562.1: -.
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FIKRVSKVII 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                               MUTAGENESIS.
MEDLINE: 91264793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
110
119
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MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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METAL
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtills.";
Electrophoresis 18:1451-14(4):1451-14(4):1951-1
-: CATALYTIC ACTIVITY: SUCCIINTE - COA + ATP - SUCCINTL-COA + ADP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIS OF SUCCENTL-COA SYMESTASE O ATP CITRATE-LYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
115-JUL-1999 (Rel. 13, Last annotation update)
BETA-LACTAMASE, TYPE II PRECURSOR (EC 3.5.2.6) (PERIC: LINASE).
BACALlus Sp. (Strain 170).
BACALlus Sp. (Strain 170).
BACHELIA: Firmicutes: Bacilius/Clostridium group:
Bacallus/Staphylococcus group: Bacilius/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ċ
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-!- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
-!- SIMILARIIY: BELONGS IO THE CLASS-B BETA-LACTAMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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60.6%: Shore 57; DB 1: Length 299;
Best Local Similarity 46.2%: Short No. 1.196+00;
Matches 5: Conservative : Mismatches 2: Indels
                                                                                                                                                                *L/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker
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2EB28DB9DD177D15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCNIT: IETRAMER OF TWO "PHA AND TWO RETA CHAINS (BY SIMILARITY).
-1- SUBCNIT: CO CHER ALE SUBUNITS OF SUCCINYL-COMO OF MALATE-LOAD LIGASE AN 0 APP CLIRATE-LYASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: AJ000975; CAA04420.1; -.
BMBL: AJ9112; CAB13483.1; -.
HSSP: PC7459; 1SCU.
SUBTILIST: BG12681; SUCD.
PROSITE: PS01215; SUCCINYL_COA_LIG_1; 1:
PROSITE: PS01215; SUCCINYL_COA_LIG_1; 1:
PROSITE: PS01215; SUCCINYL_COA_LIG_1; 1:
PRAM: PF03549; 1;qase-COA. 1:
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                                                                                                    Foulger D., Errington J.: Submitted (OCT-1997) to the telement of the submitted (OCT-1997) to 
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SEQUENCE FROM N.A.
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Ambler R.P., Canlel M., Fleming J., Hermoso J.M., Pang C., Waley S.G.;
"The amino acid sequence of the zinc-requiring beta-lactamase II from the baccerium Bacilius cereus 569.";
FEBS 1ett. 189:207-211(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 88137841.
MEDLINE: 88137841.
Sutton B.J., Artymikk P.J., Cordero-Borboa A.E., Little C.,
Phillips D.C., Waley S.G.;
Phillips D.C., Waley S.G.;
"An X-ray-crystallographic study of beta-lactamase II from Bacilius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hussain M., Carlino A., Madonna M.C., Lampen C.C.,
"Cloning and sequencing of the retallothioprotein beta-lactarase !!
gene of Bacillis cerous 569/H in Escherichia coli.";
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20-MAR-1987 (Rel. 04, Last sequence update)
20-MAR-1987 (Rel. 04)
15-FEB-2000 (Rel. 04)
19-FE in PRECURSOR (EC 3.5.2.6) (PENICTLLINASE)
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ن
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                                                                                                                                                                                                                                          BETA-LACIAMA E, TYPE II.
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
W. 23EERBOCO45AES7! CRC64:
                                                                                                                                                                                                                                                                                                                                                                           Length 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria: Firmicutes: Pacillus/Clostridium group:
Bacillus/Staphylococcus group: Bacillus.
                                                                                                                       EMBL: WISSSC: AAA22275.1: -.
PIR: A24331 PMS2S.
PIR: A24331 PMS2S.
PROSITE: PS00743: BETA_CATAMASE_B_1: 1.
PROSITE: PS00744: BETA_CACTAMASE_B_2: 1.
PROSITE: PS00753: Lactamase_B3: 1.
Hydrolase; Zicc: Actibiotic resistance: Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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C
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 164:223-229(1985).
                                                                                                                                                                                                                                                   115
118
10 1120
1179
240
240
28153 MM: 2
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Biochem. J. 248:181-188(1987).
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Local Similarity 70.0%:
                                                                                                                                                                                                                                                                                                                                                                                                        7: Conservative
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                                                                                                                                                                                                                                             105 FOKRVIDVII 114
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BLM.
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MEDLINE: 86008356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus cereus.
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PC4190;
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SEQUENCE
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                                                                                                                                                                                                                            MEDLINE; 98400945.
Fabiane S.W., Sohi M.K., Wan T., Fayne D.D., Bateson D.B.,
Mitchell S.W., Sohi M.K., Wan T., Fayne D.D., Bateson D.B.,
"Crystal structure of the zinc-dependent beta-lactamasm from barrilus cereus at 1.9-Å resolution: binuclear active site with reatures of a monopuclear enzyme."
Biochemistry 37.12464-12411(1998).
                                                                                                                                                                                                                                                                                                                                                                          Gaps
MEDLINE; 96067120.
Carfi A., Pares S., Duee E., Galleni M., Duez C., Frere J. M.,
Dideberg O.;
The 3-0 structure of a zinc metallorbetarlactamase from Bachlius
cereus reveals a new type of protein fold.":
EMBO J. 14:4914-4921(1995).
                                                                                                                           Carti A., Juee E., Gallen, M. Frere J.-M., Dideberg G.,
1.85-A resolution structure (the zinc (II) betarlandase (10)
Bacillus cereus.")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R EMEL; M1189: AAA22276.1: -.
R PIR: A01006: PNBSU2.
R PDB: IBMC; 28-463-96.
R PDB: IBMC; 29-5EP-98.
R PDB: IBMC; 23-5EP-98.
R PDB: IBMC; 23-5EP-98.
R PDB: IBC2: 14-70T-58.
R PDB: IBC2: 20-4PR-99.
R PRESITE: PSU074: BETA.IAMANE_F... 1.
R PRAM: FR00753: 1amane=28: 1.
R PGM: AMICIANASE_S: 1.
R PGM: AMICIANASE_S: 1.
R PGM: AMICIANASE_S: 1.
R PGM: AMICIANASE_S: 1.
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116 ZINC I, HIGH-AFFINITY.
120 ZINC I, HIGH-AFFINITY.
179 ZINC Z, LOW-AFFINITY.
179 ZINC Z, HIGH-AFFINITY.
178 ZINC Z, LOW-AFFINITY.
240 ZINC Z, LOW-AFFINITY.
240 ZINC Z, LOW-AFFINITY.
28092 MW: 266EBFB7DDA45431 CRC64;
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                                                                                                          X-RAY CRYSTALLOGRAPHY (1.85 P. DSTROMS)
MEDLINE: 98437525.
                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.7 AN SIROMS).
                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                  Acta Crystallogr. D 54:313-323(1998)
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larity 70.0%;
Conservative
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Best Local Similarity
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FIKRVSNVII 11

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Score 55: DB 1; Le
Pred. No. 3.11e+60;
6: Mismatches 2;
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                                                                                                              58.5%:
38.5%;
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nes 5; Conservative
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                                                      PIR; D27212; W2BE4
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connell M.;
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YOK7 C
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Matches
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Davison A.J. Scott J.E.;
The complete DNA sequence of varicella-zoster virus.";
J. Gen. Viroi. 67.1759-1816 (1986)
1. S.MILARITY: BELONGS TO FAMILY THAI GROUPS TOGETHER HSV-1 UL54,
HSV-2 UL54. EHV-1 5, V2V 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
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                                                                                                                                                                                                                                                                                                       This SWIS.-PROT entry is copyright. It is produced through a collaboration between he Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license arreement (See http://www.isb-sib.ch/announce/or sond an email to license@isb-sib.ch).
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                                                                                                                               Nitrobacter vnigaris.
Bacteria: Proteobacteria: alpha subdivision: Bradyrhizobium group.
                                                                                                                                                                                                                Streeker M., Sickinger E., English R.S., Shively J.M., Bock E., Submitted (XXX-1994) to the EMBL/GenBank DDBJ databases.
-:- CATALYTIC ACTIVITY: ATP + D-RIBJIOSE 5-PHOSPHAIE - ADP +
-:- THBUIOSE 1,5-BISPHOSPHAIE.
-:- PATHWAT: CALVIN CYCLE.
-:- PATHWAT: CALVIN CYCLE.
-:- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0478; PHRIBLKINASE.
PROSITE: PSGC567; PHOSPHORIBULCKINASE: 1.
PFAM: PFGC485; PRK; 1.
Iransferase: Kinase: Calvin cycle: ATP-binding; Photosynthesis.
NP_ESND 12 23 ATP (POTENTIAL).
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د:
                                                      01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
PHOSPHORIBULDKINASE (EC 2.7.1.19) (PHOSPHOPENICKINASE) (PRK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.6%: Score 55; UB 1; Length 230; Best Local Similarity 41.7%; Pred. No. 1.93e-00; Matches 5; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BINC 12 20 ATP (POTENTIAL).
SEQUENCE 290 AA: 32908 MW; 9E29722319A2841C CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Varicella-zoster virus (strain Dumas) (VZV).
Viruses; dSDNA viruses, no RNA stago: Herpesviridae:
Alphaherpesvirinae: Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1969 (Rel. 10, Created)
01-MAR-1986 (Rel. 10, Last Sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
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                             290 AA
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                                                                                                                                                           Nitrobacteraceae; Nitrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: 122884; AAA25506.1: -. HSSP; P12033: 1A73.
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD
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                          KPPR_NITVU
P37100;
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P09269:
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL: X04370: CAA27887.1:
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STRAIN-H37RV;
MEDLINE; 98295987.
Cole S.I., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saps
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Actinomycetales; Corynebacterineae; Mycobacterlaceae; Mycobacterium
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Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caencrhabditis
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P71558:
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
SUCCINVL-CGA SYNHETASE ALP: CHAIN (EC 6.2.1.5) (SCS-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 50:0%, Pred No. 3 lier(U)
Matches 6: Conservative 1: Mismatches 1: Indels
                                                                                                                                                                                                                                                                     Length 452:
                                                                                                                                                                                                                                                                                                                                     2: Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 59.4 KD PROTEIN 05662.7 IN CHROMOSCHE III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: U23177; AAA64334.1; -.
WORMPEP: C56G2-7; CE01876.
WYPOChetical protein.
SEQUENCE 55G AA: 59367 MW: 878847A58EFOAEE8 CRC64:
                                                                                                                                                                rranscription regulation.
SEQUENCE 452 AA; 51543 MW; 42926E4A71E380B4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Peulwell T., Gentles S., Hamlin N., Holrcyd S., Hornsty T., Jacels K., Krogh A., McLean J., Moule S., Murphy L., Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skeiton S., Squares S., Sqares R., Sulston J.E., "Deciphering the biology of Mycobacterium tubercuicsis from the complete genome sequence."

**Nature 193:537-544 (1598)**

**Institute Activity: SUCCINAIE + COA ** AIP - SUCCINYL-COA ** ADP **

**OPTIVITY: SUCCINAIE + COA ** AIP - SUCCINYL-COA ** ADP **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
MEDINE: 88139192.
Aldrich T.L., Chakrabarty A.M.;
*Iranscriptional regulation, nucleotide sequence, and localization of the promoter of the catBC operon in Pseudomonas putida.";

[3]

[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STATAIN-PRESCUES:
MEDIINE: 97277391.
Aldrich T.L., Frantz B., Gill J.F., Klibane J.J., Chakrabarty A.M.;
Cloning and complete nucleotide sequence determination of the catB
gene encoding cis.cis.muconate lactonizing enzyme.";
                                                                                                                                                                                         -1- SCBUNIT: IETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY SINLLARITY).
--- SINLLARITY: TO CHER ALPHA SCBUNITS OF SCCCINYL-COA SYNTHETASE.
OF MALATE: -COA LIGASE AND TO ATP CITRATE-LYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria: Proteobacteria: gamma subdivision; Pseudomonas group:
Pseudomonas.
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Pred. No. 4.98e+CO;
6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL: 279700: CAE01999.1; -. HSSP: PC7459, 1SCU.
PROSTITE: PS01216; SUCCINYL_COA_LIG_1: 1.
PROSTITE: PS0399; SUCCINYL_COA_LIG_2: 1.
PFAM: PFC0549; 1,44886-COA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 AA; 31229 MM;
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Host Local Similarity 38.5%;
Matches 5: Conservative
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                     Goldman A., Ollis D.L., Steitz I.A.;
Grystal Structure of muconate lactonizing enzyme at 3-A resolution. T.
J. Mol. Biol. 194:143-153(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aromatic hydrocarbons catabolism, is metuse: Manganese: Obstructorolism: 0 0 170 170 170
                                                                                                                                                                                                                                                                                                                                                -:- COFACTOR: REQUIRES MANGANESE.
-:- PAI WAY: SECOND SIEP IN THE DEGRADATION OF CAIECHUL TO SUCCINATE
AND ACEIYL-COA IN THE BET -- KETCADIFATE PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                      -!- FUNCTION: CATALYZES A SYN CYCLOISOMERIZATION.
-!- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE - CIS.CIS-
HEXADIENEDIOATE.
                                                                                                                                  Heifs S., Kahn P.C., Guta B.L., Mallows D.J., Goldman A.,
"The refired X-ray structure of muchate lactonizing enzyme from
Pseudomonas putida PR22000 at 1.85-A resciution.";
J. Mol. Biol. 254:998-94:(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBUNIT: HOMOOCTAMER.
-:- SIMILARITY: BELONGS TO THE MANDELATE RACEMASE / MUCHATE LACTONIZING ENZYME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1; Length J...
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S -> T (IN REF. 2).
MISSING (IN REF. 1).
MW: A7767A865EACD38C CRC64:
                                                                                                                                                                                                             SIMILARITY TO MR.
MEDLINE; 91015392.
Neidhart D.J., Kenyon G.L., Gerit J.A., Petsko G.A.;
"Mandelate racemase and mucchate lactonizing enzyme at mechanistically distinct and structurally homologous." Nature 347:692-694(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYSN.ECOLI STANDARD: PRT: 475 AA. P23845: 01-NOV-1991 (Rel. 20, Created) 01-NOV-1992 (Rel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANGANESE.
MANGANESE.
MANGANESE.
                                                                                        X-RAY CRYSTALLOGRAPHY (1.85 ANSSTROMS)
CRYSTALLOGRAPHY (3.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M1('6C; AAA25765.1; --
EMBL, M1(.85, AAA25765.1; --
EMBL, A27316; A27316.
PIR, A28630; A28630.
PDB, IMUC; L1_UUL-96.
PDB, ZMUC; 04-NOV-98.
PDB, 3MUC; 04-NOV-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00908; MR_MLE_1; 1:
PROSITE; PS00909; MR_MLE_2; 1:
PFAM; PF01188; MR_MLE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.48;
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374 AA;
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                                                                                                                       MEDLINE: 96107379.
                87283908
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              MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- FUNCTION: MAY BE THE GIPASE, REGULATING ATP SULFURYLASE ACTIVITY.
-:- CATALYTIC ACTIVITY: ATP + SULFATE - PYROPHOSPHATE -
ADENYLYLSULFATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: SELONGS TO THE GTP-BINDING ELCNGATION FACTOR FAMILY. CYSN/NODQ SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
SECUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE: 9742611 / MG1655;
Blattner F.R. Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R. Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R. Plunkett G. III, Bloch C.A., Roylew G.F.,
Riley M., Collado-Yides J., Glasner F.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                               SIRAIN-K12:
MEDLINE: 92268080.
LEYN T.S., Voqt T.F., Suo Y.;
T.T. Sano Y.;
T.T. Sano Y.;
T.T. Sano T.S.
T. Sano T.S.

                                                                                                                                            Escherichia coli.
Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 88115389.
Leyh T.S., Taylor J.C., Markham G.D.;
The sulfate activation locus of Escherichia coli Ki2: cloning,
genetic, and enzymatic characterization.";
J. Biol. Chem. 253:2409-2416(1988).
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GTP-binding.
15-DEC-1998 (Rel. 37, Last annotation update)
SULFATE ADENYLATE TRANSFERASE SUBUNIT 1 (EC 2.7.7.4) (ATP-
SULFURYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.4%: Score 53: DB 1: Length 475: Best Local Similarity 54.5%: Pred. No. 7.91e+00: Matches 6: Conservative 3: Mismatches 2: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
91E983E49732AA15 CRC64;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-5
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113 117 GTF
169 171 GTF
475 AA; 52558 MW;
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ECOGENE; EG10194; CYSN.
PRINTS: PRG0315; ELONGATNFCT.
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EMBL: U29579: AAA69261 1; -.
EKBL: AE000358; AAC75793.2; -.
PIR: JN0327: JN0327.
HSSP: P02990: lETU.
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                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
SIRAIN-S2807 / AB972:
SIRAIN-S2808 / AB972:
Pavello A., Andrews S., Brinkman R., Gooper J., Diny H., Du Z.,
Favello A., Fulton L., Gattung S., Greco I., Kirsten J., K.caba T.,
Hallsborth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Lat. Wille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Ries L.,
Taich A., Trevaskis E., Viquati D., Wilcox L., Wohldman P., Vaudin M.,
Wilson R., Waterston R.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium transport: Transport: Symport
                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae Taker's yeast).
Bukaryota: Fungi: Ascomyc --: Saccharomycetes: Saccharomycetaies:
Saccharomycetaceae; Saccha. myces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delius F., Hebling U.;
Submitted (SEP-1995) to the E: ML/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109369 MW: AD0B86D483DCDD89 CRC54;
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Pred. No. 7.91e+00:
                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                               NA(+)/H(+) ANTIPORTER.
NHAI OR YER138W OR L3149 OR L9606.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 145-985 FRCM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: U538E1: AABE2392.1;
EMBL: X91259; CAA62653.1;
EMBL: Z73310; CAA97709.1; -:
EMBL: Z73311; CAA97711.1; -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 36.4%;
Matches 4; Conservative
                                                                                                                                  STANDARD;
419 IFIDRLSNVTV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320
362
411
985 AA:
                          1 VFIKRVSNVII 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                NAH1_YEAST
099271;
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Gaps

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE K.A., Smith A.G., Gasser C.S.;
Budeller K.A., Smith A.G., Gasser C.S.;
Sudeller K.A., Smith A.G., Gasser G.S.;
Sudeller K.A., Gasser G.S., Gasser G.S.;
Sudeller K.A., Gasser G.S., Gasser G.S.;
Sudeller K.A., Gasser G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
STATE DEFECCEMENT-SPECIFIC PROTEIN 9612.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spernatophyta: Magno.lophyta: eudicotyledons;
core eudicots: Asteridae: euaslerids I; Solanales: Solanaceae;
solanum.
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Pred. No. 1.25e-01;
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                                                                                                                                                     9612_EYCES STANDARD: PFI: 404 AA. P24336: 01-MAR-1992 (Roll. 21, Created) 01-MAR-1992 (Roll. 21, Last sequence update) 15-501-1999 (Roll. 38, Last annotation update) SIYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44298 MM:
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PIR: $12209: $12209.
PFAM: PFO0544: pec_lyuser.i.
PRINTS: PROC867: AMARLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match
Local Similarity 63.6%;
Nes 7: Conservative
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27
37
291
404 AA:
338 IFLRRIPAVMI 348
                                                1 VEIKRVSNVII 11
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SIGNAL
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Search completed: Mon Jun 19 16:16:23 2005 Job time : 5 secs.

162 IHHTSNIIIHG 172

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:16:40 2000; MasPar time 8.57 Seconds 105.118 Willion cell updates/sec Rom on:

Tabular output not generated.

>US-09-142-524A-13 (1-13) from USO9142524A.pep 94 1 VFIKRVSNVIIHG 13 Description: Perfect Score: Sequence:

PAM 150 Gap 15

Scoring table:

225878 seqs, 69334122 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries Catabase:

sptrembll2
1.sp_archea Z.sp_bacteria 3.sp_tingi 4.sp_buman
5.sp_invertebrate 6.sp_mamrai 7.sp_mhc 8.sp_organelle
5.sp_invertebrate 6.sp_mamrai 7.sp_mhc 8.sp_organelle
9.sp_phage 10.sp_piant 11: o_rodent 12.sp_unclassified
13.sp_vertebrate 14.sp_virus

Mean 25.111; Variance 31.885; scale 0.919 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No	9.02e-02	1.50e-0	4.07e-0	4.07e-5	1.08e+00	1.76e+0C	4.52e+00	4.52e+00	4.52e+00	7.20e+00	7.20e-00	1.14e+0	1.79e+0	1.79e+01	1.79e-0	1.79e+0]	1.79e-01	1.79e+0	1.79e+0	1 790+01
Description	ORF MSV077 HYPOTHETICA	HYPOTHETICAL 41.5 KD P	POLLEN MAJOR ALLERGEN	CHAC1 PRECURSOR.	F12F1.22 PROTEIN.	BETA-N-ACETYLGLUCCSAMI	GLYCOSYLIRANSFERASE GT	PUTATIVE FLIPPASE.	K07A12.2 PROTEIN.	PROLYL AMINOPEPTIDASE.	TIFIS.3 PROTEIN (EC 2.	MAT1.	VIRULENCE ASSOCIATED P	TRANSCRIPTIONAL REGULA	THYMIDYLATE SYNTHASE C	CODED FOR BY C. ELEGAN	HYPOIHETICAL 41.2 KD P	PITA.	PLASMID GRO4970, COMPL	PROTEIN
10	09YW15	675260	092NU7	686369	055388	09ZH39	P96565	09XDK3	P90920	032449	064795	082590	P72994	CLZM60	066883	922917	Q9YW11	022370	045322	P90755
# C	7.	N	10	1 0	0.7	7	7	(4	'n	7	0.1	0	7	7	a	'n	14	10	10	'n
y Glery Match Length	598	360	367	375	366	783	4 C8	511	861	317	1894	45.	75	Co	317	327	357	405	411	674
¢ Clery Match	68.1	67.0	54.9	64.9	62.8	61.7	29.6	9.69	9.69	58.5	58.5	57.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4	56.4
Score	54	m Y	61	61	s S	58	26	26	99	55	55	54	53	53	53	S)	53	53	53	e S
Result No.		7	m	4	Ś	φ	7	æ	6	10	11	12	13	7.4	15	16	17	18	19	20

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                                                                                                                                  KALAMBARETI T., BULACH D.M., RAJAKUMAR K., ADLER B.;
Generic Organization of the Lippoplysaccharled Oranigen Biosynthetic
"Generic Organization of the Lippoplysaccharled Oranigen Biosynthetic
"Generic Organization of the EMBL/GenBank/DDBJ databuses."
Submitted (UCL-1998) to the EMBL/GenBank/DDBJ databuses.
EMBL: AF078135, AAD12950.1:
Hypotherical protein
SQUENTE 360 AA: 41546 MW. 822CIEEJ CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M., KOMIYAMA N., ITOH M., ITOH H., SONE I., KUNO K., TAKAGI I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OHIA N.:
OHIA N.:
"Purification, characterization and molecular cloning of Cha o 1, a
major allergen of Chamaecyparis obtusa (Japanese cypress) pollen.";
Mol. Immunol. 33:451-460(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8380
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BROCKS E.G.;
Molecular cloning of mountain cedar (Juniperus ashel) pollen major alleges to the letter of mountain cedar (Juniperus ashel) pollen major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LI 3

PRELIMINARY:
092NU7

092NU7

01-MAY-1999 (TEMBLrel. 10, Created)
01-MAY-1999 (TEMBLrel. 10, Last sequence update)
01-MAY-1999 (TEMBLrel. 12, Last annotation update)
01-NOV-1999 (TEMBLRel. 12, Last annotation update)
10-Nov-1999 (TEMBLRel. 12, Last annotat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chamaecyparis obtusa.
Swaryota, Viridplantae: Streptophyta: Embryophyta; Tracheophyta;
euphy.lophytes: Spermatophyta; Coniferopsida: Coniferales;
Taxodiaceae: Chamaecyparis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oucry Match 67.0%: Score 63: DB 2: Length 360: Rest Local Similarity 56.7%; Pred. No. 1.5 e-01: Matches 8: Conservative 2: Mismatches 2: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 ....
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR106663; AR03609-1;
EMBL, AR106669; AR003609-1;
EMBL, AR10669; AR003608-1;
EMBL, 36544; Junas;1988;36544;
MENDEL: 36548; Junas;1988;36544;
MENDEL: 36548; Junas;1989;36545;
SEQUENCE: 367 AA; 59324 MW; 402DB630 C 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update;
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Pred. No. 4.07e:01
7: Missatches
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10 Q96385
10 Q96385
11 Q963865
11 G1-FEB-1997 (TrEMBLrel. 02, Created)
12 G1-FEB-1997 (TrEMBLrel. 02, Last sequent of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Rest Local Similarity 46.2%;
Matches 6: Conservation
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     SEQUENCE FROM N.A.
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MEDLINE; 96265194.
SUZUKI M., KOMIYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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TECHKARNJANARUK S., GOODMAN A.E.;
Cloning, sequence analysis and characterisation of genes involved in
Cloning, sequence analysis and characterium, Pseudoalteromonas sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y.
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euphyllophytes: Spermatophyta: Maquel:ophyta: eudicotyledons:
core eudicots: Rosidae: eurosids II: Brassicales: Brassicaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-CV. CCLUMBIA:
STRAIN-CV. CCLUMBIA:
STRAIN-CV. CCLUMBIA:
VSSTSAIA V.S., OSBORNE B.II., SCHWARIZ J.R., TGRICMI M., VI 3.
KWAN A., OST D., LIG. S., BUEHLER E., G'NWAY A.B., CUNNAY A.R.,
DEWAR K., FENG J., KIM C., KURTZ D., PALM C.J., LI Y., SHINN P.,
SCN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.R.
SUBMILLED (MAY-1998) to the EMBL/Genhank/UCBJ databases.
EMBL: ACOOLJ31, AAC17625.1.*
MENDEL: 29024: ATALN:1088:29024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudoalteromonas sp. 59.
Bacteria: Proteobacteria: gamma subdivision: Alteromonadaceae:
Pseudoalteromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March Local Structure 72.7%, find his mental tending the mental response to Conservation 2. Most conservation tending the second conservation of the second 
                                                                                                                                                                                                                                                                                                                                        Length 375
                                                                                                                                                                                                                                                                                                     Score 61, DB 10; Length 375
Pred. No. 4.07e-01;
Transce 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AGG-1998 (TrEMBLrel. 07, Created)
01-AGG-1998 (TrEMBLrel. 07, Last sequence update)
01-NCV-1999 (TEMBLrel. 12, Last amonation update)
F12F-122 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10. Created; UMAY-1999 (TrEMBLrel. 10. Last sequence update) 01-NOV-1999 (TrEMBLrel. 12. Last annotation update) BEIA-N-ACETYLGLUCOSAMINIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 AA: 43354 MW. ECF32F54 CRC32;
                                                                                                                                                                                                                             CHAIN 22 375 CHAOL
SEQUENCE 375 AA: 40258 MW: A0981492 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       783 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                              PULENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MENDEL, 29024; Arath 1088:25024.
PFAM: PF00544: pec_lyase: 1.
PRINTS: PRC6807; AMBALLERGEN.
EMBL: D4540; BAAC8246.1; --
MENDEL: 7626; Chaob.: 5084:7626.
PFAM: PF00544; PeC. 19ase: 1
PRINTS: PRO0807; AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiology 3:0-0(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 LFMRIVSHVILHG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VEIKRVSNVIIHG 13
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SEQUENCE FROM N.A.
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68HZ6O
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SIGNAL
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Aminopeptidase.
SECUENCE 317
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                                                                                               K07A12.2
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P90920
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EMBL: U84350; AAB49299....
                                                                                                                                                                                                                                                        Amycolatopsis orientalis.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae:
Actinomycetalos; Pseudonocardineae: Pseudonocardiaceae: Amycolatopsis.
                                                                        Gaps
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SEQUENCE FROM N.A.
MEDLINE: 9940714.
COMSTOCK L.E., COYNE M.J. TZIANABOS A.O., PANTOSTI A.,
COMSTOCK L.E., COYNE M.J. TZIANABOS A.O., PANTOSTI A.,
ONDERRONK A.B., KASPER D.L.;
Analysis of a capsular polysaccharide biosynthesis locus
Bacteroides fragilis...
Infect. Immun. 671355-5321(1999).
EMBL: AFO469742.1.
SEQUENCE 511 AA: 58642 MW; D4196E8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55: DB 2; Length 511:
Pred. No. 4.52e+00;
4: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56: DB 2; Length 408; Pred. No. 4.52e+00; 4; Mismatches 2: Indels
                                             Score 58: DB 2: Length 783;
Pred. No. 1.76e+00;
2: Mismatches 2: Indels
                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. G3, Created)
01-MAY-1997 (TrEMBLrel. G3, Last sequence update)
01-AG2-1999 (TrEMBLrel. 07, Last annotation update)
G1YCOSYLTRANSFERASE GIFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteroides tradilis.
Bacteria, Cytophagales, Bacteroidaceae: Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYXXXX
QYXXXX
01-NOV-1999 (TEMBLrei, 12, Created)
01-NOV-1999 (TEMBLrei, 12, Last Sequence update)
01-NOV-1999 (TEMBLrei, 12, Last annotation update)
WINTITVE FLIPPASE.
                                                                                                                                                                                                                                                                                                                                                                                            408 AA; 43042 MW; 8F3A4D0B CRC32;
EMBL: AF072374: AAC83237.1; -.
HSSP: P06865: 10BC.
SEQUENCE 783 AA: 88856 MW; FF87EDF8 CRC32:
                                                                                                                                                                         408 AA
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larity 54.5%;
Conservative
                                              Query Match
Best Local Similarity 63.6%:
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8%;
Matches 7: Conservative
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 VLFRRVAAVIHHG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VFIKRVSNVIIHG 13
                                                                                                 391 FIKRVSQ11KQ 401
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                                                                                                                        2 FIKRVSNVIIH 12
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P96565
P96565:
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Q9XDK3
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SEQUENCE FROM N.A.

X MEDLINE; 94150718.

A WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COLLEON A.,

CRAXTON M., DERR S., DU Z., DURBIN R., FAVELLO A., FULTON E.,

A GARDNER A., GREEN P., HARMINS T., HILLIER L., JIER M., JOHNSTON L.,

A JONES T., KERSHAW J., LAISTER N., LAIRELLE P.,

A LIGHTNILG J., ILLOYD C., MCMU RAY A., MORTIMORE B., O'CALLAGGIAN M.,

RA PARSONS J., PERCY C., RIFFERN L., FOLPRA A., SAUNDERS D., SHOWNEEN R.,

RAMALDON N., SMITH A., SONNHAWER E., STABEN R., WATERSTON R.,

HIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

HATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,

Elegans J.,

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MEDLINE; 98006313.
KABASHIMA T., KITAZONO A., KITANO A., ITO K., YOSHIMOTO T.;
FROIY] aminopeptidase from Serratia marcescens: cloning of the enzyme gene and crystallization of the expressed enzyme.";
J. Blochem. 122:601-605(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saps
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                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota: Metazoa: Nematoda: Secernentea: Rhabditia: Rhabditida:
Rhabditina: Rhabditoidea: Rhabditidae: Peloderinae: Caenorhabd:tis
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032449
DRELIMINARY: PRI; 317 AA.
032449
O1-34N-1998 (TEMBLEE). 05. Created;
01-3AN-1999 (TEMBLEE). 05. Last sequence update;
01-3N-1999 (TEMBLEE). 12. Last annotation update;
PROUVI. AMINOPERTIDASE.
Serialia marcescens.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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Pred. No. 4.52e+00:
5: Mismatches 2: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCI-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                      Last sequence update)
Last annotation update)
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EMBL; Z81098; CAB03182.1; -.
PFAM; PF00560; LRR; 14.
SEQUENCE 961 AA; 165365 MW; 750352FU CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AA; 35083 MW: FAE10431 CRC32;
961 AA
                                                                                                  Created)
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                                    P90920;
01-MAY-1997 (TEMBLEEL 03.
01-JAN-1998 (TEMBLEEL 05.
01-MAY-1999 (TEMBLEEL 10.
KO7A12.2 PROTEIN.
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Best Local Timilarity 46.2%:
Matches 5: Conservative
     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                            I VFIKRVSNVI 10
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P72994
P72994:
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DOELSCH N.A., THOMPSON M.D., HALLICK R.B.;
"A maturase-encoding group III twintron is conserved in deeply rooted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA:
VYSOTSKAIA V.S., SCHWARTZ J.R., FORIUMI M., YU G., OJI. O, KWAN A.,
LIU S., LI J., ARACJO R., AU M., BRENDEL V., SUEHLER E., CONWAY A.B.,
CONWAY A.R., DEWAR K., FENS J., KIM C., KURTZ D., LI Y., PALM C.J.,
SHINN P., SCN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A.,
THEOLOGIS A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantee: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Marooliophyta: eudicotyledons:
core eudicots: Rosidae: curosids II: Brassicales: Brassicaceae:
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-!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE INTPROSENATE - N PROPHOSOHATE - NDA(N).
-- EMBL: ACCO4393: AAC + 10A(N).
-- PROSTITE: PSO0116: DNA_POLYNERASE_B: 1.
-- PFAM: PF00136: DNA_POLYNERASE_B: 1.
-- PFAM: PF00136: DNA_POLYNERASE_B: 1.
-- PFAM: PF0016: DNAPCLB: 1.
-- PFAM: PF0016: DNAPCLB: 1.
-- PFAM: PF0016: DNAPCLB: 2.1
-- DNA-GILGCLG AA: 2.1137 NW: 3C1AFDS2 CRG32:
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Eukarycta; Euglenozoa; Euglenida: Euglenales; Lepocinclis
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Last sequence update)
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01-A05-1998 (TrEMBLrel, 07, Last sequence update)
11-NOV-1999 (TrEMBLrel, 12, Last annotation update)
11-F15 3 PROTEIN (EG 2.7.7.7),
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01-NOV-1998 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel. 02-NOV-1998 (TrEMBLrel. 04-NAT1.
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2 FIKRVSNVIIHG 13
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STRAIN-CV. OCLUMBIA:
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SEQUENCE FROM N.A.
MEDILNE: 99287316.
NELSON K.E., CLAYION R.A., GILL S.R., GWINN M.L., DODSON R.J.,
NELSON K.E., CLAYION R.A., GILL S.R., GRISON W.C., KETCHUM K.A.,
MCDONALD L., UTIERBACK T.R., MALEK J.A., LINNER K.D., GARRETT M.K.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDBLEBERG J., SOTTON M.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.
SMITH H.O., VENIER J.C., FRASER C.M.;
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                                                                                                                                                                                                                       20.00
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MEDLINE: 97051201.
MEDLINE: 97051201.
MINDLINE: 97051201.
MIYAJIMA N., HIROSAWA M., SUSTURA M., SASAMUTU E., NAKAMUTA Y., MIYAJIMA N., HIROSAWA M., SUSTURA M., SASAMUTU S., KIMUWA T., MIYAJIMA N., HIROSAWA M., MUWAKI A., NAKAZAKI N., NAKUG K., UKUMIWA SHIMPO S., IAKEUCHI C., WADA I., WATANABE A., YAMADA M., YASULA M., TABATA S.,
Euglenoid species: Are group III introns the chicken or the eduth: Submitted (OCT-1997) to the EMBL/Gensank/20BJ databases.
EMBL: 29884; CAB16599.1; -. S2368 FW; RE943A2F CRC32;
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Submitted (JUN-1996) to the EMBL/JenHank/FDFBJ databases
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Bacteria: Oyanchacteria: Chrochocystis
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01-FEB-1997 (TEMBLIEL) 62, Last segmente update)
01-JAN-1999 (TEMBLIEL, 65, Last accordation update)
VIRULENCE ASSOCIATED PROTEIN B.
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2 34; No. 1,79e-01;
3; Misharmes 1
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Bacteria: Thermotogales: Ther: toga.
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SEQUENCE 75 AA; 8539 MW;
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Local Similarity 45.5%;
les 5: Conservative
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Best Local Similarity 50.0%;
Matches 5: Conservative
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                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
HAFT D.H., BICKEY E.K., PETERSON J.D., NELSON R.C., KETCHUM K.A.,
HAPT D.H., BICKEY E.K., PETERSON J.D., NELSON R.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARREIT M.M.,
HEIDELBERG J., SUTTON M.D. PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON M.D., PRATT M.S., PHILLIPS C., SALZBERG S.L.,
SMITH H.O., VENNER J.C., FRASER C.M.;
SLDMILLER (JUN-1995) to the EMBL/GenBank/DDBJ databases.
ENBL: AEO01449; AAD35805.1:
SEQUENCE 190 AA: 22492 WW. B32D7ZDO CRC32;
"Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of Thermotoga maritima.":
Nature 399:323-329(1999).
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MEDLINE: 98196666.
MEDCKEXI G., WARREN P.V., GAASTERLAND T., YOUNG W.G., JENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AJJAY M., HUBER
FELDMAN R.A., SHORT J.M., OLGON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
acolicus.";
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DECKERT G., MARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
SCRAHAN D.E., CVERBEER R., SNEAD M.A., KELLER M., AUGKY M.,
FELDMAN R.A., SHORT J. W., GLESON G.J., SWANSON R.V.,
SUBMILLE G. (JUL-1997) to the EMBL/GenBack/DDBJ databases,
EMBL: AEGONTOG: AACO6547.1.
SEQUENCE 317 AA: 37642 MW; 6E749GF4 CRC32;
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                                                                                                                                                                                                                                                                                   Query Match 56.4%: Score 53: DB 2: Length 190: Best Local Similarity 58.3%: Pred. No. 1.79e+01: Matches 7: Conservative 2: Mismatches 3: Indels
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 16:05:16 2000, MasPar time 2.77 Seconds 102.539 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-142-524A-6 (1-12) from US09142524A.pep 72 1 ISLKITSGKIAS 12

Description Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

188953 seqs, 23685106 residues

Searched:

a-deneseq35 l:geneseqp Database:

Mean 16.610; Variance 49.150; scale 0.338 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.46e-01	2.45e-01			2.46e-01	4	7	2.45e-01	2.45e-01	2.46e-Ci				4.90e+00	4.90e+00	8.32e+00	32	8.32e+00			3.97e+01	3.97e+01	3.97e+01
Description	Japan cedar pollen mat	Residues 341-355 of Cr	Cedar polien allergen	Sugi allergen protein	Multi-epitope peptide	Japonicum allergen res	Japan cedar polien Cry		Japonicum allergen.	Japanese cedar pollen	polle:	Cedar pollen allergen	Cedar pollen allergen	Japanese cedar pollen	Japan cedar pollen mat	T-cell epitope peptide	Chamaecyparis obtusa p	ss poll	Sugi allergen protein	allergen	Juganese cedar pollen	Japanese cedar pollen	Sugi allergen protein
d1							R93599			R53690		R81577		W14301		W42197		W42122	W80342	W80344	W14302	4	W8C341
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Cuery Match	100.0	100.0	100.0	10C.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.3	90.3	84.7	84.7	81.9			'n.	ŝ	73.6	ص	73.6
Score	7.5	72	7.2	7.2	25	72	7.5	72	2.	72	72	65	65	61	61	59	59	65.	54	54	53	53	ς, 13
Result No.	7	2	ε.	•7	ชา	T)	7	90	17/	10	11	12	13	77	15	16	17	18	61	20	21	22	23

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411474888888888888888888888888888888888	4 4 4 4 1 W 4 10

## ALIGNMENTS

RESULT	בן
	R97939 standard; peptide; 15 AA.
S S	R97939;
	I amino acids
	.X 1 11:
	Sug1 pollinosis; diagnosis; tratment.
	Cryptomeria japonica.
	J08047392-A.
	20-FE3-1996.
	G7-NOV-1994; 297840.
	65-NOV-1993; CP-276773.
	26-MAY-1994; JP-134868.
PA	(MEIP ) MEIJI MILK PROD CO 1.
DR	WPI; 96-166249/17.
	Japan cedar pollen allergen Dr. j II epitope - comprises at leas:
ΡŢ	part of specified 450 amino acid protein
PS	Claim 8; Fig 5; 17pp; Japanese.
S	R97871-R97960 are overlapping peptides used for the epitope mapping
CC	of the Japan cedar police alleran Gry ( 11. Cry ) II and alleranic
S	peptides of it are useful in the diacousts, prevention and treatment
O)	of Sugi politicosis, the a proje reaction to Japan redar pollen.
S	Significant regions of the Lilerage were identified using the
Ü	overlapping peptides of the full epitope derived from a Cry 5 ::
00	antiden-specific T cell line. Amino acids 66-80 (R97884) and 186-200
S	(R978908) of the full mature 460 amino acid allerges are the most
8	allergenic of the 90 peptides tested
SO	equence 15 AA:
2 8	Query Match 100.0%; Score 72; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 2.45e-0;
.¥a	12; Conservative 0: Misma
qa	4 ISLKLTSGKIAS 15
ò	1 ISLKLISGKIAS 12
RESULT	2
ü	W57770 standard: peptide; 15 AA.
<b>A</b> C	457770;
51	(first entry)
30	341-355 of Cry j 2.
Κ¥	Cry j 2; Japanese cedar pollen antigen: allergy: immunotherapy:
X.	Η
SO.	Cryptomeria japonica.
S.	WC9826902-A1.

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12-MAY-1998.
12-NOV-1997. UG4129.
13-NOV-1997. UG4129.
13-NOV-1997. UG4129.
14-NOV-1997. UG4129.
15-NOV-1998.
15-NOV-1998.
16-NOV-1998.
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18-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide(s) derived from codar pollen allergens - activate allergen-specific T-cells, but not allergen-specific IqE antibodies, used for treating codar pollinosis claim 4: Page 29: 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cedar pollen allerger peptide II (T-cell epitope).
Cedar: Cryptonoria japonica: pollen: allergen: immunoglobulin E:
IgE: T-cell epitope: antibody: pollinosis therapy: immunotherapy.
Synthelic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic peptides based on portions of cedar pollen allergens A (R81586) and B (R81587) were tested for their ability to activate cedar allergen-specific Toells, but not allergen-specific IgE antibodies.

These peptides (R81580-R81585) were identified as Toell epitopes. These peptides, plus subsequences (R81573-79) essential for Toell recognition, and homologous peptides (R81588-96) can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevent cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.46e-01;
0; Mismatches 0; Indels
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pollinosis, avoiding side-effects such as anaphylaxis.
Sequence 17 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1996

08-SPF-1995: 306295.

10-SPF-1996: JP-242137.

14-JUD-1999: JP-20022.

14-JUD-1999: JP-20022.

(HAYB.) HAYASHIBARA SKIBUTSU KAGAKU.

(HAYB.) RAILU S, TALIGUCKI KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R81583 standard: Peptide: 17 AA.
R81583;
24-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Bost Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sucry Match
100.0%;
Rest Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ISEKETSSKIAS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ISLKLISCKIAS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hino K. Saitu S.
WPI: 96-140976/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-700929-N2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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Periode immunocitierapelic au., to treat allerand diseases to contains milti-epitope periode contains of cell epitope revisors

Tontains milti-epitope periode containing T cell epitope revisors

Solaim 6: Page 31, 58pp. Japanese.

The present sequence represents a multi-epitope peptide which is used as a new immunotherapeutic agent. It comprises T cell epitope revisors from 2 or more different alleragement (presents) insked via arginine or tysine dimers), where the T cell epitope regions have a posit vity index or more different alleraged in a patient group responding to the allerage, have at least 70% reactivity with lymphocytes from patients responding to the allerage, and are not reactive with immunoglobulin E (195) antibodies from patients responsive to the alleragen. The agent can be used to prevent and treat a vide variety of allerage. The agent can be used to prevent and treat a vide variety of allerage and seases. e.g. by describitation. Side effects, e.g. those mediated by 19E, are reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sugi-pollinosis
Claim 7; Page 18: 21pp: Japan.
W80339-58 represent epitopes. T cells, derived from the sugi alleraen procesins Cryyl (W80339-44, W80340-44, W80340-44, W80350-58) and W80356-58) and Cryyl (W80354-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic resction of the body to pollen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W27369;
24-MAR-1998 (first entry)
Multi-epitope peptide used as imminotherapeutic agent #1.
Multi-epitope peptide; immunotherapeutic agent; ellergic disease;
T-cell epitope region; allergen: lymphocyte; immunoglobatin E.
                                                            for T cells.
.: Cryl2: treatment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                    used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72: DB 1: Length 17:
Pred. No. 2.45e-01:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 1; Length 80; Prr1. No. 2.46e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 2.46e-01;
Mismatches 0;
   il-JAN-1999 (first entry)
Sugi allergen protein Cryf2 dellyed epitope fo
T cell epitope; Sugi allergen proteins Cryll: segi-poliinosis; allergic reaction; polien.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e A. Sone In
                                                                                                                                                                                                                       29-SEP-1998.
22-DEC-1997: 353448.
24-DEC-1996: JP-343441.
24-DEC-1996: JP-343441.
(ARVB.) HAYASHIBARA SEIBUTSU NATAKU.
(SANY.) SANKYO CO LTD.
WPI: 98-577037/49.
A linked I cell epitope pepti . used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-1997.
1C-MAR-1997. J0074C.
1C-MAR-1996. JP-080702.
(MEIP) MEIJI MILK PROD CO LT
Dairiki K. Iwama A. Kino K. K. &
WPI: 97-470495/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W27369 standard; peptide; 80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0%;
Matches 12; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AA:
                                                                                                                                                                                                  J10259198-A.
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SOCOCO STANDARD SEED TO SOCOCO O SOCOCO SOCOCO SOCOCO SOCOCO SOCOCO SOCOCO SOCOCO SOCOCO SOCO
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JT 6 R69791 standard; Protein; 460 AA.

RESULT

RESULT 4 10 W80345 standard; peptide: 17 AA.

1 :SLKLTSGKIAS :2

SLKLTSGKIAS

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Gaps

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0: Indels

Page

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r. 8
R74333 standard; Protein: 514 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77-SEP-1965 (first entry)
Japonicum allergen, induced P
Japonicum allergen, induced P
Japonicum sp.
Japonicum sp.
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Match 100.0%:
Local Similarity 100.0%;
nes 12: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                   Cryptomeria japonica.
BP-65550-A.
31-MAY-1995.
03-NOV-1994; 308117.
05-NOV-1993; JP-299151.
20-DEC-1993; JP-346596.
27-DEC-1993; JP-346814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB: 084045, 084046
                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 ISLKLTSGKIAS 409
398 ISLKLISGKIAS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ISEKETSSKIAS 12
              Kurimoto M, Namba
WPI; 95-195588/26.
                                                                                                                                                                                                                                                                                                                                                                                      514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kino K, Kohno Y,
WPI; 95-067159/09
                                                                                                                                                                                                                                                                                N-PSDB; 290156
                                                                                                                                            desensitizer.
                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                         R74333;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japan cedar pollen allergen Crv j II epitope - comprises at least part of specified 460 anino acid protein Claim 1, Page 10-11: 17pp: Japanese. 183599 is a Japan cedar pollen Cry j II allergen which is useful in the diagnosis, prevention and treatment of Sugi pollinosis, the allergen were identified using overlapping peptides of the full epitope derived from a Cry j II antispens peptides of the full epitope derived from a Cry j II antispens peptides of the full speption derived from a Cry j II antispens period 185-200 (R9789C8) of the full mature 460 amino acid allergen are the most allergenic of the 90 peptides tosted.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                 Disclosure: Pages 26-27; 46pp: Japanese.

949644 encodes R6991 Japonicum allerqen residues 55-514, from which the annializergic peptides R6945-R69809 were derived. The peptides ability to inhibit the cross-linking of an allergen, to an IgE antibody can be used in the prevention and treatment of allergic diseases.
                                                                                                                                                                                                      Peptide antiallergic agent - inhibits cross-linking of allergen with lag antibody
Disclosure, Pages 26-27, 46pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cry ) II: cedar pollen:
              27-SEP-1995 (first entry)
Japonicum allergen residues 55-514.
Japonicum allergen: redidues 55-514: induced histamine release:
antiallergic poptide: 19E cross-linking inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
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Pred. No. 2.46e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  Score 72; DB 1; Length 460;
Pred. No. 2.46e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-1995 (first entry)
Japan cedar pollen Cry 3 11 allergen.
Allergen: epitope, overlapping peptide:
Sugi pollinosis: diagnosis: treatment.
Cryptomeria japonica.
                                                                                                                                                               Kino K, Kohno Y, Komiyama N, Sone I:
WPI: 95-067159/09.
N-PSDB: Q84844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*]abel= sid_peptide
55. .514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1996.

37-NCV-1994: 297846.

05-NCV-1993: JP-276773.

26-MAY-1994: JP-134868.

(MEIP.) MELIX MILK PROD CO LTD.

WPI: 96-166249/17.

N-PSCB: F18102.
                                                                                                     15-JUL-1994; JO1164.
16-JUL-1993; JP-177028.
01-SEP-1993; JP-217725.
07-ARR-1994; JP-069336.
(MEIP.) MEIJI MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R93599 standard: Protein; 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                    Match
Local Similarity 100.0%:
les 12: Conservative
                                                                                                                                                                                                                                                                                                                                                                                      344 ISLKLTSGKIAS 355
                                                                                                                                                                                                                                                                                                                                                                                                              1 ISLKLTSCKIAS 12
                                                                  Japonicum sp.
WO9502412-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J08047392-A
                                                                                         26-JAN-1995
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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                                                                                                                                                                                                                                                                                                                                                             Matches
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Sequence 514 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 New Japanese cedar polien aliergen polypeptide - and DNA coding for useful for treatment and diagnosis of cedar polien allergy claim 5; Page 26-28; 41pp; English. The gene encoding an allergen of Japanese cedar pollen was isolated by PCR amplification using primers based on portions of the allergen protein. The gene was used for recombinant allergen production in E. coli (vector plasmid pKR-223-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                induced histamine release; antiallergic pertide:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide antialiergic agent - Inhibits cross-linking of allergen with IgE antibody
Example 3: Pages 27-28: 46pp: Japanese.
01-NOV-1995 (first entry)
Japanese cedar pollen allergen.
Japanese cedar: pollen: allergen: allergy: therapy: diagnostic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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Pred. No. 2.46e-01;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 514:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 1: 1
Pred. No. 2.46e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0: Mismatches
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                                                                                                                                                                                                                                                                                                                         (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOSSCA12-A.
26-JAN-1995.
15-JUL-1994. JOHNER.
16-JUL-1993. JP-177008.
07-SPR-1594. JP-069336.
07-APR-1594. JP-069336.
(MEIP.) MELUI MILK PROD CC LID.
                                                                                                                                                                                                                                                                                                                                                  Namba M, Torigoe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R69792 standard: Proteis: 514 AA
R69792:
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398 ISLKLTSGKIAS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) derived from cedar pollen allergens - activate
allergen-specific Treels, but not allergen-specific IgE antibodies.
I used for treating cedar pollinosis
claim 5 Page 29/30; 86pp; English
Synthetic peptides based on portions of cedar pollen allergens A
(R81566) and 5 (R81587) were tested for their ability to activate
cedar allergen-specific Treels, but not allergen-specific IgE
antibodies. 6 Peptides (R81589-88158) were identified as Treel
cedar allergen-specific and homologous peptides (R81588-96) can
be used as immunotherapeutic agents to treat or prevent cedar
C pollingsis, avoiding side-effects such as anaphytaxis.
Sequence 5:4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ္ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caps
                                                                                                                                                                                                                                                           Allegenic (.y.) II protein and iraquents from Japanese cedar pollon - used to diagnose, treat and prevent Japanese cedar pollinosis.
Claim 2: Fig 4: 69pp: English.
The sequence is of a Japanese cedar pollen allegen Cry j
II. The protein and its fragments can be used for diagnosis and irearcent of Japanese cedar pollinosis and treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cedar pollen allergen A. Cedar, pollen allergen. Immuncalobalin E. 19E: I-cell epitope: antibody: pollensis: thetapy: Immunciherupy. Cryptomeria. Juponica. EP-100929-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72: DB i: Length 514:
Pred. No. 2.45e-01:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72: 0B 1: Legath 514;
Pred: No. 2.46e-61;
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1996.
08-SEP-1995.
10-SEP-1995.
10-SEP-1995.
14-JUL-1995.
14-JUL-1995.
14-JUL-1995.
14-JUL-1995.
14-JUL-1995.
14-JUL-1995.
14-JUL-1995.
A (HAYB.) HAYASHIRARA SEIBUISU KAGAKU.
                                                                                             Ol-FEB-1995 (first entry)
Japanose cedar police ullergen Cry 1 ll
Cedar polinusis: diagnostic.
Cryptomeria Japonica.
                                                                                                                                                                                                                        Pollock J, Yeung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R81586 standard; Protein; 514 AA
                                                                  R53690 standard: Protein: 514 AA
                                                                                                                                                                26-MAY-1994.
12-NOV-1993: U1100C.
12-NOV-1992: U5-975179.
(IMMC.) ZMGLOGTC PHARK CORP.
Brauer A. Kuo M. PCIlock J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match
Pest Local Similarity 100.0%:
Matches 12: Conservative
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hest Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1996 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 ISLKLTSGKIAS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ISTKLTSGKIAS 12
                                                                                                                                                                                                                                   WPI: 94-183513/22.
N-PSDS: Q66(18.
Altergenic ..y ) II
                                                                                                                                                                                                                                                                                                                                                                          See also R53692-6.
Sequence 514 AA;
1 ISEKETSGKIAS
                                                                                 R53690:
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13. MAR 1995.
10. SEP-1995; 306295.
20. S. SEP-1995; 306295.
20. S. SEP-1995; 306295.
20. S. S. S. JP-200221.
20. S. JP-200222.
20. S. JP-200222.
20. S. JP-200202.
20. S. JP-200202.
20. S. JP-200202.
20. MPI; 96-140976/15.
20. Synthetic peptides based on portions of cedar polien allergens A cedar allergens-specific Teells, but not allergenspecific gE cedar allergens-specific Teells, but not allergenspecific gE cedar allergens-specific Teells, but not allergenspecific gE cedar allergens-specific Teells.
20. MPI; 96-140976/15.
20. MPI; 96-140976/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mew peptidics) derived from cedar police altergens - activate allergen-specific T-cells, but not altergen-specific T-cells, but not altergen-specific 198 antibodies. Claim 3: Page 27: 36pp. Enqlish.
Synthetic poptides based on portions or cedar police alteraces A (R8159) and B (R81587) were tested for their ability to antivate cedar altergen-specific T-cells, but not altergen-specific 19E antibodies. These peptides (R81890-R8155) were televillified as T-cell for T-cell recognition, and lomologous peptides (R81899-95; can be used as Immunotherapoutic anoths to treat or provent, redured an used as Immunotherapoutic anoths to treat or provent, redured an activation of the televillinosis, avoiding side-effers such as anaphylaxis.
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Cedar pollen allergen peptide 22 (horologue).
Cedar: Cryptomeria japonica; pollen: allergen: inminoglobilin E:
Ige: T-cell epitope: antibody; pollinosis; therapy; immunotherapy.
                                                                                                                                                                                                                                           24-MXY-1996 (first entry)
Cedar polien aliergen peptide 5.
Cedar Cryptomeria japonica: pollen; allergen; immunoglobulin E
igE: antibody: pollinosis: therapy: immunotherapy.
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Pred No. 1.67c+00:
0: Mismarchae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
10 Rel594 standard: Peptide; 17 AA.
AC Rel594:
                                                                                                                                           J 12
R81577 standard: Peptide: 11 AA.
R81577:
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Best Local Similarity 100.0%:
Matches 11, Conservative
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08.SEP-1995: 306295.
10.SEP-1994; JP-242137.
14.JUL.1995; JP-200221.
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| ISLKLISGKIAS
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US-09-142-524A-6.rag

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                                                                                                                               Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAYE) HAYASHIBATA SEIBUISU KAGAKU.

(SANY ) SANKYC CO LTD.

WELL 97 195487799.

Peptide allerand derived from Japanese cedar pollen - causes I cell
response specific to redar pollen, for treatment of pollenosis
Claim 29. Page 20: 21pp: Japanese.
The present sequence is one of 24 claimed peptides which were
synthesised based on Japanese cedar pollen sequences. This peptide
was shown to have Japanese cedar pollen antigen I cell epitope
activity by using I cells isolated from a cedar pollinosis patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
that contain 1 or more amino acid substitution(s) ran be used as immunotherapeutic agents to treat or prevent celar pollinosis, avoiding side-effects such as anaphylaxis. Sequence 17 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-1996 (first entry)
Japan cedar pollen mature allergen Cry j II amino acids 346-35C.
Allergen: epitope: overlapping peptide; Cry j II: cedar poilen:
Sugi pollinosis: diagnosis; treatment.
Cryptcmeria japonica.
                                                                                                                                                                                                                                                                                           W1430];
30-APF-1997 (first entry)
30-APF-1997 (first entry)
Japanese cedar pollen allergen-derived peptide 20.
Japanese cedar such pollen; pollinosis; pollenosis; allergen;
allergy; Treel epitope; TCR: Troeli receptor; activation;
immine tolerance; Cry;
Cryptomeria japonica.
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                                                                                        Score 65: DB 1: Length 17: Pred. No. 1.67e+50: 0: Indels 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           query Match 34.7%; Score 61: DB 1; Length 12: 3est Local Similarity 100.0%; Pred. No. 4.90e+00; Matches 10: Omservative 6: Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The peptide produces little or no anaphylaxis.
Sequence 12 AA;
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R97940 standard: peptide; 15 AA.
R97940:
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W14301 standard: peptide: 12 AA.
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07-NCV-1994: 297840.
05-NCV-1995: JP-276773.
26-MAY-1994: JP-134868.
(MEIP.) MELJI MILK PROD CO LTD.
WPI: 96-166249/17.
                                                                                          Query Match
Best Local Similarity 100.0%;
Matches II; Conservative
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07-APR-1995; JP-082519.
                                                                                                                                                                  3 SUKLISCKIAS 13
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overlapping peptides of the full epitope derived from a Cry ] II antigen specific T cell line. Amino acids 65-80 (R97884) and 186-200 (R978968) of the full mature 450 amino acid allergen are the most allergenic of the 90 peptides tested.
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                                                                                                                                                                   0: Indels
                                                                                                                                   Length 15:
                                                                                                                                Score 51; DB 1; Le
Pred. No. 4.90e+60;
5; Mismatches 0;
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                                                                                                                                  Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                   Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Tue Jun 20 13:34:47 2000; MasPar time 2.23 Seconds 77.802 Million cell updates/sec Tabular output not generated. MFsrch_pp Run on:

>US-09-142-524A-6 (1-12) from USO9142524A.pep 72 | ISLKLTSGKIAS 12 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Post-processing: Minimum Match 08 Listing first 45 summaries

145341 segs, 14437480 residue

Searched:

a-:ssued
1:5A_CCMB 2:5B_COMB 3:5_CO: v 4:PCT_COMB 5:backfiles1 Mean 15.504; Variance 46.068; scale 0,337 Statistics: Satabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Pred. No.	8.720+01	8.72e+01	1.12e+02	1.12e+02	1.12e+02	1.12e+02	1.12e+02	1.12e+02	1.12e+02	1.12e-02	1.12e+02	1.12e+02	1.i2e+02	1.12e+02	1.12e+02	1.12e+02	1.12e+02	1.12e-02	1.12e+02	1.12e+02	1.12e+02	1.44e+02	1.44e+02
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SUMMARIES	CI	US-08-993-	US-09-032-	US-08-407-	CS-08-719-	US-08-719-	US-08-719-	US-08-346-	US-08-719-	US-07-721-	PCT-US91-0	0S-08-339-	US-08-503-	US-08-576-	rs-08-839-	US-08-972-	PCT-US93-1	US-08-357-	-065-80-SD	US-08-485-	US-09-184-	-966-80-sn	PCT-US95-1	US-08-208-
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24 45 62.5 331 1 Ut 8.330 Sequence 4, Applicatio 1.444-02 25 44 51.1 1098 1 US-08-409 Sequence 2, Applicatio 1.444-02 28 43 59.7 1489 5 518345-2 atent No. 5183745 2.374-02 39 43 59.7 1794 5 518375-6 atent No. 5183745 2.374-02 31 42 58.3 247 5 5455030 atent No. 5183745 3.034-02 31 42 58.3 318 2 US-08-93 Sequence 3, Applicatio 3.034-02 31 42 58.3 318 2 US-08-93 Sequence 3, Applicatio 3.034-02 31 42 58.3 318 2 US-08-23 Sequence 5. Applicatio 3.034-02 31 42 58.3 460 1 US-08-93 Sequence 5. Applicatio 3.034-02 31 42 58.3 460 1 US-08-93 Sequence 5. Applicatio 3.034-02 31 42 58.3 40 1 US-08-93 Sequence 5. Applicatio 3.034-02 31 42 58.3 3075 2 US-08-93 Sequence 5. Applicatio 3.034-02 31 42 58.3 3075 2 US-08-93 Sequence 5. Applicatio 3.034-02 31 42 58.3 3075 2 US-08-93 Sequence 5. Applicatio 3.034-02 42 58.3 3075 2 US-08-93 Sequence 5. Applicatio 3.034-02 42 58.3 3075 2 US-08-93 Sequence 5. Applicatio 3.034-02 44 44 1 1 US-08-08-93 Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 42 58.3 10.034-03- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-83- Sequence 2. Applicatio 3.034-02 44 44 1 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-02 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-03 44 41 56.9 476 2 US-08-803- Sequence 2. Applicatio 3.034-03 44 41 56.9 476 2 US-08-803- Sequence 3. Applicatio 3.034-0	ALIGNMENTS SULT 1 GS-08-993-318A-7 STANDARD: PRJ: 572 A	US-08-993-318A-7 STANDARD: PRT: 5 xxxxxx Sequence 7, Application US/08993318A	Sequence 7, Application US/C8993318A Patent No. 5998333 GENERAL INFORMATION: APPLICANT: Pedersen, Alien APPLICANT: Schoelder, Palien APPLICANT: Cherry, Joel IIILE OF INVENTION: Les MUTANTS CORRESPONDENCES: 10 CORRESPONDENCES: 10 COUNTRY: USA STREET: 405 Lexication Avenue CITY: New YOR LEXICATION Avenue CITY: New YOR COMPITER: BORDER COUNTRY: USA ZIP: 10174 COMPUTER READABLE FORM: WEDION TYPE: FORPY disk COMPUTER: ParentIn Release #1.0, Version #1.30 (EPC) CURRENT APPLICATION DATE: December 18, 1997 CLASSIFICATION UNBER: US/OB/993.318A FILING DATE: December 18, 1997 CLASSIFICATION UNBER: 33, 28 RETERRACE/DOCKET NUMBER: 5032.200-US TELEFAX: 212-867-012 TELEFAX: 212-867-012 TELEFAX: 212-867-012 TELEFAX: 212-867-012 TELEFAX: STABMIN CALIGS: LENGTH: 572 amino acids ITYPE: amino acids TTYPE: amino acids
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Sequence 2. Application US/0 07544
Patent No. 5741657
GENERAL INFORMATION:
APPLICANT: TSLED, ROGER Y.
APPLICANT: TSLED, ROGER Y.
APPLICANT: LOKATON: ELUOROGENIC SUBSIRATES FOR
TITLE OF INVENTION: BETA-LACIAMASE AND METHODS FOR THE REFERENCE AND USE NUMBER OF SEQUENCES: Z
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08719697

Patent No. 592888
GENERAL INFORMATION
GENERAL INFORMATION: Michael A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SENSITIVE
TITLE OF INVENTION: AND RAPID, FUNCTIONAL IDENTIFICATION OF GENOMIC
TITLE OF INVENTION: POLYNUCLEOTIDES AND SECONDARY SCREENING CAPABILITIES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy c.sb
COMPUTER: IBM PC comput ole
OPERATING SYSTEM: PC-D, VMS-DOS
SOFTWARE: Patentin Reje de #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/6/407,544
FLLING DATE:
                                                                                                                                                                                                     AUDIESSEE: C/O RObbins, burinner & Carson SIREET: 210 N. Figuero: Street, Suite 500 CITY: Los Angeles COTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match
Local Similarity 70.0%; Prvd. No. 1.124+02;
Nes 7: Conservative 0. Mismatches 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ENCE 263 AA: 28907 MW: 327899 CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATJORNEY/AGENT INFORMATIO:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1279
TELECOMMUNICATION INTORMATION:
TELEFUNE: (213) 977-10-1
TELEFAX: (213) 977-10-1
INFORMATION FOR SEQ 15 NO: 2: SEQUENCE CHARACTERISTICS:
                                                          Sequence 2, Application US/08: 7544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08719697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 263 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09012315
Patent No. 59e5818
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Vu, Fend
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONLENCE ADORESS:
ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America, Inc.
SIREE: 455 Lexington Avenue
CITY: New York
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0
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                                                       Score 47: DB 2: Length 572;
Pred. No. 8.72e+01:
5: Misratches 0: Indels
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Pred. No. 8.72e+01;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER SEADABLE FORM:
MEDIUM TYPE: Diskette
COMPOTIER: IBM Compatible
(PPERATING SYSTEM: DGS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
TILING DATE: 27-FEB-1998
CLASSIFITATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 AA.
                                                                                                                                                                                                   572 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: ROZGE, CAFO)
RESISTENCY/OFFER: 36,993
REFERENCY/COCKE: NUMBER: 5200.200-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 212-867-0123
TELEFAX: 212-867-0123
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 572 AA: 63747 MW: 1718990 CN:
TOPOLUGY: linear
MOLECULE:YPE: protein
SEQUENCE 572 AA: 63747 MW; 1728990 CN;
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                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09032315
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TYPE: amino acid
STRANDEDNESS: single
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Pest Local Similarity 54.5%;
Matches 6: Conservative
                                                     Guery Match
Hest Local Similarity 54.5%;
Matches 6: Conservative
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                                                                                                               25 NUKISNGK: AP 35
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2 SLKLTSGK:AS 12
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ID US-09-032-315-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY
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ID US
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NAME: Haile, Lisa A. REGISIRATION NUMBER: 38,347
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70.0%;
                                                                                                                      y Match
Local Similarity 70.0%;
                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                            amino acid
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                                                                                      linear
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Best Local Similarity
                                                                                                                                                        24 IELDLNSGKI 33
                                                                                                                                                                        1 ISEKLTSGKI 10
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                                                                                                                                                                                           RESULT 6
ID US-08-719-697-6
XX
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                                                                                                      SEQUENCE
                                                                                                                      Query Match
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                                                                                                                                                                                                                              xxxxx
                                                                                                                                        Matches
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Sequence 2. Application US/08719697
Patent No. 592888
GENERAL INVERMATION
APPLICANT: Whitney, Michael A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SENSITIVE
TITLE OF INVENTION: POLYNUCLEOTIDES AND SECONDARY SCREENING CAPABILITIES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
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                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:

ZIP: 92037
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                            Score 46: DB 2: Length 264: Pred. No. 1.12e+02; 0: Mismatches 3: Indels
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/719,697
FILING LATE: 26.5EP-1996
CLASSIFICATION: 435
ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                            ATTCRNEY AGENT INFORMATION:
NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
REFER WISTORNEY NUMBER: 08366/003001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERSTICS:
LENGTH: 264 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                   MCLECULE TYPE: protein
JENCE 264 AA; 29039 MW; 333868 CN:
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 70.0%;
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CA
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                                    COUNTRY
                          STATE
                                                                                                                                                                                                                                              SEQUENCE
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Sequence 6, Application US/18719697
Patent No. 592888
GENERAL INFORMATION
APPLICANT: Whitney, Michat. A.
TITLE OF INVENTION: METHOLS AND COMPOSITIONS FOR SENSITIVE
TITLE OF INVENTION: METHOLS AND COMPOSITIONS FOR SENSITIVE
TITLE OF INVENTION: POLYNUCLEOTIDES AND SECONDARY SCREENING CAPABILITIES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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Pred. No. 1.12e+02:
0: Mismatches 3: Indels
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NAME: Haile, Lisa A.
REI ISTANTION NUMBER: 38 347
REFERENCE/COCKET NUMBER: 08366/063001
TELECOMMUNICATION INFORMATION:
TELEFAN: 619/678-5070
TELEFAN: 619/678-5070
INFORMATION FOR SEQ ID NO: 0: SEQUENCE CHARACTERISTICS:
LENGTH: 265 aming acids
               100806/99880
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HENCE 265 AA; 29120 MW; 336091 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 265 AA; 29125 MW; 333037 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT
REFERENCE/DOCKET NUMBER: 0836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ 10 NO: 2:
SEQUENCE CHARACTER 15ICS:
LENGTH: 265 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08719697
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US-09-142-524A-6.rai

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APPLICANT: Whitney, Michael A.

TILLE OF INVENTION: METHCUS AND COMPUSITIONS FOR SENSITIVE
TILLE OF INVENTION: AND RAPID, FUNCTIONAL IDENTIFICATION OF SENDINITION: POLYNOCLEGITIDES AND SECONDARY STREENING CAFABILITIES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish's Richardson P.C.
STREEL 425 Executive Square, Salte 1400
CITY: La Joila
STATE: CA
COUNTRY: USA
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Patent No. 5180666
GENERAL INFCRMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronaid N.
APPLICANT: No. 5180566ak, Raymond F.
TITLE OF INVENTION: MITHOD AND CELL LINE FOR TESTING
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-FOS/MS-DOS
PC-FoS/MS-DOS
n Release #1.0, Version #1.30
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TELECON UNICATION INFURMATION:
TELE :0NE: 619/678-5070
TELEFAX: 419/678-5099
INFORMATION FOR SEQ ID NO: 40
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: CS/08/719.697
FILING DATE: 26-SEP-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTANTION NUMBER: 38.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
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MOLECULE TYPE: protein
FENCE 286 AA: 31570 MW: ***420 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCFIWARE: Patentin Release #1.
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                                                                                                                                                                                 Sequence 4, Application US/08719697
Patent No. 5928888
GENERAL INFORMATION:
                                                                                                                      Sequence 4, Application US/08719697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Ficppy d sk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-FOS/WS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 286 amino acids
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Sest Lonal Similarity 70 0+
Matches 7: Conservative
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GENERAL INCRMATION:
APPLICANT PAISALLI IImochy
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: Methods for modification on interaction of
TITLE OF INVENTION: Methods for modified polypephides with target substrates.
TITLE OF INVENTION: encoded modified polypephides with target substrates.
NUMBER OF SEQUENCES: 86
CCRESSIN: Richard F. Irecartin
STREET: 4 Embarcadoro Center, Suite 3405
CLITT: San Francisco
STATE: 731 [Crinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 1.120+02;
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   Indels
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COMPUTER: ISM PC COMPATIBLE
CPERATIN: SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.6, Version #1.25
CORRENT APELICATION DATA:
                                                                                                                                                                                                                                                   285 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/602.158
FILLING (AFF) 22-401-1990
ATTORNEY ALGERT INFORMATION
NAME: Legartin, Richard F.
REGISTARION NUMBER: 318".
REGISTARION NUMBER: 318".
REFERENCE/DOOKET NUMBER: A 53469/RFT
TELECOMMUNICATION INFORMATION
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/039,501 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/346.3333
FILING DATE:
                                                                                                                                                                                                                                                   PRT
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286 AA; 31466 MW: 387468 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08346333
Patent No. 5677153
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08346333
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Sest Local Similarity 70.0%; Pred.
Matches 7; Conservative 0; 3
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TELEFAX: (415) 398-3249
INFORMATION FOR SEC ID NO: 16: SECUENCE: CHARACTERISTICS: LENGIH: 286 amino acids
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                                                                                                                                                                                                                                                   STANDARD:
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PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER HEADABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: ISM PC COM
   7) Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                                                              24 IELDLNSGK: 33
                                                                                                                      1 ISEKETSCK: 10
                                                                                                                                                                                                                                                   US-08-346-333-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
10 US-08-719-697-4
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      Matches
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ID US
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STREET: P.O. Box 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2. Application US/0P33558
Patent No. 552482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Rohald N.
APPLICANT: HINES, Rohald N.
APPLICANT: No. 5525462ak, Raymond F.
ITILE OF INVENTION: METHOD AND CELL LINE FOR TESTING
ITILE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 4; Length 286
Pred. No. 1.12e+02;
      NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31 R?1
REFERENCE/DOOKET NUMBER: FP-53469-PC/RFT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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JENCE 286 AA: 31466 MW. 387468 CN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08339658
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TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
                                                                                                                          TELEPHONE: (415) 781-1399
TELEFAX: (415) 398-3249
INFOREMATION FOR SEQ 1D 0: 16:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                           LENGTH: 286 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.9%;
Best Local Similarity 70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7: Conservative
                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-339-658-2
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                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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STATE: M
CCUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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ID US
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      Sequence i6. Application PC/TUS9107506

GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Balzkili, Timothy
TITLE OF INVENTION: Wethods for modifying DNA and for
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: encoded modified polypeptides with target substrates.
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Richard F. Irecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
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ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton STREET: P.O. Box 4390 CITY: Troy
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDICM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAITMG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C7/721.775A
FILING DATE: 19910627
CLASSIF:CATION: 4356
ATTORNEY/AGENT INFORMATION:
NAME: KOAD, KENDELD:
RECISTRATION NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Juery Match 63.9%; Score 46: DB 1: Length 286; Best Local Similarity 70.0%: Pred. No. 1.12e+02; Marches 7: Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UNMER: PCT/US91/07506
FILING DATE: 19911021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 286 AA; 31557 MW; 391925 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application PC/IUS9107506
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                                                                                                                                                           ZIP: 46099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                STAIE: Michigan
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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PCT-US91-07506-16
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APPLICANT: Gerardy-Schahn, Rita; Fikuda, Minoru;
APPLICANT: Nakayama, Jun: Eckhardt. Matthias
TITLE OF INVENTION: Isolated Polysialy! Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
TITLE OF INVENTION: Production and Use
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saps
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2019: 10022
CCMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
CORBUTER: UBM PS/2
CORBUTER: Wordperfect.
CURRAING SYSTEM: PC-DOS
SOFTWARE: Wordperfect.
CURRAIN APPLICATION DATA:
APPLICATION 105/8/575,775A
FILING DATE: 21-December: 1995
Thest FICATION: 1710.
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359 AA
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Best Local Similarity 75.0%; Pred. No. 1.12e+02;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION UATA:
APPLICATION NOMBER: 08/7 5,133
FILING DATE: 17-2019-14-7
PRIOR APPLICATION DATA:
APPLICATION NOMBER: PC 94/3428
FILING DATE: 22-Decert 1594
ATTORNEY/AGENT INFORMATI:
5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 359 AA; 41227 MW; 690704 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an D.
                                                                                                                                                      Sequence 2, Application US/08576775A Patent No. 5849994 GENERAL INFORMATION:
                                                                                                                    Sequence 2, Application US/0857675A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08899545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | IELEPHONE: (212) 688-9200
| TELEFAX: (212) 838-3884
| INFORMATION FOR SEC ID NOT 2.
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CIIY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, NO. 584%+
REGISTRATION NUMBER: (U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTIC
LENGTH: 359 amino acids
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
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US-08-576-775A-2
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US-08-899-545-2
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                                        XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gerardy-Schaho, Rita: Fukuda, Minoru;
APPLICANT: Wakayama, Juc. Eckhardt, Matthias
APPLICANT: Nakayama, Juc. Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysially| Transferases,
TITLE OF INVENTION: Nucleic Acid Wolecules Coding Therefor, Methods of
TITLE OF INVENTION: Production and Use
NUMBER OF SEQUENCES:
ADDRESSE: Rolfe & Lynch
STRET: 805 Third Avenue
CTTY: New York City
STATE: New York City
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                              Gabs
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Pred. No. 1.12e-02;
2; Mismatches 0; Indels
                                      Length 286;
                                                                            3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10022

ZIP: 10022

COMPUTER REABALE FORM:

MEDIUM TYEE: Diskette. 3.5 inch. 360 kb storage

COMPUTER: IRM PS/2

OPERATING SYSTEM: PC-DUS

SOFTWARE: PC-DUS

SOFTWARE: OF COMPUTED:
                                                                                                                                                                                                                                         359 AA
                                  Score 46: DB 1: 16
Pred. No. 1.12e+52:
U: Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hanson, NO. 5747326man D. REGISTRAIION NUMBER: 30,946
REPERBNCE/DOCKET NUMBER: BOER 1056
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/503.133A FILLNS CARES: 27-3CLV-1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION UNMBER: PGI/EP94/04289 FILLNS CARE: 22-2E0-1994 ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           PRT:
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359 AA; 41227 MW; 690704 CN;
286 AA: 31557 MW; 391925 CN;
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                                                                                                                                                                                                                                                                                                                                                              Sequence 2. Application US/38503133A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 359 amino acids IYPE: amino acid
                                                                                                                                                                                                                                           STANDARD
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                                    Cuery Match
Hest Local Similarity 70.0%;
Matches 7: Conservative
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GENERAL INFORMATION:
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SEQUENCE 2, APPLICA

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SQUENCE OS
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Search completed: Tue Jun 20 13:34:52 2000
Job time : 5 secs.
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Patent No. 5y59078
GENERAL INFORMATION:
APPLICANT: Gerardy-Schahn. Rita: Fukuda, Minoru:
APPLICANT: Makayana, Jun: Eckhardt, Matthias
TILLE OF INVENTION: Isolated Polysialyl Transferases,
TILLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
TILLE OF INVENTION: Production and Use
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADREES:
ADDRESSEE: Felfe & Lynch
SIREET: 805 Third Avenue
CITY: New York City
GENERAL INCRMATION:

APPLICANI

GENERAL INCRMATION:

APPLICANI

GENERAL SCHAHN, Rita: Fukuda, Minoru:

APPLICANI

TILLE GET INVENTION:

TILLE OF INVENTION:

TILLE OF INVENTION:

Nucleic Acid Adjustally Transferases,

TILLE OF INVENTION:

Nucleic Acid Acid Adjustally Transferases,

CORRESPONCES:

ADDRESSE:

ADDRESSE:

FELSE Lynch

STREET:

STREET:

STREET:

STATE:

New York City
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                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 36C kb storage
COMPUTER: 18M PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 AA
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PKION APPLICATION DATA:
APPLICATION NUMBER: 08/503.133
FILING DAIE:
ATIONNEY/AGENT INFORMATION:
NAME: HA:SON, NO. 502020lman D.
REGISTRAIION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1050
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCLECULE TYPE: protein
SEQUENCE 359 AA: 41227 MW; 690704 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08972498
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 359 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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ID US-08-972-498-2
                                                                                                                                                         COUNTRY
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Gaps
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                                      inch, 360 kb storage
                                                                                         COMPUTER REACABLE FORM:
MEDIUM TYPE: Diskette, 4.5 inc), 36.
COMPUTER: IBM PS/2
OPERATING SYSTEM: FG-L;
SOFTWARE: MONOTHERIFECT
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/972,498
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 359 AA; 41227 MW; 690704 CN;
New York
                    10622
                                                                                                                                                                                                                                                                                                                                                                                              348 ALKLTTGK 355
                                                                                                                                                                                                                                                                                                                                                                                                             2 SIKLTSGK 9
STATE: N
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4624, Applica

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CS-08-467-CS-08-468-CS-08-467-CS-08-257-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-226-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-238-CS-08-

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2. Application 134. Application 2. Application 5. Application 22. Application 22. Application 22. Application 25. Application

2, Applicatio 134, Applicat 134, Applicat 134, Applicat 134, Applicat

2284, Applica 2714, Applica 2714, Applica 25733, Applica 38423, Applica 5184, Applica 5184, Applica 5684, Applica 8461, Applica 8461, Applica

Sequence edneuce

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protein - protein database search, using Smith-Waterman algorithm
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1.PCT 2:06 3:060 4:07 5:080 6:081 7:082 8:083 9:084A
10.0842 11:085 12:086 13:087 14:088 15:089 16:090 17:091
18:092 19:093 20:094 21:095 22:NEWP 2 .NEWD60 24:NEWU8
25:NEWD9
                                                                                                                                                                                                                                Mon Jun 19 15:23:50 2000; MasPar time 14.77 Seconds 81.852 Million cell updates/sec
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1393-1598 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mean 18.571: Variance 42.966: scale 0.432
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Perfect Score:
Sequence:
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STAIE: MSALINGUES.
STAIE: D.C.
COUNTRY: USA
ID: 2000 CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
CLASS:FICATION DATA:
APPLICATION DATA:
RELING DATE: 10-SEP-1994
FILING DATE: 10-SEP-1994
FILING DATE: 14-JUL-1995
FILING DATE: 14-JUL-1995
FILING DATE: 14-JUL-1995
FILING DATE: 14-JUL-1995
ATONNEY/AGENT INPORMATION:
NAME: 14-JUL-1995
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ATONNEY/AGENT INPORMATION:
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GENERAL INFORMATION:
APPLICANT: SALTO, Saburo
APPLICANT: TANIGUCHI, YOSHIYUMI
APPLICANT: TANIGUCHI, YOSHIYUMI
APPLICANT: KURIMOTO, MASASHI
TITLE OF INVENTION: PEPTILE AND USESS OF THE SAME
NUMBER OF SEQUENCES:
UCORRESPUNDENCE ADJAMESS:
                                                                                                                                                         ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., CITY, Washington, STATE: D.C. COUNTRY: USA
                                                                                                                                                         PRT
ALIGNMENTS
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                                                                                                                                                         STANDARD:
                                                                                       RESULT 1

XX AXXXX

XX XXXXX

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XX SEQUENCE 11, APP11

XX SEQUENCE 11, APP11

XX APPLICANT: BA

APPLICANT: BA

APPLICANT: BA

APPLICANT: TA

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CC APPLICANT: TA

CC APPLICANT: TA

CC COUNTRY: US

CC COUNTRY: US

CC COUNTRY: US

CC CONDUTER REDAD

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CC CONDUTER APPLICATION

CC CONTREDICATION

CC RELING DATE:

CC RETARE

CC RETADOR

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BROWDY, Roger L.

US-C7-975-US-C8-526-US-08-350-

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SEQUENCE
                                                                                         Query Match
                                                                                                                                                                                                             XXXXXX
                                                                                                           Matches
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GENERAL INFORMATION:
APPLICANT: Griffeth, irwin J.;
APPLICANT: Griffeth, Janes:
APPLICANT: Bond, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Wounder Changy
APPLICANT: Wency, Marichard D;
APPLICANT: Wency, Marichard D;
APPLICANT: Wency, Julian F.;
APPLICANT: Wency, Julian F.;
APPLICANT: Wency, Julian F.;
APPLICANT: Wency, Steven F.
TILLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Allergenic Proteins And Peptides From TITLE OF INVENTION: Allergenic Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESSONDENCE AUDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation, i.c.
STRRET: 416 Lincoin St.
GITTE: Waltham
                                                                                                                                                                      ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Ja:e E. Remilard
REJESTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 38,872
RELEMBNOSMIONION INFORMATION:
TELEDPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
                                                                                                                                                Score 72: DB 11; Leggth 17; Sect 17: DB 11; Leggth 17; Sect Local Similarity 100:0%; Pred: No. 1.63e-01; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCUNTRY: USA
CCUNTRY: USA
CCUNTRY: 0.8A
CCMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,697
FILING DATE: June 6, 1995
                                                                                                                                                                                                                                                   24 AA.
                                                                                                                                                                                                                                                   PRT:
REGISTRATION NUMBER: 25.619
REFERENCY/COCKET NUMBER: SAITO-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                             Sequence 192, Application US/08467697
                                                                                        TYPE: arino acid
STRANDEDNESS: single
DPOLOGY: linear
MCHEGGLE TYPE: peptide
SEQUENCE IT AA: 1778 MW: 1362 CN:
                                       TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                   STANDARD:
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US:68-467-697-192
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GENERAL INFORM
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.,
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.,
APPLICANT: Woo, March H.;
APPLICANT: Woo, March H.;
APPLICANT: Woo, March H.;
APPLICANT: Exley, Siu-im H.;
APPLICANT: Exley, Mark H.;
APPLICANT: Exley, Mark H.;
APPLICANT: Powers, Sieven F.
TITLE OF INVENTION: Albergenic Proteins And Peptides From ITILE OF INVENTION: Japanese Cadar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immulcaic Phiritants
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STATE: MA
CJUNITY: JSA
CJUNITY: JSA
TIP: C214
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DASPET PROPONDATE:
COMPUTER: DASPET DASPET IN REPEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,006
FILICO DATE: June 6. 1995
CLASSITICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/35: 225
FILIOR DATE: December 6, 194
APTORNEY/AGENI INFORMATION:
NAME: DECEMBER: 08/35: 225
FILICOMUNICATION NUMBER: 025.6 USD6 (IMI-028CPD6)
TELEFONNINICATION NUMBER: 38,72
FILICOMUNICATION NUMBER: 38,73
FILICOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.
1.
                                                                                                                                                                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 24 AA: 2551 WW: 3329 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD
                                                                     LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            Match
Local Similarity 100.0%;
les 12: Conservative
                                                                                                                                                           inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 ISLKLTSGKIAS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ISEKLTSGKIAS 12
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Gaps

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APPLICANT GILIECTA JUNIO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maceutical Corporation, Inc
                                                            Query Match 150.0%; Sc. e 72; DB 10: Length 24; Best Local Similarity 100.0%; Pr\sim: No. 1.63e-01; Matches 12: Conservative 3: Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CMPUTER: 1BM PC compatible CONSTRUCTION MEDIUM TYPE: Floppy disk CMPUTER: 1BM PC compatible CMPUTER: 1BM PC compatible CMPUTER: 1BM PC compatible CMPUTER: 1BM PC compatible CMPUTER: 1BM PC CMPUTER: 1BM PC CMPUTER: 1BM PC CMPUTER: 1BM 1994

APPLICATION NUMBER: 05/08/26.244A

FILING DATE: April 8, 1994

PRIOR APPLICATION NUMBER: 07/938,990

FILING DATE: September 1, 1992

APPLICATION NUMBER: PCT/US93/06139

FILING DATE: January 15, 1993

ATORNEY/AGENT INFORMATION: NAME: Darlene A. Vanstone REGISTRATION NUMBER: 35,799

REPEROMOUNICATION INFORMATION: TELEFOND: (617) 466 6040

INFORMATION FOR SEQ 1D NO: 192: SEQUENCE CHARACTERISTICS: 1993

INFORMATION FOR SEQ 1D NO: 192: SEQUENCE CHARACTERISTICS: 1903
                                                                         .63e-01;
.hes û; Indels
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                                                                                                                                                                                                                                                                     24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 192, Application US/08226249A GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.:
APPLICANT: Pollock, Joanne;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 192, Application US/U8226248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 72;
FRAGMENT TYPE: internal
JENCE 24 AA; 2551 MW; 3329 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T TYPE: internal
24 AA: 2551 MW; 3329 CN;
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ImmuLogic P. STREET: 610 Lincoln St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 24 amino acids
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MOLECULE TYPE: peptide
FRAGMENT TYPE: inferration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
STATE: MA
                                                                                                                                          13 ISLKLTSGKIAS 24
                                                                                                                                                                    1 ISLKLTSGKIAS 12
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US-08-226-248A-192
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ZIP: 02154
                     SEQUENCE
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                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBJECT INTERPRETATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne,
APPLICANT: Bond, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Kuo, Mei-Chang:
APPLICANT: Yeung, Slu-mei H.;
APPLICANT: Yeung, Slu-mei H.;
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Andrew:
APPLICANT: Brauer, Aleven P.;
APPLICANT: Brauer, Aleven P.;
APPLICANT: Braver, Steven P.
TILLE OF INVENTION: Allergenic Proteins And Peptides From TILLE OF INVENTION: Japanese Cedar Poilen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immulogic Pharmaceutical Corporation, Inc.
                                                                                                   :
:
                                                            Score 72; DB 10; Length 24;
Pred. No. 1.63e-01;
C: Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM : YPE: Floppy disk

COMPUTER IN PE: Floppy disk

FLING DATE: Floppy disk

APPLICATION NUMBER: US/08/468,940

FLING DATE: APPLI 8, 1994

APPLICATION NUMBER: 08/226,248

FLING DATE: APPLI 8, 1994

APPLICATION NUMBER: 07/938,990

FLING DATE: SEPTEMBER: 1,1992

APPLICATION NUMBER: PCI/US93/C0139

APPLICATION NUMBER: PCI/US93/C0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Darlene A. Vanstone
REGISTRATION NUMBER: 35,729
REFERENE/JOCKET NUMBER: 025.6 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 192, Application US/08468940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 466-6000
INFORMATION: (617) 466-6000
INFORMATION FOR SEQ ID NO: 192: SECUENCE CHARACTERISTICS: LENGTH: 24 amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 192, Application US/08468940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
  FRAGMENT TYPE: internal SEQUENCE 24 AA: 2551 MW; 3329 CN;
                                                                                                                                                                                                                                                                 STANDARD:
                                                          Query Match
Best Local Similarity 100.0%:
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 510 Lin
CITY: Waltham
STATE: MA
                                                                                                                                          13 ISLKLTSGKIAS 24
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US-06-468-940-192
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13 ISLKLTSGKIAS 24

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                  Gaps
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APPLICANT: BOUND JULIAN F.C.
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Powers, Steven P.:
APPLICANT: Brauer. Addrew:
APPLICANT: Powers, Steven P.:
ITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SOJUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSE: Immilengic Pharmaceutical Corporation, inc.
STREE: 51G Lincoin St
COMPRESS: ADDRESS:
ADDRESSE: Immilengic Pharmaceutical Corporation, inc.
STREE: 51G Lincoin St
COMPRESS: ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: MACOUNTRY: WA
COUNTRY: WA
COUNTRY: WA
COUNTRY: WA
COUNTRY: TOWN
MEDIJU TIVE: Floppy disk
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MEDIUM 17PE: Floppy disk
COMPUTER: 19M PC COMPATIBLE
COMPUTER: 19M PC COMPATIBLE
COMPUTER: 19M PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATONIE Release #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/350,225
FLING TATION FATON: 424
PRILING TATE: PC-COMPATION FATONIES 1994
APPLICATION NUMBER: 01/934
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/GC139
FILING DATE: Canuary 15, 1993
ATIONEY AGENT INFORMATION:
NAME: DATABED A. VASSENCE
REGISSERENCE/DOSCKET NUMBER: 025.6 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
TET PROMONICATION INFORMATION:
TET PROMONICATION INFORMATION:
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuery Match 100.0%; Score 72; DB 8; Length 24; Fest Local Similarity 100.0%; Pred. No. 1.63e-01; Matches 12; Conservative 0; Mismatches 0; Indels
 Pred. No. 1.53e-01;
0; Mismatches 0;
                                                                                                                                  24 AA.
                                                                                                                                  PRT:
                                                                                                                                                                                                                                                Application US/08350225
                                                                                                                                                                                                                       Sequence 192, Application US/08350225
                                                                                                                                                                                                                                                                             Griffeth, Irwin J.;
Pollock, Joanne;
Bond, Julian F.;
Garman, Richard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 24 AA: 2551 MW: 3329 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPANONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 192:
SKOUENCE CHARACITERISTICS:
LENGTH: 24 amino acids
                                                                                                                                  STANCARD:
Rest Local Similarity 100.0%;
Matches 12; Conservative
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GENERAL INFORMATION
APPLICANT: Griffe
                                             13 ISEKETSCKIAS 24
                                                             1 ISLKLISCKIAS 12
                                                                                                                      JT 6
US-08-350-225-192
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                                                                                                                                                        APPLICANT Griffeth, Irwin J
APPLICANT Griffeth, Irwin J
APPLICANT Griffeth, Irwin J
APPLICANT Bond, Julian F;
APPLICANT Bond, Julian F;
APPLICANT Garman, Richard D;
APPLICANT Kung, Mei-Chang;
APPLICANT Foung, Siu-mei H.;
APPLICANT Exley, Mark A;
APPLICANT FOWErs, Steven P;
ITILE OF INVENTION: Alleraenic Proteins And Peptides Fiur TITLE OF INVENTION: Appaiese Cedar Pollen
NUMBER OF SEQUENCES: 26;
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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COMPUTER: Florey disk
COMPUTER: Florey disk
COMPUTER: Florey disk
COMPUTER: Florey disk
COMPUTER: Parentin Relace #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/ /467.024
FILING DATE: US/ /467.024
FILING DATE: US/ /467.024
FILING DATE: US/ /467.024
FRITCATION NUMBER: US/ /467.024
FRITCATION NUMBER: US/ /467.024
FRITCATION NUMBER: US/ /467.024
FRITCATION NUMBER: US/ /467
FRITCATION NUMBER: US/ /467
FRITCATION NUMBER: US/ /467
FRITCATION NUMBER: US/ /467
FRIEDPHONE: (617) 227-7467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stc : 72: DB 10: Length 24:
Pre. No. 1.63e-01:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ImmiLogic Pharmacentical Corporation, STREET: 610 Lincoln St. CITY: Waltham
                 24 AA
                 PRT;
                                                                                                                                    7023
                                                                                                       .023
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FRAGMENT TYPE: internal
SEQUENCE 24 AA; 2551 MW; 33:9 CN;
                                                                                                       Sequence 192, Application US/UP
                 STANDARD:
                                                                                                                                  Sequence 192, Application US/
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%;
Local Similarity 100.0%;
es 12; Conservative
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           US-08-467-023-192
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STATE: M.
COUNTRY:
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APPLICANT

GIFFEL, Irwin J.,

APPLICANT

GIFFEL, Irwin J.,

APPLICANT

GOORESPONDENCE,

APPLICANT

GOORESS. 261

CORRESPONDENCE,

APPLICANT

APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 72; PB 10; Length 127; Best Local Similarity 100.0%; Pred. No. 1.63e-61; Matches 12; Conservative 0; Mismatches 6; Indels
                                     COMPUTER: IBM PC COMPATIBLE COMPUTER: PATCHTIB RE: ISF #1.0, Version: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/39/467.006 FILING DATE: June 6, 1995 CLASSIFICATION HORER: 06/350.225 FILING DATE: December 6, 1994 APPLICATION NUMBER: 08/350.225 FILING DATE: DECEMBER: 08/350.225 FILING DATE: NECHMATION: REGISTRATION NUMBER: 38,872 REFRENCE/COCKET NUMBER: 38,872 REFRENCE/COCKET NUMBER: 38,872 REFRENCE/COCKET NUMBER: 30.556 USD6 (IMI-028GPD6) TELECOMMUNICATION INFORMATION: TELEFAX: (617) 227-5941 INFORMATION E (617) 227-5941 INFORMATION E (617) 227-5941 INFORMATION COURTED CHARACTERISTICS: LENGTH: 127 amino actids TOPOLOGY: Island
                                                                                                                                                                                                                                                                                                                                                                                                            025.6 USD6 (IMI-028CPD6)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rele se #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
UENCE 127 AA; 14435 MW; 84298 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 190, Application US/08350225
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ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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US-08-350-225-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                   APPLICANT: Kume, Akinori
APPLICANT: Kume, Akinori
APPLICANT: Kume, Akinori
APPLICANT: Kume, Akinori
APPLICANT: Kume, Akinori
APPLICANT: Kume, Akinori
APPLICANT: Kume, Akinori
APPLICANT: Kino, Kohsuke
ITILE OF INVENTION: Peptide-based Immunotherapeutic Agent For Treating
ITILE OF INVENTION: A.1.ergic Diseases
FILE REFERENCE: Docket No. SPO-103
CURRENT FORTION NAMBER: US/09/142.524
CURRENT FILING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: B/80/702
EARLIER APPLICATION NUMBER: PCT/JP97/0074C
EARLIER FILING DATE: 1996-03-10
NUMBER OF SEO ID NOS: 5
SOSTWARE: PALCUTIN VET. 2.0
SEO ID NO 1
LENTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garis
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APPLICANT: Yeung, Stu-mei H.:
APPLICANT: Yeung, Stu-mei H.:
APPLICANT: Brauer. Andrew:
APPLICANT: Brauer. Steven P.
APPLICANT: Powers, Steven P.
IITLE OF INVENTION: Alleraenic Proteins And Peptides From VIMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism:peptide
SEQUENCE 80 AA: 9067 MW: 30888 CN;
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ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 17; Length 80;
Pred. No. 1.6 >-01;
C: Mismatch 0; Indels
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                          80 AA.
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                          PRT;
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne:
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 190, Application US/08467006
                                                                                                                                                                                                                        Sequence 1, Application US/09142524 GENERAL INFORMATION:
                                                                                                                                                                             Sequence 1, Application US/09142524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%:
Matches 12: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 ISLKLTSGKIAS 63
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                        US-09-142-524-1
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STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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APPLICANT: Griffeth Irwin J.;
APPLICANT: Griffeth Joanne;
APPLICANT: Bood, Julian F.;
APPLICANT: Garman, Richard P.
APPLICANT: Garman, Richard P.
APPLICANT: Face, New Change
APPLICANT: Face, Strict H.
APPLICANT: Framer, Androw
APPLICANT: Framer, Androw
APPLICANT: Framer, Androw
APPLICANT: Fowers, Stevens F.
ITTLE OF INVENTION: Allorgenic Proteins And Peptides From
ITTLE OF INVENTION: Allorgenic Proteins
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ć,
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION DATA
APPLICATION DATA
APPLICATION NUMBER: 08/156.225
FILING DATE: December 6, 1994
ATTOREX/AGENT INFORMATION:
NAME: BECSISTATION NUMBER: 38,872
RESERVE/COCKET NUMBER: 625.6 USD2 (IMI-C28CPD2)
TELECPANDICATION INFORMATION:
TELEPANCIALIZAPANO
TELEPAN: (617) 227-5941
INFORMATION FOR SEQ ID NO: 290:
SEQUENCE CHARACIFELSITOS:
LENGTH: 127 amino acids
TOPPIC APPLICATION OF SECULATION OF SEQUENCE CHARACIFELSITOS:
LENGTH: 127 amino acids
TOPPIC APPLICATION OF SECULATION OF SEQUENCE CHARACIFELSITOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 127
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Pred. No. 1.63e-01:
0: Mismatches C: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE 127 AA: 14435 MM; 84298 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ImmuLogic P?
STREET: 610 Lincoln St
Cliff: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best local Similarity 100.0%.
Matches 12: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ISEKETSGKIAS :2
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                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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CENERAL INELHATION

APPLICANT STITECT. ITWIN 0.1

APPLICANT Bond, Julian F.1

APPLICANT Reus, Stumer B.1

APPLICANT Reus, Stumer B.2

APPLICANT Reus, Stumer B.3

APPLICANT Reus, Stumer B.3

APPLICANT Reus, Stumer B.4

APPLICANT Reus, Stumer B.3

APPLICANT Reus, Stumer B.4

APPLICANT Reus, Stumer B.4

APPLICANT Reus, Stumer B.7

ADSRESSER Immunication Pharmaceutical Corporation, Inc.

STATE: Mailtham

CCUNTRY: Waltham

CCUNTRY: Waltham

CCUNTRY: Waltham

CCUNTRY: Waltham

CLOWERSON CORPORATION CORPORATION CORPORATION CORPORATION CORPORATION COMPANY CONTRY: WALTHAM

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CCUNTRY: WALTHAM

CLOWERSON CORPORATION CORPORATI
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Sest Local Similarity 100.0%; Pred. No. 1.63e-61;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02154
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PARENTE: Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.023
                                                                                                                                                                                                                                                                                                                                                    REFERENCE FOR THE STATE OF THE SECRET STATE OF TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTER STICS:
LENGTH: 127 anino acids
TOPOLOGY: 110-azid
                                                                            PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (68/26,248
FILING CATE: APPLI 9, 1994
APPLICATION NUMBER: 07/938,990
FILING CATE: September 1, 1992
APPLICATION NUMBER: PCI/US93/03139
FILING DATE: January 15, 1993
ATDRAES/ALENT INPORATION:
NAME: CATCORE A VAGSTORE
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.X.
                                  APPLICATION NUMBER: US/08/350,225
FILING DATE: December 6, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 127 AA: 14435 MW: 84298 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD:
          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISEKTTSGK:AS 12
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10 US-08-467-023-190
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APPLICANT: SOUND, APPLICANT: SOUND, APPLICANT: Young, Siu. H.;
APPLICANT: Young, Siu. H.;
APPLICANT: Brauer, Andrew:
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TILLE OF INVENTION: Alberge.ic Proteins And Peptides From TILLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF STOURENES: 26:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ebundSSEE: Immelodir Profrancistical Corporation. Uni
STREET: 610 innovin St.
CITY: Watther
                                                                                                                                                                      Score 72: DB 10: Length 127:
Pred. No. 1.63e-01;
0: Mismatches 6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SCFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Darlene A. Vanstone
REJISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.6 US (IMI-028CP2)
                                                                                                                                                                                                                                                                                                                                   127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: December 6, 1994
APPLICATION NUBBER: 08/226,248
FILING DATE: April 8, 1994
APPLICATION NUBBER: 07/98,990
FILING DATE: September 1, 1992
APPLICATION NUBBER: PCT/VS93/00139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 190, Application US/08468949
GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Poilock, Joanne:
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, R. 11d D;
                                                                                                           MOLECCIE TYPE: peptide
FRAGMENT TYPE: internal
IENCE 127 AA; 14435 MW: 84298 :N:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 190. Application US/08468940
 TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NOT 1501
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                        STANDARD:
                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative
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02154
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US-08-468-940-190
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TITLE OF INVENTION: Allocannic Proteins And Poptides From TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      ..
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STREET: 610 Lincoln St
CITY: Waitham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,697
FILING DATE: Jane 6, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING EATE: December 6, 1994
ATTORIEY/AGENT INVORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: 025.6 USD4 (IMI-028CPD4)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     Query Match 100.0%: Score 72: DB 7; Length 127; Sest Local Similarity 100.0%: Pred. No. 1.63e-61: Matches 12: Conservative 0: Mismatches 0: Indels
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Datafere A. Vanscoor
REGISTATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP)
TELECOMMUNICATION HYPERMATION:
TELEPHONE: (617) 466-6000
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 mainto acids
TORGE: ACID acids
TORGE: ACID acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                               127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 190. Application US/08467697
GENERAL INFORMATION:
APPLICANT: GITECHI, ITWIN J.,
APPLICANT: Policack, Joanne:
APPLICANT: Bond, Julian F.:
                                                                                                                                                                                                         MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 127 AA; 14435 MW: 84298 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 190, Application US/08467697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuo, Mei-Chang;
I: Yeung, Siu-mei H.)
I: Brauer, Andrew:
I: Exley, Mark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garman, Richard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                  1 ISUKLISCKIAS 12
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US-08-467-697-190
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ADDRESSEE: OBLOW. SPIVAK, MCCLELLAND, MAIER & NEUSTADI, ADDRESSEE: P C.
STREE: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
STREE: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
STREE: VA.
COUNTRY: OSA
CONDUTRY: DAVIS HIGHWAY, SUITE 400
STREE: LAND OSA
COMPUTER: PALABLE FORM:
MEDIUM 1VFE: FIDENCY GISK
COMPUTER: PALABLE FORM:
MEDIUM 1VFE: FIDENCY GISK
CURREMT PARLATION BATA:
APPLICATION NUMBER: US/08/571,978
FILING DATE: 16-JAN-1996
CLASSIFICATION NUMBER: US/08/571,978
FILING DATE: 16-JAN-1996
CLASSIFICATION NUMBER: US/08/571,978
FILING DATE: 15-JUL-1994
PRIOR APPLICATION NUMBER: US/08/571,076
FILING DATE: DAPPLICATION DATA:
APPLICATION NUMBER: 19 6-069336
FILING DATE: OSEP-1993
APPLICATION NUMBER: 29 5-17708
FILING DATE: US-SEP-193
ATTORNEY-MORTH INFORMATION:
NAME: CRION, NORMER: 24-618
RECERENCE/JOCKET NUMBER: 77318-002-0 PCT
FELEPHONE: 703-413-3200
                                                                                                                                                         Score 72: DB 10: Length 127;
Pred. No. 1.63e-01;
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08571978
GENERAL INFORMATION:
APPLICANT: KINO, KOHSUKE
APPLICANT: KONYYAMA, NAOK:
APPLICANT: KOHNO, YOICHI
TILLE OF INVENTION: ANTI-ALLERGIC AGENTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           460 AA
                                                                                                                                                                                                                                                                                                             .......
                                                                                      TOPOLOGY: linear
MOLECOLE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 127 AA: 14435 MM; 84298 CN:
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08571978
TELEPACH (617) 466-6000
TELEPACH (617) 466-6040
INFORMATION FOR SED ID NO. 150:
SEQUENCE CHARACTERISTICS:
                                    STANDARD:
                                                                                                                                                         Query Match
Bost Local Similarity 160.0%;
Matches 12; Conservative
                                                                                                                                                                                                                       11 ISLKLTSGK:AS 22
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US-08-571-978-1
                                                                                                                               SEQUENCE
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CC INFORMATION FOR SECID NG: 1:
CC SEQUENCE CHRRACTERISTICS:
CC LENGTH: 460 amino acids
CC TYPE: amino acid
CC TYPE: amino acid
CC TYPE: single
CC TYPE: single
CC TYPE: peptide
SQ SEQUENCE TYPE: peptide
SQ SEQUENCE 460 AA; 59446 MW; 1058702 CN;
OUSTY MAIC: 100.0%: Score 72: D5:11: Length 450;
Matches 12: Conservative : Mismatches 0; Indels U: days
Db 344 ISEKLTSGKIAS 355
Db 344 ISEKLTSGKIAS 355
Dj 345 ISEKLTSGKIAS 355
UP 11:11|11|11|
Qy I ISEKLTSGKIAS 12
Search completed: Mon Jun 19:16:24:10.2000
Job time: 20 secs.
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| ****                                                                             | '          |
| ********                                                                         | <u> </u>   |
| *******                                                                          |            |
| ********                                                                         | [          |
| *********                                                                        |            |
| · 在这个,我们的,我们们的,我们们的人们的,我们们们的,我们们的,我们们的自己的现在分词,我们的自己的现在分词,我们的自己的,我们们的自己的的,我们们的自己的 |            |
| *******                                                                          | 1          |

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 3.89 Seconds 145.422 Million cell updates/sec Mcc Jun 19 16:04:40 2000: Run on:

Tabular output not generated.

>US-09-142-524A-6 (1-i2) from USO9142524A.

1 ISLKLTSGKIAS 12 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

142080 segs, 47172406 residues Searched:

Misimum Match 0% Listing first 45 summaries Post-processing:

pir62 lipirl 2:pir2 3:pir3 4:pir4 Database:

scale 0.893 Mean 23.729: Variance 26.562; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1.81e-05 1.781e-05 2.90e-00 2.90e-00 2.90e-00 7.94e-00 7.94e-00 7.94e-00 1.30e-01 1. Pred. No second major allergen Cry j II protein Ja Mypothetical protein membrane-bound iron(I Mypothetical protein hypothetical protein
ABC transporter. AIPprobable membrane pro
hypothetical protein
major structural core
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G protein-coupled rec conserved hypothetica N-carbamyl-L-amino ac leucyl aminopeptidase Description 0 Score Result No. 

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| AAAA<br>BB65894<br>S8449894<br>S8449899<br>S84499999<br>S844999999<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8449<br>S8 | ALIGNMEN, ype comp.e. aliergen cryptomerik sequence_ri 6, A60147 Sone, I.: hys. Res. and expres li86                                                                                                                                         | 1abe; KOM<br>lake KOZ<br>1 Inchye,<br>0 45:309-<br>n of the 1<br>2988                                                 | signal se second m MAT\ Si e Carj                                   | . <b>x</b>                   |
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| 44444444444444444444<br>ΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NS<br>NS<br>Ors<br>ors<br>ssion<br>Ssion                                                                                                                                                                                                     | molecule.  residues.  residues.  residues.  residues.  e residues.                                                    | 9<br>60,472<br>Match<br>Match                                       | 12: .<br>ISLKLTSG            |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | RESULT<br>ENTRY<br>TITLE<br>ORGANISM<br>DATE<br>ACCESSIO<br>REFERENC<br>*Auth<br>*titl<br>*titl                                                                                                                                              |                                                                                                                       | FEATURE<br>FEATURE<br>155-46<br>55-46<br>8UMMARY<br>Ouery<br>Best L | atch<br>3                    |

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1 ISLKLTSGKIA

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Colo. S.T., Brosch, R., Parkhill, J., Garnier, T., Chircher, C., Harris, D., Gordon, S.V., Elgimeier, K., Gas. S., Barry, J., C.E., Tekaia, F., Badcock, K., Bashar, J., Brown, D., Millimworth, T., Cornor, R., Davies, R., Devlin, K., Voltwell, T., Gordor, R., Maries, R., Devlin, K., Noltwell, T., Gordor, S., Hamin, N., Holroyd, S., Harrisch, T., Garels, K., Krugh, A., Mchean, J., Molle, S., Marpey, L., Cilver, S., Stasbone, J., Qaari, M.A., Rajor, S., Startel, S., Seqer, K., Skolton, S., Squres, S., Squres, S., Sarrell, H.G., Miltehead, S., Barrell, H.G., Marier (1998) 391537-54 Mycobacterium tuberculosis from the complete genome sequence.
                                    Cry ) II protéli - Japanese cedar
#Icrmal_name Cryptomeria japonica #common_name Japanese cedar
07-May-1995 #sequence_revision 21-Jui-1995 #text_change
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                                                                                                                                                                     #authors Narbal M.: Kurose, M.: Torique, K.: Hino, K.: Taniguchi, Y.: Fukuda, S.: Usui, M.: Kurimoto, M. FERS Lett. (1994) 353:124-128 #title Moiecular cioning of the second major allergen, Cry j II, across-reterences MulD:95010777
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hypothetical protein Rv6513 - Mycobacterium tuberculosis
(strain H378V)
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Pred: No. 1.81e-05;
0; Mismatches 0; Indels
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17.0x1-1996 #sequence_revision 17.0x1-1996
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                        *type complete
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#accession F70509
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Hest Local Similarity 100.0%;
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Standenmaier H: Van Hove: B.: Yaraqhi, Z.: Hraun. V

Fjournal J. Bacteriol. (1989) 1712646-2633

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Fille proteins suggest a the feeDOBE genes at lications of the proteins suggest a periphasmic-binding protein-dependent transport mechanism for iron(III) diritate in Escherichia coi:

Facoss-references MUID:89213950
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PID:9537128
**note the nucleotide sequence was submitted to the HMHL Fata
Library, August 1994
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ATP: Iron transport: membrane protein; nucleotide binding:
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#region nucleotide-binding motif A (P-loop)
#length 255 #molecular-weight 28190 #checksum 283
                               QRECN3 #type or plete membrane-bound iro: [11] dicitrate transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #Journal Science (1997) 277 [148 to 45].
#fille The Complete Denomin Sequence of Eschetichia Coll K
#foressite Frances NOID:97426917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal Nucleic Acids Res. 1995) 23:2105-2119
#title Analysis of the Escherichia col. genome VI: INA
the region from 9.18 through 100 minutes.
#cross-references MID:95334362
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18-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46/3: 75/2: 144/3: 181/1: 242/3: 284/3
F20816.290
#Superfamily ADP.ATP carrier protein: ADP.ATP carrier protein
                                                                                                                                                                                                                                                                                                                                                                            Bavan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.;
Mewes, H.W.; Mayor, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, March 1999
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hypothetical protein F20819.290 - Arabidopsis thallana
#formal_name Arabidopsis thallana #common_name mouse-ear
                         Gaps
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05-bec-1997 #sequence_revision 05-bec-1997 #fext_change
05-un-1998
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=length 325 #molecular.weight 36551 #checksum 6140
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Pred. No. 7.94e+06:
2: Mismatches 3: Indels
                         Indels
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                       4: Mismatches
    Pred. No.
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##residues 1-407 ##label KLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.1%;
Rest Local Similarity 58.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                                 21 VSLSLPIGKITA 32
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                                                                                                         1 ISLKLISCKIAS 12
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Augent, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alioni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alioni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bototin, A.; Borcheri, S.; Borissa, R.; Borissar, E.; Brans, A.; Brain, M.; Brigheil, S.; Bolissar, E.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizor, P.; Connerton, R.M.; Dueste-hoff, A.;
Ehrlich, S.D.; Emrerson, P.I.; Entian, K.D.; Errington, J.;
Fabrer, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, Y.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, Y.; Glaser, P.; Goffeau, A.; Gollichily, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Hada, M.; Halech, G.; Husono, S.; Hallo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, S.; Kuann, A.; Korita, K.; Lapidus, A.; Lardinois, S.; Kradno, M.; Korita, K.; Lapidus, A.; Lardinois, S.; Kradno, M.; Mosell, D.; Nokai, S.; Mallado, R.; Prinscott, C.; Mediae, C.; Mediae, M.; Mosell, S.; Prinscott, S.; Prinscott, S.; Rose, S.; Prinscott, D.; Nokai, S.; Prinscott, S.; Prinscott, D.; Nokai, S.; Prinscott, S.; Rose, S.; Prinscott, A.; Prinscott, M.; Proscott, B.; Rose, M.; Prinscott, M.; Tamakoshi, A.; Tamakoshi, R.; Takemazu, K.; Takeuchi, M.; Tamakoshi, A.; Tamakoshi, T.; Takahasi, T.; Takendari, T.; T
**cross-references GB:AE001016; GB:AE000782; NID:g2689339; FID:g2649302;
TIGR:AF1278
Y *length 407 *molecular-weicht 44931 *checksum 1:4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-carbamyl-Lamino acid amidohydrolase homolog yar8 - Bacillus subtilis
#formal_name Bacillus subtilis
10-Sep_1999 *sequence_revision i0-Sep-1999 *text_vhange
12-Sep-1999
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PIDN:CAB15243.1; PID:e1184332: PID:92635750
##experimental_source strain 168
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                                                                                                                                                                          Score 49: DB 2: Length 407: Pred. No. 7:94e-00: 1: Mismatches 1: Indels
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Nature (1997) 390:249-256
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*cross-references MUID:98044033
                                                                                                                                                                          Query Match 68.1%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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**molecule_type mRNA
**#residues 20-573 **label HIL
**#residues 20-573 **label HIL
**recrear reteronces EMBLIX67845; NID:q21486; PIDN:CM48038.1; PID:g21487
**cxperimentul_source strain desiree
**cxperimentul_source strain desiree
ASSIFICATION **cperfamily cytosol aminopeptidase
EFWORDS alpha-arinoacylpeptide hydrolase
**Recrear **Recreation **Company **Com
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Beran, M.: Terryn, N.: Ardiles, W.: Buysshaert, C.:
Dasseville, R.: De Clerck, R.: De Keyser, A.: Neyt, P.:
Souze, P.: Van Den Daele, H.: Villarcel, R.: Gielen, J.:
Van Montagu, M.: Hohelsel, J.: Mewes, H.W.: Mayer, K.F.X.:
Schueller, C.
Schueller, C.
Schueller, C.
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Fauthors Hildmann, T.: Ebneth, M.: Pena-Cortes, H.: Sanchez-Serrano, J.J.: Wilmitzer, L.: Prat, S.
Fjournal Plunt Cell (1992) 4:1157-1175
fittle Gueral Toles of absciste and jasmonic acids in gene activation as a result of mechanical wounding.
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hypothetical protein F26P21.20 - Arabidopsis thaliana
*tormal_name Arabidopsis thaliana #common_name mouse-ear
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                                                                                                                                                                                                                                                                                                                                  S41376 *type complete

[cost] aminopeptidase (EC 3.4.11.1) - potato

woind-induced protein (clone 17)

***Forl999 *sequence_revision 10-Sep-1999 *text_change
10-Sep-1999
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                                                                        Gaps
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##FESIGUES 1-573 ##Jabel HER
##Cross-references EMBL:X77015: NID:q443978; PIEN:CAA54314.1;
##Cross-references EMBL:q443979
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Score 49, DB 1; Length 412;
Pred. No. 7.94e+60;
3; Mismatches 1: Indels
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$41376
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Hest Local Similarity 60.0%;
Matches 6: Conservative
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**molecule_type_DNA
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Fraser, C.M.) Casjens. S.: Bland, W.M.: Sittin, G.: Fraser, C.M.) Casjens. S.: Bland, W.M.: Sittin, G.: Fraser, C. Bathigra, R.: White, O.: Kerchur, K.A.: Tomb. Dodgoon, R.: Fichschmann, R.D.: Richardson, D.: Peterson, T.: Kerlavage, A.R.: Quackenbish, J.: Salzberg, S.: Banson, W.: Vugt, RV. V.: Palmer, N.: Adams, M.D.: Googne, G.: Weidman, J.: Citerback, T.: Watthey, L.: McDonaid, L.: Arthach, P.: Bowman, C.: Garland, S.: Fijii, C.: Cotton, M.: Harst, Roberts, K.: Kaberrs, K.: Kaberrs, K.: Kaberrs, K.: Kaberrs, M.: Brist, Mature (1997) 340:580-586
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ABC transporter, ATP-binding protein homolog - Lyme disease
spirochete
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probable membrane protein YGR168c · yeast (Saccharomyces
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*formal_name Saccharomyces cerevisiae
17-May-1996 *sequence_revision 17-May-1996 *text_change 21_Nov-1997
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F26P21.20
#length 215 #molecular-weight 23517 #checksum
**experimental_source cultivar Columbia: BAC clone F26P21
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2: Mismatches 1: Indels
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OS ATP: P-loop
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##cross-references GB.AECCLITT, 3H
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Best Local Similarity 77.8%;
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Best Local Similarity 70.0%:
Matches 7: Conservative
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MIPS:YGR168c
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TIGR:BB0261
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hypothetical protein BB0261 - Lyme disease spirochete
#formal_name Borrelia burgdorferi #common_name Lyme disease
*spirochete
*spirochete
10.58p.1999 #sequence_revision 10.58p.1999 #text_change
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CLASSIFICATION #superfamily hypothetical protein BB0261; tetratricopeptide
repeat homology
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Rieger, M.; Mueller-Auer, S.; Brucckner, M.; Schaefer.
submitted to the Protein Sequence Database, May 1996
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Database, May 1996
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Pred. No. 1.30e+01;
                                                                                                                                                                                 *authors Hobling, U.; Hofmann, B.; Deilus, submission submitted to the Protein Sequence *accession 564482
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##residues 1-376 ##label HEB
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Best Local Similarity 58.3%;
Matches 7; Conservative
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H71664 *type complete transcription-repair coupling factor (mfd) RP598 - Rickettsia
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#title Nuclectide sequence of rice dwarf virus (8DV) demont S3 codius sequence of rice dwarf virus (8DV) demont S3 codius for 14 K mejor core protein.
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atypical #label 175\
#domain tetratricopeptide repeat homology #labe:
#length 450 #molecular-weight 54024 #checksum 9100
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##residues 1-303/S/305-1019 ##label YAM
##cross-references EMBL:DCG607: NID:0222500: PIDN:BAACC482.1.
PID:d1000937: PID:g222501
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##residues 1-1019 ##label SU2
##cross-references GB:X54620: NID:q61467; PIDN:CAA38440...
ENCE S12826
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Pjourna, Nucleic Acids Res. (1990) 18:6419
*title Nuclectide Sequence of rice dwarf virus genome stross-references MIID:91057125
*accession 512826
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                                                                                                      1.30e+01;
                                                                                              DB 1: Length 46
                                                                                                                        Pred, No. 1.30e-
1: Mismatches
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major structural core protein
#formal_name rice dwarf virus
                                                                                                 Score 48;
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                         Query Match
Best Local Similarity 77.8%:
Matches 7; Conservative
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Arioss, F. Johnsawara, N.; Moszer, I.; Albertini, A.K.;
Alichi, J.; Arcvedo, V.; Bertero, M.G.; Bessieres, F.;
Anichi, A.; Borchett, S.; Bories, R.; Berouillet, S.;
A.; Brann, M.; Brighell, S.; Bories, S.; Brouillet, S.;
Fruschi, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.M.; Denzerson, P.I.; Entian, K.D.; Erington, J.;
Enrich, S.D.; Emmerson, P.I.; Entian, K.D.; Erington, J.;
Enrich, S.D.; Emmerson, P.I.; Entian, K.D.; Erington, N.J.;
Choise, C.; Foulger, D.; Fritz, C.; Fulfar, A.;
Enrich, S.D.; Emmerson, P.I.; Entian, K.D.; Erington, J.;
Enrich, S.D.; Emmerson, P.I.; Entian, K.D.; Erington, J.;
Enrich, S.D.; Emmerson, P.I.; Entian, K.D.; Erington, J.;
Edser, P.; Goffeau, A.; Gollightly, E.J.; Grand, G.
Culseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein G.; Kroph, S.; Kumano, M.;
Karita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medina, N.; Mellado, R.P.; Mizuno,
W.; Mohl, T.M.; Portetelle, D.; Nawillado, R.; Prescont,
A.M.; Pressecan, E.; Pujic, Porvolity, G.; Rophort, G.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sexiguchi, J.;
Schweska, A.; Sernor, S.J.; Sernor, P.; Shin, B.S.; Sodo,
B.; Sorokin, A.; Facconi, E.; Takapi, T.; Takahashi, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross_references GB:AJ235272; GB:AJ235269; NID:q3861033: PID:e1342886;
PID:q3861142
##experimental_source strain Madrid E
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                                                                                                                                                                                                                                                                            *journal Nature (1938) 396:133-146
*title The genome sequence of Rickettsia prowazekil and the origin of mitochondria.
*cross-references MUID:99039499
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We sporfamily transcription-repair coupling protein; DEAD/H

we shorfamily transcription-repair coupling protein; DEAD/H

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                                                                                                                                                   Andersson, S.S.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.; Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kuriand
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phacerelated protein homologyqbo - Bacillus subtilis
#!comal_name Bacillus subtilis
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Matches 7; Conservative
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Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;

Terpstra, P.; Toqnoni, A.; Tosato, V.; Uchiyama, S.;

Vandenbol, M. Vannier, F.; Vassarctti, A.; Vant., A.;

Wambutt, R. Wedier, E.; Wedler, H.; Weitzeregger, T.;

Winters, P.; Wija, A.; Yamamoto, H.; Vamane, K.; Yasarcto,
K.; Yata, K.; Yoshida, R.; Yoshikawa, H. F.; Zunstein, E.;

Yoshikawa, H.; Danchin, A.

*title The complete genome sequence of the Gram-positive bacterium.

Bacillus subtiits.

**Cross-references MUID:9804433
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                                                                                                                                                                                                                                                                                                  *molecular-weight 171029 #checksim
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Matches 7; Conservative
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Release 7.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MFsrch\_pp

Mcn Jun 19 16:03:48 2000: MasPar time 2.83 Seconds 129.156 Million cell updates/sec Rup on:

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1 ISLKLTSGKIAS 12 :eduenbes

FAM 150 Gap 15 Scoring table:

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8:857 seqs. 36454973 residues

Searched:

swiss-prot38 l:swissprot Catabase:

Variance 23.745; scale 1.018 Mean 24.176; Statistics: Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result     |       | Query |                 |                |            |                        |           |
|------------|-------|-------|-----------------|----------------|------------|------------------------|-----------|
| NO.        | Score | Match | Match Length DB | 23             | A          | Description            | Pred. No. |
| -          | 7.2   | 100.0 | 514             | г              | MPA2_CRYJA | POSSIBLE POLYGALACTURO | 1.09e-06  |
| 2          | 53    | 73.6  |                 | -              | Y248_CAEEL | HYPOTHETICAL 33.7 KD P | 2.36e-01  |
| 3          | 51    | 70.9  | 255             | r 4            | FECE_ECOLI | IRON(III) DICITRATE TR | 7.49e-01  |
| 4          | 2,    | 68.1  | 573             | ٠,             | AMPL_SOLTU | CHLOROPLAST AMINOPEPTI | 2.30e+00  |
| S          | 8.3   | 65.7  | 376             | -1             | YG3W_YEAST | HYPOTHETICAL 44.3 KD P | 3.98e-00  |
| Ą          | 8.7   | 66.7  | 1019            | -1             | VP3 RDV    | MAJOR 114 KD STRUCTURA | 3.98e-00  |
| ۲-         | 48    | 66.7  | 1120            | ٦              | MFD RICPR  | TRANSCRIPTION-REPAIR C | 3.98e-00  |
| <b>o</b> o | 8     | 65.7  | 1585            | ~4             | YQBO_BACSU | HYPOTHETICAL 171.0 KD  | 3.98e+00  |
| σ          | 47    | 65.3  | 530             | Н              | UL21_HSVEB | GENE 40 PROTEIN.       | 6.82e+00  |
| 10         | 47    | 65.3  | 572             | П              | LAC3_THACU | LACCASE 3 PRECURSOR (E | 6.82e+00  |
| 11         | 47    | 65.3  | 648             | , <del>,</del> | PEX6_SCHPO | PROBABLE PEROXIN-6.    | 6.82e+00  |
| 12         | 46    |       |                 | ٠,             | YF39_PYRHO | HYPOTHETICAL PROTEIN P | 1.16e+01  |
| 13         | 46    | ~     |                 | -1             | Y214_MEIJA | PUTATIVE HYDROGENASE E | 1.15e+01  |
| 14         | 46    | 63.8  |                 | -              | AGGB_ECOLI | AGGB PROTEIN PRECURSOR | 1.15e+01  |
| 15         | 46    | 63.9  | 208             | ~              | FISQ_STRGR | CELL DIVISION PROTEIN  | 1.16e+01  |
| 16         | 46    |       |                 | 1              | SNUCECOLI  | HIGH-AFFINITY ZINC UPT | 1.16e+01  |
| 17         | 45    | 63.9  |                 | ~              | BLAT_ECOLI | BETA-LACTAMASE PRECURS | 1.16e+01  |
| 18         | 46    |       | 316             | ٦              | TALB_ECOLI | TRANSALDOLASE B (EC 2. | 1.16e-01  |
| 19         | 46    | ٠     |                 | -              | PST_CRIGR  | ALPHA-2,8-POLYSIALYLTR | 1.16e+01  |
| 20         | 46    | 63.9  |                 | -              | PST_HUMAN  | ALPHA-2,8-POLYSIALYLTR | 1.16e+01  |
| 21         | 46    | 63.9  |                 | -              | PST_MOUSE  | ALPHA-2,8-POLYSIALYLTR | 1.16e+01  |
| 22         | 46    | 63.9  |                 | -              | REFR_VARV  | RIFAMPICIN RESISTANCE  | 1.16e+01  |
| 23         | 46    | 63.9  | 551             | -              | REFR_VACCV | RIFAMPICIN RESISTANCE  | 1.16e+01  |

| 1.16e+01<br>1.16e+01     | 1.156+01                                      | 1.15e-01   | 1.94e-01                                    | 10        | 1.946-01   | 3,40                   | 10.946.1     | 12                     | 1.94e-01               | 1.940-01               | 1.946-01               | 1.94e-01               | . 94                   | 3.23e-01               | . 23                   | 3.23e-01      | 3.23e+01               | 3.23e+01               |
|--------------------------|-----------------------------------------------|------------|---------------------------------------------|-----------|------------|------------------------|--------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|---------------|------------------------|------------------------|
| OH                       | PROBABLE DONB DEPENDEN PROBABLE DNA POLYMERAS | CAL 153.8  | NEGATIVE REGULATOR OF NEGATIVE REGULATOR OF | S PRECURS |            | THYMIDINE KINASE (EC 2 | RF4 PROIEIN. | TYPE I RESTRICTION ENZ | 2,3-BISPHOSPHOGLYCERAT | 2,3-BISPHOSPHOGLYCERAT | DNAK PROTEIN (HENI SHO | CELL SURFACE PROJEIN P | XANTHINE DEHYDROGENASE | HYPOTHETICAL ABC TRANS | CALPONIN, ACIDIC ISOFO | AGAS PROTEIN. | HYPOTHETICAL 74.3 KD P | VITELLOGENIN 11 PRECUR |
| NUSM_STRPU<br>YL4K_CABEL | DPFR_ASCIM                                    | YM , YEAST | FILM SACIY                                  | CALLANAT  | Y456_METUA | KITH_HSV23             | RF4_KLULA    | T1S_SALPO              | PMG1_RICCO             | PMG1_10BAC             | DNAK_RHILE             | SLAP_ACEKI             | XDH_DROME              | YRBF_ECOL:             | CLRAI                  | AG. S_ECOLI   | - T                    | V1 Z_CHICK             |
| -1-1                     | -4 - 4                                        | , <i>.</i> | ٦.                                          |           |            |                        | _            | _                      | ٦                      | ٦                      | _                      |                        | _                      | 1                      | _                      | _             | _                      | ~                      |
| 637<br>836               | 1202                                          | 1361       | 2. (2<br>L- L-                              | 330       | 352        | 376                    | 428          | 463                    | 556                    | 559                    | 638                    | 762                    | 1335                   | 269                    | 330                    | 384           | 629                    | 185C                   |
| م م ه                    |                                               |            |                                             |           |            |                        |              |                        |                        |                        |                        |                        |                        | ٦.                     | ٦.                     | ٦.            | ٦.                     | ۲.                     |
| 63                       | 63                                            | 63         | 2 6                                         | 52        | 62         | 62                     | 62           | 3                      | 62                     | 62                     | 62                     | 6.2                    | 62                     | 6                      | 61                     | 61            | 61                     | 61                     |
| 44.<br>00/               |                                               | 4.5        | 44 4<br>N R                                 | 4 5       | 45         | 4.5                    | 4.5          | 4.5                    | <b>4</b>               | <b>*</b>               | <b>4</b>               | 4.5                    |                        | 4 4                    | 44                     | 7 7           | 44                     | 44                     |
| 4.55                     | 27                                            | 28         | 2 K                                         | 31        | 32         | 33                     | 34           | 35                     | 36                     | 37                     | 38                     | 36                     | 40                     | 4.1                    | 42                     | <b>4</b>      | 44                     | 5.45                   |

## ALIMMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Komiyama N., Sone T., Shimizu K., Morikubo K., Kino K.; "coMa clothing and expression of Cry j II the second major allergen of Japanese cedar pollen."; Biochem. Biophys. Res. Commun. 201:1021-1028(1994).
                                                                                                            01.NOV-1995 (Rei. 32, Created)
01.NOV-1995 (Rei. 32, Last seq.ecce update)
01.NOV-1997 (Rel. 35, Last seq.ecce update)
01.NOV-1997 (Rel. 35, Last an .tation update)
POSSIBLE POLYGALACTUROMSE PRI URSOR (EC 3.2.1.15) (PG) (PECTINASE)
(MAJOR POLLEN ALLERGEN CRY J 1) (CRY J II).
CYPCHOMETA Japonica (Japanese cedar).
ELNATYOTA: VIrialplantae: Streptophyta: Embryophyta: Iracheophyta: euphyllophytes; Spermatophyta: Coniferopsida: Coniferales: Iracodiaceae: Cryptomeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakaguchi M., Inouye S., Taniai M., Ando S., Usui M., Matuhasi I.:
"Identification of the second major allergen of Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Namba M., Kurose M., Torigoe K., Hino K., Taniquchi Y., Fukuda S.,
Usul M., Kurimoto M.,
"Moleoular clonning of the second major allergen, Gry [ 11. trum
Japanese cedar pollen.];
FESS Lett. 353:124-128(1994).
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-!- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-ALPHA-D-
-!- GALACTOSIOURONIC LINKAGES IN PECTATE AND OTHER GALACTORONANS.
-!- SUBCELLULAR LOCATION: SECRETED OR AMYLOPLAST (POTENTIAL).
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
(POLYGALACTURONASES).
                                               514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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                                               STANDARD:
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MEDLINE; 95010777.
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MEDLINE; 94271186.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                      EMBL; D29772; BAN6172.i; PROSITE; PROSITE; PS005.22 POLYGALACTURGNASE: 1.
PFAM; PF00295; Glycolhydrol28: 1.
Applicate; Glycolhydrol28: 1.
Amylcolase; Glycolhore; Geli wall; Signal; Zymogen; Fruit ripening; Amylcolase; Glycoprofein; Allegen.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoai Neratoda: Secermentea: Rhabditta: Rhabdittida.
Rhabditina: Rhabdittoidea: Rhabdittidae: Feloderinae: Caenorhabditis
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Pred. No. 2.36e-01:
4: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 514;
                                                                                                                                                                                                                                                                                                                                 DI -> VV (IN REF. 2).
0 -> K (IN REF. 2).
N -> S (IN REF. 2).
K -> E (IN REF. 2).
K -> E (IN REF. 2).
C -> R (IN REF. 2).
C -> R (IN REF. 2).
R -> I (IN REF. 2).
R -> C (IN REF. 2).
R -> C (IN REF. 2).
W, 624511C3FA8D6302 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BRISTOL N2:
Greco I., Bradshaw H., Keppler D.;
Submitted (WN-1999) to the EMB./GenBank/DDB./ databases.
-- SIMILARITY: BELCONGS TO THE UPFOC99 FAMILY.
                                                                                                                                                                                                      POSSIBLE POLYGALACTURONASE POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AF067936; AAC19215.1; -.
WORMPEP: C2466.8; CE77464.
Hypothetical protein.
Hypotherical protein.
Hypotherisal AR: 33689 WW: 20E4FA3D52B4EFB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
14yPOTHETICAL 3+7 F KD PROTEIN CA466-8 IN CHRONOSOME V.
                                                                                                                                                                                                                                 PROGRAGE.
PROBABLE.
POTENTIAL.
F -> L (IN REF. 2).
V -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 1; Ld
Pred. No. 1.09e-06;
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Best Local Similarity 58.3%;
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Best Local Similarity 100.0%:
Matches 12: Conservative
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076387:
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CARBOHYD
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7: Conservative

209 MSLKMGTGKIAA 220

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or send an email to license (String)
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"Nucleotide sequences of the fedBCUE games and locations of the
"nucleotide suggest a periplasmic-binding-protein-dependent transport
medianism for iron[III] dictitate in Escherichia coli.";
J. Bacteriol. 171:2626-2633(1999).
                                                                                                                                                                                                                                                                                                                                                                Bacteria: Proteobacteria: gamma subdivision; Enterobacterianeae.
Escherichia.
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EMBL: D10003: AAA97183.1.

EMBL: AE000499: AAC7243.1:

PIR: JS0115: ORECM3

ECOGENE: EG10290: FECE

PROSITE: FG00211: ABC_IRANSPORTER: 1.

PFAM: PFC0005: ABC_LTAN: 1.

Iron transport; Transport; Inac membrane: ATP-binding.

Iron transport; Transport; AAP (BY SIMILAR.TY).

71:07 MP (BY SIMILAR.TY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 9534362.
Burland V.D., Plunkett G. III. Soffa H.J., Daniels D.L.,
Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 70.8%: Score 51: DB 1: Length 255.
Local Similarity 50.6%: Pred. No. 7.49e-01:
les 6: Conservative 4: Mismatches 2: Indels
                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1997 (Rel. 35, Last annotation update)
IRON(III) DICHIRATE TRANSPORT ATP-BINGING FROTEIN FECE.
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                                                                                                                     255 A.A.
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                                                                                                                     STANDARD;
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D FECE_ECOLI

D O1-APR-1990

DI O1-NAV-1997

DE IRON(III) D1

GN FECE.

CS Bacterial Process

CS CARAIN-K12;

RX MEDLINE: 892

RX MEDLINE: 893

RX MEDLINE
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                                                                                                                                                                                                                                                                                            RECUENCE OF 19-573 FROM N.A.

SEQUENCE OF 19-573 FROM N.A.

STRAIN-CV. DESIREE: TISSUE-LEAF;

A HIDMINE TO BE SERVER TISSUE-LEAF;

HIDMINE TO BE SERVER TISSUE-LEAF;

WILLIME 1905 OF dascaigle and jasmonic acids in gene activation as a recurst of mechanical wounding.

TESUIT of MATTER TISO (1992).

FINCTION: PRESCHABLE INVOLVED IN THE PROCESSING AND REGULAR TISONOVER OF INTRACELLULAR PROTEINS.

CHANKOVER OF INTRACELLULAR AMINO ACIDS.

TISSUE SPECIFICITY: IN TUBERS AND FLORAL BUDS OF UNTRAIED PLANTS.

CHANKOVER OF RESIDENT OF MECHANICAL WOUNDING IS MOSTLY ACCUMULATED.

AFFER ABA TREATMENT OF MECHANICAL WOUNDING IS MOSTLY ACCUMULATED.

CHANKOVER OF A LESSER EXTERN IN STEMS, BUT NOT IN ROOTS.
01-0C1-1996 (Rel. 34, Last annotation update)
CHLOROPLAST AMINOPEPTIDASE PRECURGOR (EC 3.4.11.1) (LEUCINE
AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE)
(EC 3.4.11.5) (PROLYL AMINOPEPTIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17: 1.50 KNOWN AS THE CYTOSOL AMINOPEPTIDASE FAMILY.
                                                                                      Solanum tuberosum (Potato).
Skaryota, Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermarcephyta: Magnolitophyta: euditotyledons:
core cudicots: Asteridae: euasterids I: Solanales: Solanaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: Abrogue.

PIR: 24769: 24769.

PIR: P0040.10.

HSSP: P00727: ILAN.

PRINTS: PRC0488: LANNOPPIDASE.

PROSITE: PSC0488: CATCSCL_AP: I.

PROSITE: PSC0688: Peptidase_M17: 1.

Transit peptide: Chloroplast: Aminopeptidase: Hydrolase; Zinc.

TRANSIT 1 53 CHLOROPLAST (POTENTIAL).

TRANSIT 573 CHLOROPLAST AMINOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-ALA.
ZINC (2) (BY SIMILARITY).
ZINC (1 AND 2) (BY SIMILARITY).
ZINC (2) (BY SIMILARITY).
ZINC (2) (BY SIMILARITY).
ZINC (1) (BY SIMILARITY).
ZINC (1 AND 2) (BY SIMILARITY).
                                                                                                                                                                                                                         Herbers K., Prat S., Willmitzer L.;
"Functional analysis of a leusine aminopeptidase from Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3152145A4A7FB291 CRC64;
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                                                                                                                                                                                                                                                                     Planta 194:230-240(1994).
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431
573 AA;
                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. DESIREE:
MEDLINE: 94339796.
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ACT_SITE
SEQUENCE
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                                                                                                                                                   Solanum.
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METAL
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METAL
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DB 1; Length 573;

Score 49;

68.1%;

Query Match

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                  Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rieger M., Brueckner M., Schalfer M., Mucller-Auer S.;
Sequence analysis of 203 kilobases from Saccharomyces merevisiae
                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharorynetes: Saccharomycetales:
Saccharomycetaceae: Saccharomyces.
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Suzuki N., Watanabe Y., Kusano I., Kitagawa Y.;
"Sequence analysis of the rice dwarf phytoreovirus segment S3
transcript encoding for the major structural core protein of
KDa.;
                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
C1-NCV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 44.3 KD PROTEIN IN CLC1-PDS2 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3e
                    indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hebling J., Hofmann B., Delius H.,
Submitted (MAY 1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 208 POTENTIAL.
376 AA: 44301 MW: ADE8946D805E830F CRC64;
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tches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice dwarf virus (RDV).
Viruses; dsRNA viruses: Reoviridae: Fijivirus.
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                    Mismatches
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TRANSMEM 153 173 POTENTI
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Best Local Similarity 45.5%:
Matches 5; Conservative
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                                                                                                                                                                                STANDARD:
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                                                            139 INLRLPGGRIT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                       SIRAIN= 288C;
MEDLINE; 97435481.
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YG3W_YEAST
P53293;
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"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson J.O., Andersson S.G.E.; "Genomic rearrangements during evolution of the obligate intracellular parasite Rickettsia prowazekii as inferred from an analysis of 52015 bp nucleotide sequence."; Microbiology 143:2763-2795(1997).
                                                                                                                                                         Hibron H., CmcTa T.;
"Nucleotide sequence of rice dwarf virus (RDV) genome segment S3 coding for li4 K major core protein."
Nucleic Acids Res. 18:6700-6700(1990).
-! FUNCTION: IS THE MAJOR STRUCTURAL CORE PROTEIN.
                                                                                                                SEQUENCE FROM N.A.
MEDLINE: 91067474.
Kano H., Kolzumi M., Noda H., Mizupo H., Tsukihara T., Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                        Yamada N., Uyeda I., Kudo H., Shikata E.;
"Nucleotide sequence of rice dwarf virus genome segment 3.";
Nucleic Acids Res. 18:6419-6419(1950).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48: DB 1: Length 1019;
Pred. No. 3.98e+00;
4: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    t -> HG (IN REF. 3).
-> S (IN REF. 2).
5FE562F73E629C50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MFD_RICPR STANDARD: PRT; 1120 AA. 005959. (Rel. 37, Carcated) 15-PER-1998 (Rel. 37, Cast sequence update) 15-PER-2000 (Rel. 39, Cast sequence update) 15-PER-2000 (Rel. 39, Cast annotation update) HRANSCHPTION-REFAIR COUPLING FACTOR (TRCF). MPD OR RPS98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114290 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 132-1120 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               EMBL, X54620; CAA38440.1; -. 
EMBL, D306607; BAA60482.1; -. 
EMBL, D00693; BAA00597.1; -. 
PIR: A45341; A45341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guery Match
Rest Local Similarity 58.3%;
Matches 7: Conservative
   Virology 179:455-459(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 VSLKLISAGIG1 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1019 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ISLKLTSSKIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MADRID E;
MEDLINE: 97419517.
                             SECUENCE FROM N.A. MEDLINE, 91057125.
                                                                                                                                                                                                                                                                                                                                                                                                                                       183
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                     TEMPLATE STRAND BLOCKS THE RNA FOLYMERASE COMPLEX (RNAP). THE RNAP-DAM-RNA COMPLEX IS SPECIFICALLY RECOGNIZED BY BY THEF WHICH RELEASES RNAP AND THE TRUN'ATED TRANSCRIPT; THE TER MAY BELLAGE RNAP AT THE LESION SITE AND THEN RECRUIT THE UVRA/B/C REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.00
FUNCTION: NECESSARY FOR STRAND-SPECIFIC REPAIR, A LESIUN IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takemaru K.-1. Mizuno M., Sato I., iukeuchi M., Kobuyashi
Complete nucleotido sequence of a skin element excised by
rearrangement during sportlation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                                                                                                                    SIMILARITY: IN THE N-TERMINAL TO UVRB. SIMILARITY: BELONGS TO THE RECG SUBFAMILY OF HELICASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48: DB 1: Length 1120:
Pred. No. 3:98e+00:
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W: 09C78EBE71D00482 CRC64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria: Firmicutes: Bacillu. Tostridium droup:
Bacillus/Staphylococous droup. Macillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicase: DNA repair: ATP-binding ENA-binding.
NP_BIND 604 611 ATP (PCTENTIAL).
SITE 709 712 DEED BOX.
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EBBLS, V11783: CAA7244.1: -.
PFAM: PF00270: DEAD: 1.
PFAM: PF00271: helicase_C: 1.
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Local Similarity 70.0%;
nes 7: Conservative
                                                                                                               SYSTEM (BY SIMILARITY)
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STRAIN-168 / JH642:
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P45931;
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002079;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LACCASE 3 PRECURSOR (EC 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani). Eukaryota: Fungi: Basidiomycota: Hymenomycetes; Ceratobasidiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1; Length 1585;
Pred. No. 3.98e+00;
2: Mismatches 1; Indeis
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Pred. No. 6.82e+C0;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses: dSDNA viruses, no RNA stage: Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
GENE 40 PROTEIN.
                                                                                                                   EMBL: 032216; BAA06947.1: -.
EMBL: D844.2: BAA1241.1: -.
EMBL: 29917; CBR1544.1: -.
SUBTILIST: BG11286; Y0BO.
PFAM; PF01464; S.T.; 1.
PFOLHetical protein
SEQUENCE .585 AA: 171630 MW
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Best Local Similarity 66.7%:
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                       66.78;
70.08;
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Best Local Similarity
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UL21_HSVEB
P28972;
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                                                 Wahleithner J.A., Xu.F., Brown S.H., Golightiy E.J.,
Haikier I., Kauppinen S., Pederson A., Schneider P.,
"The identification and characterization of four laccases from the
plant pathogenic fungus Rhizortonia solani.";
Curr. Genet. 29:355-403.1966).
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                            -!- CATALYTIC ACTIVITY: 4 BENZENEDIOL + 0(2) - 4 BENZOSEMIQUINONE
                                                                                                                                             VATOCYANIN-LIKE I.

VSTOCYANIN-LIKE 2.

VSTOCYANIN-LIKE 2.

COPPER (TYPE 3) (BY SIMILARITY).

COPPER (TYPE 4) (BY SIMILARITY).

POTENTIAL.

POTENTIAL.
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:
 Ceratobasidiaceae: anamorphic Geratobasidiaceae: Rhizoctonia
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Pred. No. 6.82e+00;
5: Mismatches 0: Indels
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H -> H.

I -> V.

DF1E2AF9FF108CE4 CRC64:
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ilarity 54,5%;
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Best Local Similarity
                     SEQUENCE FROM N.A.
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Archaea: Euryarchaecta: Thermoceccales: Thermoceccaceae: Pyroceccus
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695 702 ATP (POTENTIAL).
948 AA: 106505 MW: F41DFD7DE6D391B5 CRC64)
                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Funai: Ascomycota: Schizosaccharomycetales:
Schizosaccharomycetaceae: Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROBABLE PEROXIN-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, 29849; CABILSOI.1; -.
PROSITE: PSC6574; AAA: FALSE_NEG.
PFAM; PFO0004; AAA; 2.
PETOX:SOME: ATP-binding. ATP-NPS NP_BIND 695 ATP
PEX6_SCHPO STANDARD: F
013764:
15-JUL-1998 (Fel. 36, Greated)
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This SWISS-PECT entry is copy that it is produced through a collabration between the Swiss lastitute of billionaries and the Ensh putstation the Buropean Bloomformatins institute. There are no restrictions on a last profit institutions as long as its content is in a way modified and this statement is not removed. Usage by and int connected entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
use by non-profit institut: s as long as its content is in the way modified and this statement is of removed. Usage by and for commercial entities requires a license as exact (See http://www.isb-sin.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-JALL / DSM 2661 / ATCC 43567.

MEDILE: 96337999.

Buit C.J., White O. Olsen G.J., Zhou L., Fleischmann S.L., Soruyne J.D., Sutton G.G., Blake J.A., Fitzgerald C.M., Clayton R.A., Soruyne J.D., Kerlavage A.R., Doudberty B.A., Tomb. O.F., Mams M.D., Revind J.D., Sorut J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nougen D., Cotton M.D., Roberts K.M., Hankl M.A., Kaine B.P., Borodovsky M., Clerk H.-P., Fraser C.M., Smill H.C., Woese C.R., Venter J.C., Stander B.P., Horodovsky M., Complete genome sequence of the methanogenic archaeon, Methanocorcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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%red. No. 1.16e+01;
% Mismatches 1; Indels
                                                                                                                                                                                                                                                             Scrib 46, DB 1, Length 121, Pr. 4, No. 1,15e-01, Amstratches 1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-NoV-1997 (Rel. 35, Last sequence update)
01-NoV-1997 (Rel. 35, Last senctation update)
PUTATIVE HYDROGENASE EXPRESTION/FORMAIION PROTEIN MIGGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 :00 C4-TYPE (POIENTIAL).
124 AA: 14058 MW: 1769B05D496957AD CRC64:
                                                                                                                                                                                                                   BE7129443A95F98B CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            jandaschii.";
Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO TH. HYPA/HTPL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 AA.
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PFAM: PF01155: HyPA: 1.
Hypothetical protein: Zinc finger.
ZN_FING 78 :00 C4-TY
                                                                                                                                                           EMBL: AP000005; BAA30649.1; Hypothetical protein. SEQUENCE 121 AA; 13377 MK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.9%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 60.0%;
Matches 6; Conservative
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3 LKLTSGKIAS 12
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Q57657;
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MEDLINE: 94374704.
MEDLIARION of the division-controlling gene fts2 during growth and sportlation of the filamentous bacterium Streptomyces griseus.
GROWIN: MAY INTERACT WITH FTS2, FTSA, AND PBP3 (BY SIMILARITY).
SUBCELULAR LOCATION: TYPE II MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ENDEROAGREGATIVE 17-2 / SERCITYPE 03:H2:
STRAIN-ENDEROAGREGATIVE 17-2 / SERCITYPE 03:H2:
SAVATION 94327462
ADVATION S.J., FOX P., Deng Y., Nataro J.P.;
"Identification and characterization of a gene cluster mediating enteroaggregative Escherichia coli aggregative adharence fimbria I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces griseus.
Bacteria; Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 63.9%; Score 46; DB 1; Length 145; Best Local Similarity 50.0%; Pred. No. 1.1f :+01; Matches 5; Conservative 5; Mismatch 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN 25 145 AGGB PROTEIN.
SEQUENCE 145 AA: 15837 MW; AD308CF0526F3DBF 04C64;
P46026;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 32, Last sequence update)
N-NOV-1997 (Rel. 35, Last annotation update)
AGGB PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTSQ_STRGR SIANDAPD, PRT: 208 AA. P45503: 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) CELL DIVISION PROTEIN FTSQ HOMOLOG (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: U12894; AAA57453.1; -.
Fimbria: Plasmid: Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GMKLATGRIA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SEKETSGKIA 11
                                                                                                             Escherichia coli.
                                                                                                                                 Plasmid P17-2
                                                                                                                                                                  Escherichia.
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or send an email to license@ist-sib.ch).
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                                                                    NON_TER 1 1 208 ! KTRACEULULAR (POTENTIAL).
SEQUENCE 208 AA; 21942 MW: 7CC9A96699746E82 CRC64;
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                                                                                                                         Score 45; DB 1;
Pred. No. 1.15e+0;
4; Mismatches
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                                        EMBL: UC7344; AAA55888.1: -. Cell division.
                                                                                                                        / Match 63.9%; Local Similarity 41.7%; es 5; Conservative
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Release 3.1A John F. Collins, Biccomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 6.15 Seconds 135.255 Million cell updates/sec Mon Jun 19 16:04:11 2030; Run on:

Tabular output not generated.

>US-09-142-524A-6 (1-12) from USO9142524A.pep 72 1 ISLKLTSGKIAS 12

Description: Perfect Score: Sequence:

225878 seqs, 69334122 residues Searched:

PAM 150 Gap 15

Scuring table:

Minimum Match O% Listing first 45 summaries Post-processing:

sptrembil2 l:sp\_archea 2:sp\_bacteria 3:sp\_fundi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_nc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified Catabase:

Mean 23.339; Variance 24.379; scale C.957

13:sp\_vertebrate 14:sp\_virus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |       | نعو   |        |     |        |                        |           |
|---------------|-------|-------|--------|-----|--------|------------------------|-----------|
| Result<br>No. | Score | Query | Length | DB  | ID     | Description            | Pred. No. |
| -             | 53    | 73.6  | 316    |     | 076387 | C24G6.8 PROTEIN.       | 5.98e-01  |
| 7             | 52    | 72.2  | 182    | ~   | 033358 | HYPOTHETICAL 19.4 KD P | 1.05e+00  |
| m             | 51    | 70.8  | 523    | 0.1 | 092W11 | LIK                    | 1.83e+00  |
| 4             | เร    | 70.8  | 627    | 0.7 | 09ZW09 |                        | 1.836+00  |
| 2             | 30    | 4.69  | 157    | ~   | 092HX5 |                        | 3.17e+00  |
| 9             | 49    | 58.1  | 407    |     | 028990 | CONSERVED HYPOTHETICAL | 5.446+00  |
| 7             | 49    | 68.1  | 412    | ~   | 032149 | YURH PROTEIN.          | 5.440+00  |
| တ             | 48    | 66.7  | 210    | 0.1 | 082633 | HYPOTHETICAL 23.5 KD P | 9.27e+00  |
| ው             | 4.8   | 66.7  | 309    | ~   | C51695 | ABC IRANSPORTER, ATP-B | 9.27e+00  |
| 10            | 80    | 66.7  | 460    | ~   | 051276 |                        | 9.27e+00  |
| 11            | 8     | 66.7  | 1019   | 14  | 08860  | MAJOR CORE PROTEIN.    | 9.276+00  |
| 12            | 48    | 66.7  | 1743   | 'n  | 019004 | SIMILAR TO GLUCAN 1    | 9.27e+00  |
| 13            | 47    | 65.3  | 199    | -1  | 028751 | CONSERVED HYPOTHETICAL | 1.57e+03  |
| 7,            | 4.7   | 65.3  | 298    | ~   | P73352 | LACTOSE TRANSPORT SYST | 1.570+01  |
| 15            | 47    | 65.3  | 332    | Ŋ   | Q9XTH3 |                        | 1.576+01  |
| 9             | 4.7   | 65.3  | 381    | 7   | Q9YMM5 | LDORF-102 PEPTIDE.     | 1.57e+01  |
| 17            | 47    | 65.3  | 455    | ø   | 09XS7B | T-CELL SURFACE GLYCOPR | 1.57e+01  |
| 18            | 47    | 65.3  | 529    | . 1 | 039281 | COUNTERPART OF HSV-1 G | 1.57e+03  |
| 19            | 47    | 65.3  | 694    | C)  | Q926R0 | POLYRIBONUCLECTIDE NUC | 1.578+03  |
| 50            | 47    | 65.3  | 907    | ::  | 0921P4 | ORPHAN G PROTEIN-COUPL | 1 570+01  |

Ouery Matc's 73.6%; Score 53; DB 5; Length 316; Best Local Similarity 58.3%; Pred. No. 5.98e-01;

| 2.62e-01<br>2.62e-01                      | . 526.                 | Ψ,                     | œ,                       | ψ,                    | ď,                     | 2.520-01               | 2.62e-01              | Ψ,                    | 2.52e-01              | 2.626-01               | 620-                   | ٠.          | 2.620-01   | 2.620.01               | 2.620-01 | 40                     | ď,     | 2.62e+01          | ç.               | . 52             | 2.520-01               | 4   |                      |
|-------------------------------------------|------------------------|------------------------|--------------------------|-----------------------|------------------------|------------------------|-----------------------|-----------------------|-----------------------|------------------------|------------------------|-------------|------------|------------------------|----------|------------------------|--------|-------------------|------------------|------------------|------------------------|-----|----------------------|
| R208 AMPICILLINASE GEN<br>BETA-LACTAMASE. | EXIENDED-SPECTRUM BETA | TEM-26B BETA-LACTAMASE | EXTENDED - SPECTRUM BETA | BETA-LACTAMASE TEM-43 | BETA-LACIAMASE (EC 3.5 | BETA-LACTAMASE PRECURS | ES-BETA-LACTAMASE (EC | TEM-12 BETA-LACTAMASE | BETA-LACIAMASE TEM-28 | EXTENDED-SPECTRUM BELA | BETA-LACIAMASE PRECURS | LACTAMASE C | LACTAMASE. | BETA LACTAMASE TEM6 PH | ORFS.    | FGFR1 ONCOGENE PARTNER | HRPW.  | ORFIL (FRAGMENT). | F35E2.6 PROTEIN. | DELTA ENDOTOXIN. | KIAA0674 PROTEIN (FRAG | 14  | POLYKETIDE SYNTHASE. |
| 038212<br>000522                          | 048388                 | 048488                 | 6x5x60                   | 034175                | 033677                 | P78144                 | 053043                | 248406                | Q46954                | 992FV9                 | 900626                 | 032372      | Q38058     | 047313                 | P72466   | 095684                 | 087264 | 089222            | 062230           | 045710           | Q9Y4D0                 | 17  | 031781               |
| σm                                        | ~                      | ~                      | ~                        | ~                     | ~                      | 7                      | ~                     | 7                     | ~                     | ~                      | 7                      | 7           | Q,         | ~1                     | 7        | 4                      | ~      | 77                | S                | ~                | -3*                    | m   | ~                    |
| 225                                       | S                      | 2                      | 7                        | 00                    | <b>a</b>               | ထ                      | $\alpha$              | m                     | $\alpha$              | æ                      | ന                      | æ           | ന          | æ                      | (7       | (J)                    | (7     | S)                | 869              | 18               | $\sim$                 | 28  | r-                   |
| 63.9                                      |                        | ω.                     | ۳.                       | ۳.                    | ۳.                     | m                      | ۳.                    | 'n.                   | ۳.                    | ۳.                     | ۳.                     | m.          | ٦.         | ۳.                     | ۲,       | ٠.                     | ۳.     |                   | 63.8             | ω.               | É                      | ω.  | m.                   |
| <b>4.4</b><br>6.5                         | 46                     | 4.5                    | 9                        | 4.5                   | 4.6                    | 45                     | 4.5                   | <b>4</b>              | 4.5                   | 4.5                    | 4.5                    | 9 7         | 4.5        | 4 5                    | 46       | 4.5                    | 4-6    | 4 5               | 46               | 45               | 4.5                    | 4 6 | 4.5                  |
| 21 22                                     | 23                     | 24                     | 25                       | 56                    | 27                     | 28                     | 29                    | 30                    | 31                    | 32                     | 33                     | 34          | 35         | 36                     | 37       | 38                     | 35     | 0.4               | 4 1              | 42               | 43                     | 44  | 4.5                  |

### ALIGNMENTS

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TERMINEBRISTOL NO.

RECURENCE FROM N.A.

SECURENCE FROM N.A.

SECURENCE FROM N.A.

STRAIN-BRISTOL NO.

RELECTED J. GONELL M., COPSET T., CCCPER J., C.YILSON A., COPSET T., CCCPER J., C.YILSON A., BURTON J., CONNELL M., COPSET T., CCCPER J., C.YILSON A., BONEIELD J., EDRES N., TO Z., DURSIN R. FAVELLO A., FULL N. STRAINON M., DEAR N., KERSHAW J., KIRSTEN N. LATREILLIS I., LATREILLIS I., LICKE M., CARLEARAN M., RESTEN N., LATREILLIS I., LATREILLIS I., LICKE M., CANLEARAN M., ROWERS N., CANLEARAN M., ROWINGRAY A., SAUVERS D., SHOWNKEN R., ARAZON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON N., MATSON A., WALKINSON SEROAT J., WOHLDMAN P.;

RA MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

REGGADS. T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C., elegans. T., 2.2 mb of waller 368:32-38(1994).
                                                                                                                                                      Eukaryota, Metazoa, Nematodu, Secernentea, Rhabdilla, Khabdilida, Rhabditida, Rhabdituna, Rhabditidae, Peloderinae, Geenorhabdills.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2:
WATERSTON R.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067936; AAC19215.1; -.
SEQUENCE 316 AA: 33689 FM; B8060373 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;

GRECO I., BRADSHAW H., KEPPLEF D.;

"The sequence of C. elegans cosmid C24G6.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                        Last sequence update)
                         316 AA
                                                         Created)
                         PRT;
                                                      08,
08,
0LT : PRELIMINARY: 076387 PRELIMINARY: 076387 01-804-1998 (TEWRLFE): 08 01-NOV-1998 (TEWRLFE): 08 C2456.8 PROTEIN. C2456.8 Caenorhabditis elegans.
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     RESULT
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HSSP; P02867: 1RIN.
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092W09;
092W69;
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C92HX5
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                                                                                                                                            Matches
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  Gaps
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Actinomycetaies: Corynebacterineae: Mycobacteriaceae; Mycobacterium
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PHILIPP W.J., PUCLET S., EIGLMEIER K., PASCOPELLA J.,
PHILIPP W.J., PUCLET S., EIGLMEIER K., PASCOPELLA J.,
BALASJBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
COLE S.L.,
"An integrated map of the genome of the tubercle bacillus,
"An integrated map of the genome of the tubercle bacillus,
Mycobucterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1)
SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA:
ROUNSLEY S.D., IIN X., KAUL S., SHEA I.P., FUJII C.Y., MASON T.M.,
ROUNSLEY S.D., LIN X., KAUL S., SHEA I.P., FUJII C.Y., WENTER J.C.:
"HEN M., ROONING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.:
"Arabidops:s thaliana chromosome II BAC F16F2 genomic sequence.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004561: AAC95210.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Wararyota, Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: euphyllophytes: Spermatophyta; Magnoliophyta; eudicctyledoms; core eudiccts: Rosidae: eurosids II: Brassicales: Brassicaceae;
ن:
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-1378V.
PARKHILL J. BARKELL B.G., RAJANDKEAM M.A.:
Submitted (JJL-1997) to the EMBL/GenBank/SDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BROWN D., CHURCHER C.M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                          033356 PRELIMINARY, PRT: 182 AA.
033358 (3358) (175MBLrel. 05. Created)
01-JAN-1998 (TEMBLrel. 05. Last sequence update)
101-JAN-1998 (TEMBLrel. 08. Last annotation update)
MTCY20G10.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10. Created)
01-MAY-1999 (TEMBLrel. 10. Last sequence update)
01-NOV-1999 (TEMBLrel. 12. Last annotation update)
PUTATIVE RECEPTOR-LIKE PROTEIN KINASE.
F1552:37.
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EMBL. 297831: CARLOSO.1, -.
Hypothetical procedin.
SEQUENCE: 182 Aar. 19401 MW; 2588107F CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 AA
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                             209 MSUKMCTGKIAA 220
                                                                        131 IGLKLIGGRIA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ISEKLISSKIA 11
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STRAIN-H37RV:
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  Matches
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GOPFROID F. TAMINIAU B., DANESE I., DENOEL P., TIBOR A., WEYNANTS V.
GOPFROID F. TETESSON J. J.;
TIGENTATION OF THE PETOSAMINE SYNTHECASE GENE OF BRUCELLA
MELITERISIS IS MAIN AND INVOLVEMENT OF LIPOPOLYSACCHARIDE O SIDE CHAIN IN
ENUCELLA SULVIVAL IN MICE and IN MACOPHAGES.";
INFECT. IMMUN. 66:0-0(1998).
EMBE. APO47478; RAC98623.1;
SEQUENCE 157 AA: 17565 MW: 52393578 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saps
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                                                                                                                                        Sapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ea: cress).
Mekryota: Viridiplattae: Stre: Ophyta: Embryophyta: Trac:ecptyta: euphyliophytes: Spermatophyta: Mannoliophyta: eudicotyledons: core_eudlocts: Rosidae: eurosids II: Brassica.es: Brassicacea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. COLUBBIA:
ROUNSLEY S.D., IIN KAUL S. SHEA T.P., FUJIT C.Y., MASON T.M.,
SHEN M., RONNING C.M., FRASEN U.M., SOMERVILLE C.R., VENTER D.C.,
"Arabidopsis thatiana chromosome il HAC Fi5P2 genomic sequence.";
Submitted (DEC.1998) to the EMBL/Jensank/DDBJ databases.
EMBL: ACC04561: 1800.
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                                                                                  Length 623:
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Bacteria, Proteobacteria, alpha subdivision: Rhizoblaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 527
                                                                            Score 51: DB 10: Length 623 Fred. No. 1.83e+00; 2: Mismatches 6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
76.8%: Score 51: DB 10; Length 627
Best Local Similarity 77.8%: Pred. No. 1.81c+00;
Matches 7; Conservative 2: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.4%; Score 50; DB 2; Length 157; Best Local Similarity 54.5%; Pred. No. 3.17e+00; Matches 5; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE RECEPTOR-LIKE PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrembLrel. 10, Created)
01-MAY-1999 (TrembLrel. 10, Last sequence update)
01-MAY-1999 (TrembLrel. 10, Last annotation update)
P2 158H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor: Kinase.
SEQUENCE 627 AA: 68788 MW, 7D6CCA4D CRC32;
Receptor: Kinase.
SEQUENCE 623 AA: 69216 MW: FUNAD607 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 AA
                                                                                                                                                                                                                                                                                                                                              627 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.F.
                                                                         70.8%;
Similarity 77.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY:
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                                                                                                         Local Similarity
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                                                                                                                                                                                     185 ISLRLASGK 193
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                                                                                                                                                                                                                    1 ISLKLISGK 9
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3 LKLTSGKIAS 12
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RRARRER RRARRER RRARRAR RRARRAR RRARRER RRARRE
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KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORGHET S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
BORNISSER, BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
CHCI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
DENIZOT F., DEVINE K.M., DOSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOLIGER D.,
FRITZ C., FULITA M., FULITA Y., FUNA S., GALIZZI A., GALLERON N.,
GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHILY E.J., GRANDI G.,
OUISEPRI G., GUY B.J., HAGECH J., HARMOOD C.R., HENAUT A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-VC.16 / DSM 4304 / ATCC 49558;
MEDLINE: 98049343.
METCHOW K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RECHCHOW K.A., DODSON R.J., LEE N.H., SUTTON G.G., GILL S., KITRANESS E.F., DOUGHERY B.A., MCKENBY K., ADAMS M.D., LOFICS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLOSEK A., ZHOU DVERBEEK R., GOGAYNE J.D., WEIDHAN J.F., MCDONIC) L., UTIERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADGW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.M., MASON I.M., OLSEN G.J., FRASER C.M., SMITH H.C., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                        Archaea: Euryarchaecta: Archaeoglobales: Archaeoglobaceae;
Archaeoglobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
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Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 407 AA; 44931 MW; E38F6477 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                        407 AA
                                                                                                                                                           PRT:
                                                                                                                                                                                                                                                                                       CONSERVED HYPOTHETICAL PROTEIN. AF1278.
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TIGR: AF1278; -.
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032149;
01.240.1998 (TEMBLIEL, 05, C1
01.540.1998 (TEMBLIEL, 05, L4
01.NOV-1998 (TEMBLIEL, 08, L4
VURH PROTEIN.
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                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                               Archaecglobus fulgidus
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Best Local Similarity
     43 VNLRLTGGQIA 53
                                    1 ISLKLISGKIA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 LKLKGGKIA 201
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SORESPANDO CONTRACTOR 
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RA HILBERT H., HOLSAPPEL S., FOE SO S., HULLO M.F., ITAYA M., JONES L.,
RA KORAYASHI Y., KASAH Y., KLAERF-BLANCHARD M., KLEIN C.,
RA KURITA K., LAPIDUS A., LANDIN'S S., LACBER J., LAZAREVIC V.,
LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MAZAREVIC V.,
LEE S.M., LEVINE A., LIU H., MASUDA S., NAUEL C., MASALIC V.,
RA MEDINA N., MELLADO R.P., MIZ'NO M., MOESTL D., NAKA, S. H.,
RA PRESCAN E., POULC P., PORNETELLE D., PORMOLLIK S., PRESCOTT A.M.,
RA PRESCAN E., PUJIC P., PUBNELLE B., RAPPOPORT G., REY M., KEYNÖLLS S.,
RA SATO T., SCANLAM E., SCHREEFER R., SOFFENE F.,
SCANLAM E., SCHLECH S., SCHROEFER R., SOFFENE F.,
SCANLAM S., TAKAGHI H., TAKAMAKU K.,
RA SCRIGHI J., SEKCWSKA A., SEF R S., SERROR P., SHIN B. S.,
SOROKIN A., TACCONI E., TAKAAASHI H., TAKEMAKU K.,
RA TOSATO V., UCHTYAMA S., VANG: I., MANIER F., VASSROTI A.,
VINTERS P., WARBUTT R., WEDLER H., WEDLER H., WEITZENEGER T.,
VANNIER P., VASSROTI A.,
VANNIER R., VOSHIKAMA H.F., "STEIN E., YOSHIKAMA H., DANCHIN A.,
RI The COMPLETE SEQUENCE C. The gram-positive bacterius Bacterius
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thallana (Mouser, cress).
Warayota, Virdiplantae: St.eptophyta, Erbryophyta, Trachwophyta, eubhytlophytes: Spermatophyta: Magnolishphyta; eudicotylodons: core eudloots: Rosidae: eurosids II: Brassicales: Brassinaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEVAN M., TERRYN N., ARDILES W., BUYSSHAERT C., DASSEVILLE R., DE CLEKCK R., DE KEYSER A., NEYT P., ROUZE P., VAN DEN DAELE H., VILLARDEL R., GIELEN J., VAN MONTAGU M., HOHEISEL J., MEWES H.W. MAYER K.F.X., SCHUELLER C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.1%; Score 49; DB 2; Length 412;
Best Local Similarity 60.0%; Pred. No. 5.44e+00;
Matches 6: Conservative 3: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases EMBL; 29120; CAB15243.1; SEQUENCE 412 AA: 45519 MK; 7F26E2F0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

EU ARABIDOPSIS SEQUENCING PROJECT;
Submitted (OCI-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AL031804; CAA21199.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Takt Sequence update)
01-NOV-1998 (TrEMBLrel. 08, 1 at annotation update)
HYPOTHETICAL 23.5 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein.
210 AA: 23517 MW: 7AF75A82 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 LRLTCGKITA 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LKLISCKIAS 12
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SETALINE JOUGHNAIC JULIAN STRUCK STRUC
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MEDLINE: PASSER C.M. CASSERS S., HUANG W.M., PODSON R., HICKEY E.K., GWINN M., DOUGHERTY B., TOMB J.-F., ELEISCHMANN R.D., RICHARDSON D., PETERSON J., MERRANAGE A.R., QUACKENBUSH J., SALZBERS S., HANSON M., VAN VOST R., WATTHEY L., MCDONALD L., ARITACH P., BORMAN C., GARLAND S., FULLI C., CCTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48: DB 2: Length 309;
Pred. No. 9.27e-00;
...matches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-30N-1998 (TrEMBLrel. 05. Created)
Cl.JUN-1998 (TrEMBLrel. 05. Last sequence update)
Last sequence update)
ABC TRANSPORTER. ATP-5INFING PROTEIN.
BB0754.
                                                                                                                                                                                                                                                                                                                                       Borrella burgdorferi (Lyme disease spirochete).
Bacteria: Spirochaetales: Spirochactaceae: Borrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 AA: 35183 MW: DDE96281 CRC32;
                                             309 AA
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EMBL: AE001175: AAC67099.1: -.
IIGR: BE0754: -.
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Local Similarity 77.8%;
les 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00005; ABC_tran: 1.
                                                 PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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TLT 9
051695
051695:
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             RESULT
                                                      SATE TO SERVICE SERVIC
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BONFIELD J. BURTON J., CONNELL M., COPSET T., COOFER J., COULSON A.,
CRAKTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., GREEN P., HAKKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P.,
LIGHTNING J., LLOYD C., MCWHRAR A., MORTIMORE B., O'CALLAGHAN M.,
SMALDON N., SMITH A., SCNNHAWMER E., STADEN R., SHOWNEEN R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON J.,
MATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.,
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                              0.41.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 91021050.
SUZUKI N., WATANABE Y., KUSAN- T., KITAGAWA Y.;
"Sequence analysis of the rich dwarf phytoreovirus scament S!
transcript encoding for the major structural core profess of 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
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                                  100els
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STRAIN-CHINESE.
STRAIN-CHINESE.
SHANG F., LI Y., AN C., CHEN 2.:
Submitted (SEP-1995) to the EM:L/GenBank/DDBJ databases.
EMBL: U7227, ABB17618.1; -.
SEQUENCE 1619 AA: 114102 MW. A11005B7 CR012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NeV-1996 (TERMEDRAL, 01, Prested)
CLNNV-1996 (TERMEDRAL, 01, Last Senjanca upodic)
CLNNV-1999 (TERMEDRAL, Last Last anestation update)
SIMILAR TO 3100AN 1.
                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
Fred. No. 9.27e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                  MAJOR CORE PROTEIN.
Rice dwarf virus (RDV).
Viruses: dsRNA viruses: Reoviridae: Fl)ivirus.
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                                                                                                                                                                                                                                                                    PRI: 1019 AA
                                                                                                                                                                                                                                                                                                                            02.
02.
08.
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Best Local Similarity 58.3%;
The Conservative
77.8%:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virology 179:455-459(1990)
   Best Local Similarity 77.8%:
Matches 7: Conservative
                                                                                                                                                                                                                                     11 (29830 PRELIMINARY)
998530 (0.188140)
01-FB-1997 (TERMELTC) (0.188-1997 (TERMELTC) (0.188-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 358:32-38(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISEKLTSGKIAS 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-CHINESE:
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SEQUENCE FROM N.A.
                                                                                         23 TALKLTIGK 31
                                                                                                                                        1 ISLKLISGK 9
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019004
019004;
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286 INLKLSGGNLPA 297
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SECTENCE FROM N.A.
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KC4C1.6.
                           SIRAIN-PCC6803;
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Q9XTH3
Q9XTH3:
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STRAIN-VC-16 / DSM 4304 / AICC 49558;

MEDLINE: 9804543.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DOUSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

KETCHUM K.A., DOUSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

KETCHUM K.A., DOUSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

FULLSCHMANN R.D., OWACKENBUSH J., LEE N.H., SUTTON G.G. ILL S.

KIRKNESS E.F., DCUGHERY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

FETERSON S., REICH C.I., WONEIL L.K., BADGER J.H., GLODEK A., ZHOJ L.,

OVERBEEK R., GCAZYNE J.D., WEILIACH P., KAINE B.P., SYKES S.H.,

SADOW P.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,

FOR THAN OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete genome sequence of the hyparthermophalise sulphate-
reduction archaeoch Archaeochobus fulgidus...
Nature 390:364-370(1997).
EMBL: AEO00997: AAAB89725.1.
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C
                                                                                                                              Score 48; DB 5; Length 1743; Pred. No. 9.27e+60; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Archaea: Euryarchaeota: Archaeoglobales: Archaeoglobaceae;
Archaeoslobus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47: DB 1: Length 199;
Pred. No. 1.57e-01:
3: Mismatches 2: Indels
Submitted (NOV-1995) to the EMBL/GenBank/DU 3 databases
                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria: Chroococcales: Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
P73354
AC P73352
DT 01-FEB-1997 (TEMBLTel. 02, Created)
DT 01-FEB-1997 (TEMBLTel. 02, Last sequence update)
DT 01-FEB-1997 (TEMBLTel. 09, Last sequence update)
DT 01-JAR-1999 (TEMBLTel. 09, Last amonotation update)
DE LACTOSE TRANSPORT SYSTEM PERMEASE PROTEIN LACF
CN LACF
CN LACF
CN Bacteria, Cyanobacteria, Chrococcales, Synechocystis
                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 55, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                       196517 MW: CIEBB6BF CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | protein.
199 AA; 21856 MW; 5915FA61 CRC32;
                                                                                                                                                                                                                                                                    199 AA
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                                                  Submitted (NOV-1995) to the EMBL/CEMBL: U4080C: AAA81491.1: -
EMBL: PFGAC (NOV-1995) to the EMBL/CEMBL: U4080C: 31: 1: PFAM (PFO088: trafoli; 1: 3743 AA: 196517 MM: (
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Archaeoglobus fuigidus.
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WILSON R., ANDERSON K., BAYNES C., BERKS M., MISCONGH K., ANDERSON K., PRYNES C., BERKS M., CULLSON R., BONETELD J., BURRON J., CONNELL M., COPEY T., CCOPER J., CULLSON N., BONETELD J., BURRON J., CONNELL M., THILLER I., JIER M., JCHNSTON L., GARDINER A., GREEN P., HAWKINS T., HILLER N., LATREILLE P., LOHNSTON J., STANDAN J., MISCON C., ROWURRAY A., MONTHMORE B., C'CALLAGRAN M., PRASONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWKKEN R., SMALDON N., SMITH A., SONNRAMMER E., STADEN R., SALSION J., HHERR MILG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON P., WATSON A., WEINSTOCK L., WILL INSON-SPROAT J., WOHLDMAN P., TALL STANDAN P., THOMAS M., MILL INSON-SPROAT J., WOHLDMAN P., THOMAS M., THOMAS M., THOMAS M., THOMAS M.
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(RES. 29605. BAR77383.1).
FRAM. PF05045. BAR77383.1.
SEQUENCE 296 AA: 33382 MW. E75FB074 CRC32;
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STAKIN-PCC6803.
MINLINE: 97651201.

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Rhabditina, Rhabditoidea, Rhabdítidae, Peloderinae, Caenorhabditis
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Best Local Similarity 41.7%; Pred. No. 1.57e+01;
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AINSCOUGH R.:
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 281565; CABC4583.1; -.
EMBL: 270267; CABC4583.1; -.
EMBL: 270267; CABC4583.1; JOINED.
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TAPATA S.:
Submitted (JUN-1996) to the EMBL/SenHack/USBJ databases
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01-NOV-1999 (ITEMBLrel. 12, Last sequence update)
01-NOV-1999 (ITEMBLrel. 12, L. t annotation update)
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DR EMBL, 281865; DAM94216.1; JOINED.

SQ SEQUENCE 33.2 AA; 38518 MM; JDD1SCED CRC32;

Luery Match
Hest Local Similarity 45.5%; Score 47; DB 5; Length 332;
Hest Local Similarity 45.5%; Pred. No. 1.57e+0;
Hatches 5; Conservative 5; Mismatches 1; Indels 0; Japs 0;
ED 211 ILKLSGGRVP 221
UP 1: LLKLSGGRVP 221
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

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1 MKVIVAFNÇEGPNRRVEIKR.......HDGRRVDGIIAAYÇNPASWK 105 urs-09-142-524A-2 (1-105) trom USO9142524A pep 8c6 Description: Perfect Spore: :eduenhas

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Variance 127, 35; scale 0.233 Mean 29.704; Statistics Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Pred. No.                      | 4.146-55 | 1.666-42 | $\sim$                | 4.23e-05 |       | 4.236-05              | 4.23e-06               | 36-                 | 4.230-06              | رس                     | m                      | i.35e-03              | , ,                   | $\overline{}$ | 1.05e-03 | 1.05e-03 | 1.05e-03 | 3.32e-03              | $\sim$                | $\odot$        | 1.26e-32 | 4.72e-32               | 4.720-32           |
|--------------------------------|----------|----------|-----------------------|----------|-------|-----------------------|------------------------|---------------------|-----------------------|------------------------|------------------------|-----------------------|-----------------------|---------------|----------|----------|----------|-----------------------|-----------------------|----------------|----------|------------------------|--------------------|
| Description                    |          |          | Multi-epitope peptide | A)       | cedar | Japanese cedar polien | Japan cedar polien Cry | Japonicum allergen. | Cedar pollen alleroen | Chamaecyparis obtusa p | Japanese cypress polle | Cedar pollen allergen | Japanese cedar pollen | cedar         | _        | apanes   | Cry i I. | Cedar pollen allergen | Sudi allergen protein |                | epitope  | Cry 1 I pollen allerge | y j I Japanese Ced |
| CI                             | r-       | W27371   | ۲.                    | 6979     | 9     | R74333                | R93599                 | R59792              | R81586                | WC4346                 | W42122                 | R81587                | 875388                | R60155        | R45541   | R62490   | 4        | R81581                | W80346                | R81588         | W42171   | 555                    | R82499             |
| 30<br>23                       | . 1      |          |                       |          | . 4   | e- 4                  | ٠.                     | -1                  | , ٦                   | . 1                    | ٦                      | -                     | -                     | -             | -        | -        | -        | -                     | -                     |                | -        | ~                      | ~                  |
| Lengt                          | 500      | 134      | ၁၈                    | 460      | 514   | 514                   |                        | 514                 | 514                   | 514                    | 5.14                   | 353                   | 353                   | fr.           | 374      | 374      | 374      | 17                    | 20                    | 17             | 20       | 20                     | 20                 |
| (1)<br>* (1)<br>* (1)<br>* (1) |          | 6.7.5    |                       | 21.3     | 21.3  | 21.3                  | 21.3                   | -;                  | ä                     |                        |                        | 17.9                  |                       |               | 17.9     |          |          |                       |                       | 16.3           |          | 15.4                   | 15.4               |
| Score                          | 10       | 1 45     | 372                   | 172      | 172   | 172                   | :72                    | 172                 | 172                   | 149                    | 6.5.                   | 144                   | 144                   | 144           | 144      | 144      | 144      | 138                   | 137                   | ed<br>ed<br>ed |          | 124                    | e<br>C             |
| sesult<br>No.                  | -        | ~        | ٣                     | 77       | S     | ų,                    | r-                     | ၽ                   | or                    | 10                     |                        | 12                    | 13                    | 14            | 15       | 16       | 17       | 00                    | 6.                    | 20             | 2,7      | 22                     | 23                 |

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| 5 -2- 5                | 1,740-01              | 1,740-01               | 1,240-01              | 2 526.51              | 3.020.01      | 3.726-01 | 5.226.01              | 5.226-01              | 6.270-01              | 1. JAc-50             | 1.08e-00               | 1.086+00              | 1.296-00              | 1. 296-00             | 00-8677                | 00-067                 | 1.236-00               | 1.296-00               | 00-0671                | 2.216-00               |
|------------------------|-----------------------|------------------------|-----------------------|-----------------------|---------------|----------|-----------------------|-----------------------|-----------------------|-----------------------|------------------------|-----------------------|-----------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|
| Cry ; I pollen allerge | Japanese cedar pollen | Japan cedar poller mat | Such allercen protein | Cedar polien allerden | Curs s T.     | Jun 4 1. | Gedar pollen alleraen | Sugi allerden protein | Japanese cedar polled | Residues 66-80 of Cry | Japan cedar police mat | Sudi allerged protein | Lapamese cedar pollen | Residues 76-90 of Gry | Japan dedar polien mat | Cry j I polled alledde | Cry j I Japanese Gedar | Cry j I pollen allerae | r-cell epitope peptide | Japan cedar pollen mat |
| 9753.                  | 1 535                 | 683                    | r: 77                 | R81582                | C C G G G X X | のたいい # X | R61580                | S48093                | 93.57.38              | 297578                | R: 484                 | \$5.6<br>\$5.6        | 0.75. ·               |                       | en:                    | かせい                    | ος                     |                        | W44582                 | R9788                  |
|                        | ٦.                    | _                      | -1                    | -                     |               |          | ٠,                    | -                     | _                     |                       |                        | _                     | _                     | _                     | _                      | -                      | -                      | ~                      | -                      | 7                      |
| 30                     | 7                     | 15                     | 17                    | 13                    | 367           | 370      | 1.7                   | Γ;                    | ed<br>ed              | 5.                    | 5.                     | 4.7                   | , a                   | 15                    | 15                     | 20                     | 20                     | 24                     | 30                     | 15                     |
| 15.4                   | 14.5                  | 14.5                   | 14.5                  | 14.3                  | 14.1          | 14.1     | 13.8                  | 13.8                  | 13.6                  | 13.3                  | 13.3                   | 13.3                  | 13.2                  | 13.2                  | 13.2                   | 13.2                   | 13.2                   | 13.2                   | 13.2                   | 12.8                   |
| 124                    | 117                   | 117                    | 137                   | 212                   | 114           | 1.1      | 111                   | 111                   | 110                   | 137                   | 107                    | 137                   | 106                   | 3.06                  | 90                     | 106                    | 106                    | 106                    | 901                    | 103                    |
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                                                                           24-MAR-1998 (first entry)
Multi-epitope peptide used as immunotherapeutic agent #2.
Multi-epitope peptide; immunotherapeutic agent; allergic distusc:
T-ce,l epitope region; allergen; lymphosyte; immunoalobuin E.
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W27370 standard: peptide: 105 AA
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W09732600-AL.
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LT 2 W27371 standard; peptide: 134 . W27371; RESULT ID W

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Claim b) Page 11. 58pp. Japanese.

Claim b) Page 11. 58pp. Japanese.

The present sequence represents a multi-epitope peptide which is used as a new immunoting agent. It comprises T cell epitope regions from 2 or more different allurgens (preternally linked via arginine or lysine dimers), where the T cell epitope regions: have a positivity index greater than 100 as measured in a patient group responding to the allerden; have at least 70% reactivity with lymphocyces from patients responding to the allergen; and are not reactive with immunoglobulin E (195) antibodies from patients responsive to the allergen. The agent can be used to prevent and treat a wide variety of allergic diseases, e.g. by desensitisation. Side effects, e.g. those mediated by 19E, are reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKVIVAFINUFGPNRRVFIKRVSNVIJHGRRIGIFASKNFHLUKNTIGIGKRWKNNRIWLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-1998 (first entry) as remonocherapoutic about #1. Multi-epitope peptide used as remonocherapoutic about #1. Multi-epitope poptide: immonotherapecifc agent: allergic disease: T-cel. epitope reaion: allergic disease: Synthecic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1998 (tirst eniry)
Whili---pitope peptide isod as immunotherapeutic agent #3.
Multi---pitope peptide immunotherapeutic agent; allergic disease:
Tree!! epitope region: allergen: lymphocyte; immunoglobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide immuno/therapeutic agent to treat allergic diseases contains multi-epitope peptide containing I cell epitope regions trom different allergens
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Decuth 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FAKLIGETIMARP-----IKMPMYIAGIKIPDGRRVD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                         cuery Match
test Local Similarity 85.7%; Pred, No. 1.66e-42;
Matches 90: "unservative 1: Mishatches 1
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(METP.) MELLI MILK PROD COLITD.
Dairiki K. Iwama A. Kino K. Kume A. Sone T.
WPI: 97-470495/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W27369 standard: pep'ide: 60 AA
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10-MAR-1997 (20740)
10-MAR-1996) (P-0807
                                                          Synthetic.
W09732600-A1.
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ZEGESESEZZZZZZZZSESESESESESES
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46.2%; Score 372; DB 1; Length 80;

Sequence Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure: Pages 26-27, 46pc Japanese. O84044 encodes R69791 Japanic alleracen residues 55-514. Howard teacher entrallerate peptides R6945-86989 were derived. The peptides ability to ability the prevention and treatment of to an IgE antibody can be used to the prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                              hibits pross-lipking of allerden
                                                                                                                                                                                              redidues 55-514, loduced histamice release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 2: Fig 4: 89pp. English.
The sequence is of a Japanese cedar pollen allergem Cry 3
The sequence is of a Japanese cedar pollen allergem Cry 3
The protein and its fragments can be used for diagnosis an treatment of Japanese cedar pollinosis and to identify similar sequences in other plants.
See also R53692-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allergenic Cry ; it protein and fragments from Japanese cedar pollen - used to diagnose, treat and prevent Japanese cedar
                                                            HGSSICIFASKNEHLOKNIISTUSE 5)
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                                            1 MKVIVAFNOFGPNRRVFIKRVSNVI.HGRAIDIFASKNFHLUKNTIGTGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::de::s
                                                                                                                                                                                              Japonicum allergen, redidues 55-514, jodnood histar
antjallergio peptide: jaE cross-linking imbibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 172: DH 1: Dus
Pred: No. 4.23e-06:
 No. 2.08e-24:
Mismatches 0:
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Pred. No. 4.23e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: Mismatches
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01-FEB-1995 (first entry)
Japanese redar police, allergen dry
Cedar pollinosis:
                                                                                                                                                                27-SEP-1995 (first entry)
Japonicum allerden residues 55-514
Best Local Similarity 100.0%; Pred.
Matches 51: Conservative 0, M
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15.UL-1993. D1164.
15.UL-1993. DF-17708.
01-SEP-1993. DF-217725.
07-APR-1994. UP-069336.
(MEIP.) MEIJI MILK PROD GO L 10.
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RS3690 standard: Protein, 514
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12-NOV-1992; US-975179;
(IMMC+) IMMULOGIC PHARM COKP.
                                                             1 MKVTVAFNOFGPNRRVFIKRVSN
                                                                                                                                 869791 standard: Protein: 46:
869791;
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Best Local Similarity 95.2%;
                                                                                                                                                                                                                                                                                                                                                                                              Peptide antiallergic agent with Igs antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 WKNNRIWLQFAKLIGFTLMGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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WO9411512-A.
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Best Local Similarity
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WPI: 94-183513/22.
                                                                                                                                                                                                                                                                                                                                                 Kino K. Kohno Y.
WPI: 95-067159/09.
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Sequence 450 AA
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                                                                                                                   RESULT
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13-MAR-1996.

08-SEP-1995.

10-SE-1994. 199-242137.

14-JUE-1995. JP-200294.
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WC9502412-A.
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                                                                                                                                                                                                                                                                                                                                             New Lipanness rectar pollen alleigen polypeptide - and DNA coding for it. Useful for irrealment and diagnosis of cedar pollen allergy claim 5. Page 55-28: 41pp; English.

The spice enroding an allergen of Japanese cedar pollen was isolated by PPS amplification using primers bused on portions of the allergen protect. The gene was used for recombinant allergen production in Sequence 54. AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washin codar pollon allergen Cry ) II epitope - comprises at least part of specified 46s amico acid protein claim; Pasa 10-11: ITPP: Japanese. (laim; Pasa 10-11: ITPP: Japanese. (BSS94 is a Japan cedar pollon Cry ) II allergen which is useful in the diagnosts, prevention and treatment of Susi pollicests. The diagnosts, prevention and treatment of Susi pollicests. the diagnosts reaction to Japan cedar pollen. Significant regions of the dilargen were identified using overlapping peptides of the full epitope derived from a Cry 3 if antigon-specific I cell line (see F77871-897960). Amico acids 66-80 (R97884) and 186-200 (R97898)
Saps
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16-A00-1946 (Tirst entry)
Japan cedar politen fry II alleraen
Alleraen erytelen fry III alleraen
Alleraen erytelen ovrlappion peptiden fry III neiur politen.
Staf bolloosist dianosist treament.
Tryploneria japuntou
                                                                                                                                      01-N.V-1945 (first entry)
Japanese codur pollen allergen.
Japanese endarr pollen allergen allergyr therapy: diagnostic:
Organistator:
Cryst-metta [apontea.
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Inde, s
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 Mismat nes
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55, .514
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                                                                                                                                                                                                                                                                                           (HAYE ) LAYASHIBARA SEIBUISU KACAKU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cocation/Chalifiers
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20-Nev-1994: 293840.

05-Nev-1994: 3P-296773.

26-MAY-1994: UP-194368.

MEDIA MEDIA MILK PROD CO LID.

WPI - 95-166149/17.

N-PSCH: 118102.
                                                                                                           R74345 standard: Profesm, 514 AA
                          133 WKNNRIWIQFAKUTGFIUMSK 153
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                                                     52 WKNNFIWLOPAKLIGFILMSR 72
 Conservative
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03-N:V-1944.
05-N:V-1943. UP-29451.
20-E0:1943. UP-344594.
27-E0:1943. UP-346614.
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WPI: 95-195588/26.
N-PSCH: 090195.
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 Matches
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Q84C45 encodes R69792 Japunioum allergen, from which the unitalistics peptides R69845 R69859 were ferracd. The peptides ability to inhitity to richitist the cross-liking of an all age, to an IJE antibody can be said in the prevention and treatment of allergic diseases.
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WPT: 96-140976/15
New Eptide(s) derived from the allergen-specific 1qE antituaty allergen-specific T-cells, but not allergen-specific 1qE antituative derived for treating cedir pollinosis
Claim 5: Reage 29-97, 3Epp, English.
Synthetic peptides based on portions of cedar pollen allergens A (R81586) and B (R81587) were tested for their ability to activate cedar allergen-specific 1st
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Sponitum allorgen:
Uaponitum allorgen:
U
of the full mature 460 amino sold allergen are the most alleracely of the 90 peptides tested.
Sequence - 514 AA:
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5-105-1934 301164.
16-105-1934 3P-177008.
16-105-1934 3P-277008.
16-105-1934 3P-277008.
16-105-1934 3P-2750.
16-105-1934 3P-269336.
16-105-1934 3P-269336.
16-105-1934 3P-269336.
16-105-1934 3P-269336.
16-105-1934 3P-26936.
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                                                                                                                                                                                                                                                          Score 172; UB 1: Length 5.4:
Pred. No. 4 2:e-06;
1: Mismatches C: indels
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21.3%. Score 172: DR 1: Cepath 534
Best Cocal Similarity 95.2%: Pred. No. 4.23e-06;
Matches 20: Conservative 1: Mismatches 0: Indels
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Hino K. Saito S. Taniguchi Y:
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869792 standard: Protein; 514 AA.
869792;
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[1] [1] [1] [1][] [1][]
[2 WKNNEIWIOFAKLIOFILMOF 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 WKNNRIWLQFAKLIGFTLMGK 153
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881586/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 WKNNRIWLGFAKLTGFTLMGR 72
                                                                                                                                                                                                                                                                 Query Match 21.3%;
Best Local Similarity 95.2%;
Matches 20; Conservative
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Sequence
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The piesent sequence represents Japanese cypress poliem antiqen Chad2.
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N-PSUB: 18851.

N-PSUB: 18851.

N-PSUB: 18851.

N-PSUB: 18852.

N-PSUB: 188
                                                                                                                                                                                                       Gaps
untibodies t Puppidos (R81580-R81585) were identified as Thoell epitogos. These peptidos, plus subsequences (R81575-79) essential for Threil recognition, and homologous poptidos (R81589-96) can be actual menostherapeutic agents to treat or prevent celar politicosis, unouding side-effects such as aniaphylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7-ce. epitope peptide portion of Japanese cypress pollen antidens
Chaol and Chao? - used for diagnosis and treatment of spring tree
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chanderyports obtusa polien alletaen Cha o II.
Polles alleraens Cha o II. Treell epitopes preventions treatments
polinesis.
Chanderyparis obtusa.
09-001-1996.
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W42122.
16-JUNED (IIISE entry)
Japanese (99Fess poilen untigen Chao2.
Japanese (9press poilen untigen: T-cell epilope: Chao1: Chao2.
Japanese (9press poilen untigen: T-cell epilope: Chao1: Chao2.
Japanese (9press poilen untigen: T-cell epilope: Chao1: Chao2.
Chamaeypars spring tree poilen discase: pollinesis.
W09747548-A1.
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                                                                                                                                                       Length 514:
                                                                                                                                                          Score 172 DB 1/ Length 514 Pred, No. 4.23e-06;
1/ Mismatches 0/ Indels
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12-00N-1997; J02031.
14-JUN-1996; JP-153527;
(MEIP.) MEIUT MILK PRYD CY LID.
Daithik K, Kinc K;
WPI: 98-052242/35;
                                                                                                                                                                                                                                                                                                                                                                            W04346 standard: Protein: 514 AA
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21-DEC-1994, 19-35089.
(MEIP ) MEX.1 MICK PROD TO LTD.
WPI: 96-368225/37.
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                                                                                                                                                                                                                                                                         52 WKNNRIKDOFAKOJGFICMUR 72
                                                                                                                                                            21.36:
95.28:
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28-NoV-1996 (first outry)
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                                                                                                                                                                                  Pest Local Similarity 95.2%;
Katches 20, Conservative
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HIGG K. SAILO S. TANIGUCHI Y:
REPET 96-14-996. Library STEEDISK KAGKKU
HIGG K. SAILO S. TANIGUCHI Y:
RWPI: 96-14-996. Library STEEDISK KAGKKU
New peptide(S) derived trom codar polled aliengens - activate
state for treating codar pollinosis
claim S: Page Biglist pollinosis
Synthetic peptides based on portions of cedar polled aliengenspecific library to activate
CRB1586) and B (RB1587) were tested for their ability to activate
codar allegen-specific library was been inclaimed as properly and nomologists peptides (RB1585) were identified as firely
contropes. These peptides, page 8081565) were identified as firely
contropes. These peptides (RB1585) were identified as firely
contropes as immorther agents to treat or prevent redar
collinosis, avoiding side-viter's s.m. as anaphylaxis
present invention describes peptides which correspond to the 1000. Lope sites on Japanese eppress police antidens that and the training
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
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                     epitope sites on Jaganese operess pollen antidens chall and that peptides can be used as a readent for the clasmosis of almostration operation of spring tree pollon disease in which the period involves reactivity to Japanese oppress pollen.
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Japanese cedar polich allergen Cryj I.
Dapanese cedar: polich allergen; Cryj I. T-cell epitope; peptidus:
prevention; treatment; cryptomeria pollinosis.
Cryptomeria japonica.
                                                                                                                                                                                                                                     DB 1: Length 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%: Score 144. (H.): Lenath At HS.0%: Prior No. 1 Offer54.
                                                                                                                                                                                                                                 Cuery Match 18.5%, score 144: 78 1: Lenath F14 Best Local Similarity 76.2%: Pred. No. 1.376-104: Matches 16: Conservative 2. Mishaumes 3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R81587 standard: Protein: 754 AA
R81587.
24-MAY-1996 (first entry)
cedar: ollen allerge: 5.
Cedar: rollen: allergen: 3mm modistulis E. 19EE.
antibody: pollinosis: thera; ; immenstherafy.
Cryptomeria japonica.
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/note= Treal cpitope peptide"
106. 120
146. 160
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/note= "T-cell epitope peptide'
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R75388 standard; protein: 353
R75388:
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Matches 17: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1996.

08-SEP-1995: 306295.

10-SEP-1994: JP-242137.

14-JUL-1995: JP-260221.

14-JUL-1995: JP-2602021.
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WRIT 95-203834/27

WRIT 95-203834/27

PROVIDED THE STREET AND STREET STREE
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Japanese cedar: pollen antigen: allergen: Cryjt: sugt: pollinosis.
Cryptomeria japanica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uery Match (7.9%) Score (44) DB 1/2 Length 353: Set Local Similarity 85.0%; Pred. No. 1.05e-03: Satches (7.7 Chiservative 1) Mismatches 2: Indels
                       /coter "I-cell epitope peptide" 326. .40
                                                                                              /note- "T-cell epitope peptide"
335, .346
                                                                                                                                                                   /soter "I-cell epitope peptide"
"I-cell epitope peptide"
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/iabol signal_peptide
22, .374
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R45541:
R45541:
13-JUL-1994 (first entry)
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24-MAR-1995 (first eniry)
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Sest Local Similarity 85.0%;
Matches 17: Conservative
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  /note=
2:1:-2
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19-JUL-1994.
67-JAN 1999. (VIIIS.
67-JAN-1993. UP-001116.
                                                                                                                                                                                                                        09-MAY-1995.
20-001-1993: 242526.
20-001-1993: JP-262626
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1994-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrchipp - protein r protein database search, using Smith-Waterman algorithm

nn on: Non Jun 19 15:59:53 2000: Mashar time 6.13 Seconds 405:568 Million cell updates/sec

Tabular output not generated.

111.0: 505-09-142-524A-2 Comertation: (1-105) from USO9142524A.pep Perfect Score: 606

MKVIVAFNOFGPNRRVFIKE...

se ineuce:

.....FDGRRVDGIIAAYGNPASWK 105

Schring table: 3AM 150 Cap 11

THE CONTRACTOR

Searched:

138963 seqs, 23686106 residues

Post-processing: Minimum Match 08

Listing first 45 summaries Maximum DB seq length 105

Catabase: a denesequis

Statistics: Mean 29,764; Variance 127,355; scale 0,233

Pred. No. is the number of results predicted by chance to have a score greatur than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| NO. | Score | Match | Length | 8  | 2      | Cescription            | Pred. No. |
|-----|-------|-------|--------|----|--------|------------------------|-----------|
| -   | 808   | 100.0 | 105    | _  | W2737C | Multi-epitope peptide  | 2.14e-65  |
| 7   | 372   | 46.2  |        | -  | W27369 | Multi-epitope peptide  | 2.08e-24  |
| m   | 138   |       |        |    | R81581 | ~                      | 32        |
| ₹   | 137   | 17.0  |        | -  | W80346 | Sugi allergen protéin  | 4.02e-03  |
| S   | 131   | 16.3  | :7     | 7  | R81588 | u                      | 1.25e-02  |
| ഗ   | 131   | 16.3  |        | ~  | W42171 | I-cell epitope peptide | 1.26e-02  |
| ۲-  | 124   | 15.4  |        | ~  | R45550 | I pollen               | 4.72e-02  |
| αs  | 134   | 4.85  |        |    | R82499 | 1                      | 4.72e-02  |
| ov  | 124   | 4.81  |        | 7  | 845579 | Cry j I pollen allerge | 4.72e-02  |
| 0.5 | 123   | 25.3  |        | 1  | W80357 | Sugi allergen protein  | 5.70e-02  |
| r 1 | 1.11  | 14.5  |        | ٠. | W12535 | Japanese cedar pollen  | 1.74e-01  |
| 7.7 | 117   | 14.5  |        | -  | R97887 | Japan cedar polien mat | 1.74e-01  |
| 5.7 | 1:7   | 14.5  |        | ~  | W80347 | Sugi allergen protein  | 1.74e-01  |
| 14  | 115   | 14.3  | 1      |    | R81582 | Cedar pollen allergen  | 2.51e-01  |
| 15  | 111   | 13.8  | -1     | -  | R8158C | Cedar pollen allerde:  | 5.22e-01  |
| 16  | 111   | 13.8  | -1     | ~  | W80345 | Sugi allergen protein  | 5.22e-01  |
| 17  | 110   | 13.6  | - 1    | -  | W12536 | Japanese cedar poilen  | 5.27e-01  |
| 18  | 107   | 13.3  | rı     | ~  | W5776C | Residues 56-80 of Crv  | 1.08e+00  |
| 19  | 107   | 13.3  | -1     | ٦  | R97834 | Japan cedar pollen mat | 1.08e+00  |
| 20  | 107   | 13.3  | 47     | -  | W80356 | Sudi allergen protein  | 1.08e+00  |
| 21  | 106   | 13.2  | 1      | ٦  | W12542 | Japanese cedar polien  | 1.29e+00  |
| 22  | 106   | 13.2  |        | _  |        | 76-90                  | 00.000    |

| 2.29e-90<br>1.29e-90<br>1.29e-90<br>1.29e-90<br>1.29e-60<br>2.29e-60                                                                         |
|----------------------------------------------------------------------------------------------------------------------------------------------|
| Japan cedar pollon matery ory ) I pollon allerge ory ) I Japanese Cedar Ory ) I pollon allerge T-cell epitope peptide lapan cedar pollon mat |
| R97886<br>R45549<br>R82498<br>R45580<br>F944682                                                                                              |
| eeee                                                                                                                                         |
| 25<br>20<br>20<br>24<br>30<br>15                                                                                                             |
|                                                                                                                                              |
| 1006<br>1006<br>1006<br>1008                                                                                                                 |
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Note: Post-processor removed 17 summaries from 1981 due to scarch parameters chosen.

## ALLONMENTS

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Multi-epitope peptide used as immunotherapeutic agent *[,
Multi-epitope peptide; immun therapeutic agent; allergin disease;
Theil epitope region; aller en; lymphocyte; immunoglobilin E.
                                                     24-MAR-1998 (first entry)
Militepinope peptide used as immunotherapeutic adent **.
Mailth epitope peptide immunotherapeutic adent, allergic discussor.
Theel epitope regions alleraens lymphocytes immunoaletils E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dairiki K. Iwama A, Kino K, Kume A, Sone T:
WPI: 97-4070495/43.
WPDide immuno:therapeutic agent to treat allergic discases -
contains multi-epitope peptide containing T cell epitope regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somme 806, DB 1, Length 105;
Prod. No. 2.14e-66;
0: Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FAKLIGETLMGRKIKMPMYIAGYKTEDGRHVDGIIAAYONPASWK 105
W27370 standard: peptide: 105 AA W27370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ut 2
W27359 standard: peptide: 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEIP ) MEIJI MILK PROD CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.00;
Matches 105; Conservative
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10-MAR-1997; J00740.
10-MAR-1996; JP-080702.
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                                                                                                                                                                         Synthetic.
WC9732600-A1.
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24-DEC-1996; JP-34-441.
(HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.
(SANY.) SANKYO CC LTD.
WPI: 96-577037/49.
A linked I cell epitope peptide - used for the treatment of sign-pollinosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W42171 standard; peptide: 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 94.1%;
Matches 16: Conservative
                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 94.18,
Pes 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I NRIWIQFAKIOGFILMG 17
                                                                                                                                                                                                                                                                                                                                                                                                                     1 RIWLOFAKLIGFILMGK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 RIWLOFAKLTGETLMGR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 NRIWLOFAKLIGFILMG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
EP-700929-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ON WEST
ó
              Claim 5: Page 31: 58pp; Japanese.

The present sequence represents a multi-epitope peptide which is used as mew immunity agent. It comprises T cell epitope requents from 2 or more different allergens. It comprises T cell epitope requent during the T cell epitope regions; have a positivity index attender than 100 us measured in a patient group responding to the allergen; and patient group responding to the allergen; and are not reactive with immunoglobulin E responding to the allergen; and are not reactive with immunoglobulin E (get) antibodies from patients responsive to the allergen. The agent can be used to provent and treat a wide variety of allergic diseases, e.g. by desensitisation, side effects, e.g. those mediated by 192, are reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A THAIR INTERCRETARY SERVE SO NAVAKU.

ALTO K. Salto S. Tanisuchi YI.

AR WFI: W-14097(/IS.

AR WFI: W-14097(/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-1996 (first entry)
deat politicallerae: peptide 9 (T-rel) epitope).
Tedar. Cryptheria Jabonica: polici alicigen: immunodicbulin E:
tab: T-rell epitope: antibody; pollinosis: therapy: immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-CAN-1999 (first entry)
Sudi allergen protein Cryj2 derived epitope for T cells.
Sudi allergen proteins Cryj2; treatment;
T cell epitope; sudi allergen proteins Cryj2; Cryj2; treatment;
sudiipallinesis: allergic reaction; pollen.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                     1 EKVIVAFNJEGPNRRVEIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKVIVAFWAFWAFRPPIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTOFR 51
                                                                                                                                                                                                                                                                                                                    Query Maich. 46.2%: Score 372; DB 1; Length 80: Mest Local Similarity 100.0%: Pred. No. 2.086-24; Matches 51: Posservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 138: DB 1: Length 17:
Pred. No. 3:32e-03:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mishatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-1995 UP-200221
14-JUL-1995 UP-200274
(HAYE ) HAYASHIRARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W80346 standard; peptide; 18 AA W80346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R81581 standard: Peptide: 17 AA
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Sest Local Simplarity 100.0%:
Matches 17: Conservative
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  from different allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-1995; 465295;
10-SEP-1994; 4P-242137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
EP-70/929-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P81581:
24-MAY:1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J10259198-A.
29-SEF-1998.
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                                                                                                                                                                                                                                                                             Sequence
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  MM5666666666
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Claim 7: Page 18. 21pp: Japanese. W80339-58 represent epitopes for T cells, derived from the surm willerace K80339-58 represent epitopes for T cells, derived from the Surm users cryll (K80339-44, K80350-53 and K80356-58) and Jrylz (K80340-49 and K80354-55). The peptides are useful for the treatment of Surm and Jergic reaction of the body to police. Sequence 18 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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16-20% 1998 (first entry)
16-20% 1998 (first entry)
Japanese cypress polien antigen Chao2.
Japanese cypress pollen, antigen, T-cell epitope: Chao1: Chao2.
diagnosis: allergy: spring tree pollen disease: pollinosis.
Chamaeyparis obtusa.
W909747648 A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) derived from codar pollen allergens - activate allergeneinspecific TaE antitudies. Used for treating cedar pollinosis allergen-specific TaE antitudies. Disclosure: Page 32: 36pp: English.
                                                                                                                                                                                                                                                                                                                                                  Cars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic peptides based on portions of cedar poilon alterands A (R8188) and B (R81887) were tested for their ability to activate cedar allergen-specific I-cells, but not alterancespecific [36] antibodies as Peptides (R8188-R8189) were identified as India epitopes. These peptides (R8188-R8189) were identified as India epitopes. These peptides (R8187-R9189) essential for I-cell reconfillion, and namelogies (R8187-R99) essential that contain I common ambinately as sestimated to I more ambina and a sistimately and be used. As a namenotherage cities such as anaphylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MR1588 standard; Peptide; 17 A...
RR1588.
24-MAY-1996 (first entry)
24-MAY-1996 (first entry)
Cedar pollen allergen peptide 16 (homologue).
Cedar pollen allergen peptide 15 (homologue).
Cedar pollen allergen peptide 15 (homologue).
Teeli epitope; antibod; pollinosis; therapy; imminotiviapy.
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red. No. 4.02e-03;
1: Mismatches 0. Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPY70AR 1996

10-SEP-1995; 306295;

10-SEP-1995; UP-240137;

14-JUL-1995; UP-240237;

14-JUL-1995; UP-200234;

A (HAYE) HAYASHIRAHA SEPUTKU KACAKU;

A SALLO S, TANIGUCKI Y;
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allergy
Claim 76; Fig 18; 137pp: English.
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                                                                                     Chen X, Evans S, Franzen HM.
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R45579:
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W8C357 standard: peptide: 47
              06-APR-1995; UC4249.
08-APR-1994; US-226248.
06-DEC-1994; US-350225.
(IMMU-) IMMULOGIC PHARM COR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%:
Matches 15; Conservative
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Bost Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KMPMYIAGYKIFDGR 15
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                                                                                                                                                                                                                                                                                                                                                                                           20 AA:
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19-001-1995
                                                                                                     Shaked 2:
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ID W8
AC W8
DT 11
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Laim 1. State 9 99 14pp; cladades.
The present sequence represents a Thosi epitope peptide from Japanese eypress policy antigen Chao2. The present invention describes peptides eypress policy antigen Chao2. The peptides eites on Lapanese eyptides antithems chao; and chao2. The peptides can be used as a reagent for the diabrosis of allergy to Japanese eypress pollen, and as an antigen in the treatment and prevention of spring tree policy disease in which the policies involves reactivity to Japanese eypress policy.
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The sequence is that of an isolated peptide of the Japanese bodar poller alleraem Gry 1: (amino ucids 81-100). The peptide, 001-9, can be used for the irotiment and disabosis of alleraes associated but he Japanese bedar poller. It has enhanced therapeutic proporties but reduced side effects compared to naturally occurring allergens. Sequence 20 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cry ) I Japanése Cedar póllen allergen peptide fragment (CJI-9).
Cry ) I: japanese cedar póllen allergen; modified, drug production;
allergy: Crytpomería japonica.
Crytpomería japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                (MEIP.) MEIJ: MILK PROD CO LTD.

Dairis, R. Kino K.
WPI, 94-05242/02.

Treel, epitone peptide portion of Japanese cypress pollen antigens
Chaol and Charz - used for diagnosis and treatment of spring tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU) IMMULGIT PHARM CORP.

Bond JF. Garman RD. Griffith JJ. Kuc M. Pollock J:
WPI 94-785665/04.

Antigens derived from Japanese codar polien allorgen Cry j I -
contain at least two T cell epitope(s), used to treat or diagnose
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Cry ) I polled allergen poptide CCI-9.

Japanese cedat: detection: allergy: trearment: diagnosis:

T cell epitope: Sensit.vit.y.

Cryptometra laponica.

W99401560-A.
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Pred. No. 4.72e-02:
0: Mismatches 0: Indexs
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                                                                                                                                                                                                                                                                                                                                     Jel3%: Score 131: DB 1: Length 20:
Rest Local Similarity 73.7%: Pred. No. 1.25e-02:
Matches 14: Conservative 2: Mismatches 3: Indels
                                                                                                                                            polic, disease
Claim 2: Page 39; 71pp: Capanese.
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882499 standard: Protein; 20 AA
R82499:
15-APP-1996 (first entry)
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5: PWKNNRIWIQEAKIIGEIL 69
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Best Local Similarity 100.0%:
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18-060-1997.
12-00N-1997: JF2631.
14-00N-1996: JP-153527.
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01-SEP-1992; US-938990.
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15-JAN-1993: UOD139.
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Clair i:
The sego
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RESULT

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Shaked in Shaked Cryptomeria japonicu (Dry 1) | preptiders) - uscini no proditied Cryptomeria japonicu (Dry 1) | preptiders) - uscini no predicionally cross reactive allergens or increasing allergy to japanese cedar pollen allergen or preformulation scheme to dever in uprimised duag product in the preformulation scheme to dever in uprimised duag product in the preformulation scheme to dever in uprimised duag product in the confideration of the preformulation of the confideration in allergen or an ergen which is immunologically loss reactive with Japanese ceda: len allergen Series ordinal pertudes obsesses certain characterist which render them particularly consistence of modified and unmodified are usen in R82491.882525. This petride for modified and unmodified are veen in R82491.882525. This petride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Try ) i .
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Pred: No. 4.72e-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-1994 (first entry)
Cry j I pollen allergen peptide CJI-41.
Japanese cedar: detection: allergy: treatment; diagnosis:
T cell epitope: sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 124, DB 1; Length 35;
Pred. No. 4.72e-02;
0; Mismatches 0; Indels
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15-JAN-1993: U00139.
10-JUL-1992: WG-U05661.
01-SEP-1992: US-938990.
(IMMC-) IMMUDGIC PHARM CORI
Bond JR. Garman RD. 3714f11! IJ. Kuo M. Pollock JR
WIL: 94-03-2065/04.
Antigons delived from Capanese redar polier alleraer Copinals at least two I cell epitupe(S), used to lifeat
Powers SE
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13-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Chair [0] Puber 5; 21pp; Japanese. We0339-59 from the sugi allergen We0339-59 represent upitopes for I coils, derived from the sugi allergen proteins Cryll (W80339-44, W80350-51 and W80356-58) and Cryl2 (W80345-49 and W80354-58), The poptides are useful for the treatment of sigil-pollinesis, an allergic reaction of the body to pollen. Sequence 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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(SANY) SANKYC CULID.

(SANKYC) SANKYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese cedar pollen allergen-darived peptide 4.
Japanese cedari sugi, polleni pollinosis: pollenosis: allergen:
allergy: T-rell epitope: 108: T-cell receptor: activation:
Sugi wilergen protein Cryjl derived epitope for I cells.
I cell epitope: sugi allergen proteins Cryjl; Cryj2; treatment:
sugi-pollinosis: allergic reaction; pollen.
Synthetic.
                                                                                                                                  3)40259498-A
29-SEP-1998.
22-DEC-1997.
24-DEC-1996. JP-34344.
(BAYE) BAYASHBARA SEIPHISE KAGAKU.
(SANY) SANKY. CO.111.
WPL: 98-377(37/49.
WPL: 98-377(37/49.
FAINKEG I FOLL Epitope peptide - used for the treatment of
8741-pollings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 117: DB 1; Length 14: Pred. No. 1.74e-01; U: Mismatches O: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 123: 58 1; Length 47; sest Local Similarity 57:48; Pred. No. 5.70e-52; Hatches 2: Mismatches 16: Indels Hatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKVTVAFNJEGKLISGKIASCINGLIAAYQNPASWFASKNFHLOKNI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I MXVIVAFNQEGPNRRVETKRVSNVITHG-RRIDI-FASKNFHLQKNI 45
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R9788: standard: peptide; 15 AA.
16-AJG-1996 (first entry)
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W12535 standard: poptide: 14 AA
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Hest Local Similarity 106.0%:
Matches 14: Conservative
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30-APR-1997 (first entry)
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Cryptomeria japonica.
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07-APR-1995: UP-082519.
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Scharme 5. Fig. 3. Type Japanes.

R9787-R97860 are overlapping periodes used for the epitope multiple of the Japan cedar police allerate fry 5.11. Cry 3.11 and allerate to five peptides of it are useful in the diagnosts, prevention and hierarchic of Sugisficant regions of the allerate fractions of Japan cedar politics.

Significant regions of the allerate were identified using the corresponding peptides of the full epitope derived from a fig. 3. Its configurations regentle from a fig. 3. Its configurations research from a fig. 3. Its configurations of the 90 peptides rested.

Sequence 15 AA;
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R81582:
24-MAY-1996 (first entry)
Cedar pollen allergen peptide 10 (T-ceil epitope).
Cedar: Cryptomeria japonica: pollen; allergen; immunoglobulin E;
Cedar: Cryptomeria japonica: pollen; allergen; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugi allergen protein Cryj2 / lived epitupe for 1 cells.
T cell epitope, sudi allergen proteins Cryj1; Cryj2; treatmen:
sugi-pollinosis; allergic reaction; pollen.
Synthetic.
J10259198-A.
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Pred. No. 1.74e-01;
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W80347 standard: peptide: 17 /A.
W80347:
                                                                            05-NOV-1993: JP-27673.
26-MAY 1994: JP-14868.
(MEIP.) HELK PROD CC LED
WPI: 96-166249/77.
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Matches 15; Conservative
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Matches 17; Conservative
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07-NOV-1994: 297840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 115. DB 1; Length 17:
Pred, No. 2.51e-31:
6: Mismatches 0, Indels
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14-701-1995 JP-200221
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Best Lonal Similarity 93.88:
Matches 15: Conservative
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08-SEP-1995 306299
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EP-70925-Al.
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Search ecopleted: Mod Jun 19 16:00:07 2000 Job time : 14 sees.

9 PVDGIIAAYQNPASWK 105

1 KVDGIIAAYQNPASWK 16

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protein - protein database search, using Smith-Waterman algorithm Tue Jan 20 13:38:28 2000: MasPar time 4:18 Seconds 352.971 Million cell updates/sec WPsich\_pp Ron on:

Tabblar output not generated.

-US-U9-142-524A-2 (1-105) from US09142524λ.pep 806 Title: Pescription: Perfect Score: Scywerce:

1 MKVIVAFNOFGPNRRVFIKR.....FDG5RVDGIIAAYONPASWK 105

PAM 150 Cap 11 Scoring table:

145341 seqs, 14437480 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 105 Post-processing:

a-issued lisa\_come 2:5B\_ccmB 3:6\_numB 4:PCT\_comB 5:backfiles1

Catabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 27.828; Variance 123.399; scale 0.226 Statistics

SUMMARIES

Pred. No. Result Chery No. Score Match Length DB II: Description Pred, No

No matches found.

Search completed: Tae Jun 20 13:38:33 2000 Job time : 5 secs.

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protein - protein database search, using Smith-Waterman algorithm WFsrch\_pp Mon Jun 19 15:59:18 2000: MasPar time 9.36 Seconds 529.224 Million cell updates/sec Ron on:

Tubular output not generated.

>08-09-142-524A-2 (1-105) from 0809142524A.pep 806 1 MKVIVAENDEGPNRKVEIKR......FDGRRVDGIIAAYQNPASWK 105

Description: Parfect Score: Sequence:

9AM 150 3ap 11 Scoring table:

142080 seqs. 47172406 residues Searched:

Minimur Match O% Listing first 45 summaries Maximum DB seg length 105 Post-processing:

Mean 41.762: Variance 84.448: scale 0.495 pir62 lipir1 2:pir2 3:pir3 4:p'r4 Statistics:

Patabase

Pred. No. is the number of results predicted by chance to have a scure greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No. Result Query
No. Score Mate: Lecit: CH ID

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Search completed: Mon Jun 19 15:59:36 2000 Job time : 18 secs.

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MPsrch\_pp protein : protein database search, using Smith-Waterman algorithm

Min Dig 19 15:57:58 2000; MasPar time 6.72 Seconds 475:670 Million cell updates/sec Fun on:

Tabular output not denerated.

>US-09-142-524A-2 (1-105) IIOm US09142524A.pep 806 1 MKVTVAFNOFGPNRRVFIKR......FDGRRVDGIIAAYQNFASWK 105 Title: Description: Perfect Score: Sequence:

83857 seqs, 30454973 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing Lirst 45 summaries Maximum DB seq length 105 Post-processing:

swiss-prot38 liswissprot Database:

Prod. No. is the number of results predicted I chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 42,549: Variance 75,450: scale 0,555

Statistics.

SUMMARIES

Description Pred, No. 흱 Result Clery
No. Score Match Legath DB

No matches found.

Sourch completed: Mon Jun 19 15:58:19 2000 Job time : 21 secs.

US-09-142-524A-2a.rspt

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Mon Jun 19 10:58:35 2000; MasPar time 15:33 Seconds 474.840 Million cell updates/sec Tabular output not generated. Ruth On :

JUS-09-142-524A-2 (1-105) from USC9142524A.pep 8e6 | MKVTVAFNGFGPNKRVFIKK.....FDGRKVDGIIAAYQNPASWK 105 fille: Description: Forfect Score: Sequence:

PAM 150 34P 11 Sepring table:

225878 seqs. 69334122 residues Searched:

Minimum Match O% Listing first 45 summaries Maximum D9 seq length 105 Post-processing:

Dalabase:

spirembil2 1.sp\_archea 2.sp\_bacteria 3.sp\_funal 4.sp\_buman 5.sp\_invertebrate 6.sp\_rammal 7.sp\_mhc 8.sp\_organelle 9.sp\_phage 10.sp\_blant 11.sp\_rodent 12.sp\_unclassified 13.sp\_vertebrate 14.sp\_virus

Mean 41.678; Variance 72.759; scale 0.573 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUKMARTES

Description ΙD Result Query No. Score Match Length DB ......

Pred. No.

No matches found.

Search completed: Mon Jun 19 15:59:02 2000 Job time : 27 secs.

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protein protein database search, using Smith-Waterman algorithm Mistroh\_pp

Mon Jun 19 15:58:37 2000: MasFar time 6.77 Seconds 468.570 Million cell updates/sec Rich Cho

lammiar output not aenerated.

>08-09-142 524A-3 (1-134) from USO9142524A.pep 1026 Tatte. Suscription: Perfect Score: September:

1 MKVTVAFNUEGPNRRVFIKR......KFIRRVDG1IAAYQNPASWK 134

PAM 150 Sap 11 Souring table:

188963 segs, 23686106 residues Sourchede

Minimum Match 0% Listing first 45 summaries :persshootd.ped:

aracheseg35 liacheseap

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.232

Variance 132,267;

Mode: 50.632;

Statistics

# SUMMARIES

| Pred No.            | 3.e-8             | 586-                  | .64e-2     | .30e-1      | 306-1           | 33   | .30e-1  | .33e-1 | 30        | .07e-1 | 078- | 61e-0    | .51e-0            | 3.61e-09               | .42e-0              | .32e-0             | .32e-0              | .32e-0             | 326-0             | 326-0           | .32e-5             | 3e-0            | c du                 |  |
|---------------------|-------------------|-----------------------|------------|-------------|-----------------|------|---------|--------|-----------|--------|------|----------|-------------------|------------------------|---------------------|--------------------|---------------------|--------------------|-------------------|-----------------|--------------------|-----------------|----------------------|--|
| Description         | tirepitope peptid | Multi-epitope peptide | ecolida-ii | cedar polle | ar pollen aller | J I. | e cedar | J P    | I Japanes |        | 5    | nese cyp | maecyparis obtusa | Chamaecyparis obtusa p | sell epitope peptid | conicum allergen r | edar pollen allerse | apanese cedar poli | apan cedar pollen | apanese cedar p | aponicum allergen. | at loc : . A    | ry j I Japanese Ceda |  |
| 2                   | 3.7               | 337                   | 3.5        | 3.3         | 158             | 200  | 9:0     | 554    | 249       | 557    | 557  | 2:2      | 134               | W04345                 | 468                 | 67.6               | in<br>in            | 598                | 900               | 333             | 97.9               | 554             | 549                  |  |
| <u>م</u><br>د د د   | _                 | -                     | <b>,-4</b> | -1          | -               | _    | . 1     | r 1    | . 1       | -      | . 1  |          | _                 | -                      | ~                   | -                  | ~                   |                    | _                 | -               | . 1                |                 | , 1                  |  |
| Lesgit              |                   | 300                   | ()<br>(B)  | 1/1         | LO.             | t~-  | r-      | ۲.     | ۲-        | S      | r-   | 354      | in                | 375                    | 30                  | 9                  | . 1                 |                    | , 4               | 514             |                    | O               | 2.5                  |  |
| A<br>Query<br>Match | 6                 |                       | ve.        | ń           | m.              | œ.   | 7       | æ      | (T)       | ä      | ä    | Ċ        |                   | 20.5                   | ن                   | Ġ.                 | o.                  | S.                 | Ö                 | c.              | uS.                | ıc:             |                      |  |
| Score               | .~1               |                       |            |             | 131             | . 7. |         | ()     | 1         | $\sim$ | 11   |          | $\overline{}$     | 216                    | 13                  | r                  | r·                  | t                  | 1                 | r               | 1                  | 00<br>U1<br>+ 1 | u:                   |  |
| Se sult             | . 1               | (7                    | m          | 47          | <b>L</b> O      | œ    | Ĺ       | တ      | OT.       | 10     | 11   | 12       | 13                | <b>45</b>              | 15                  | 16                 | .7                  | ωο<br>. 1          | σh<br>1           | 20              | 21                 | 22              | 23                   |  |

|                                                                            | 1.3                                    | 20            | ٠,     | 2, 476-03<br>2, 476-03                          | 5       | 47.75                   | 0.0                    | 24e-6                 | 340-0     | ç             | 336-0      | 330-0          | 3-964 | £ 38-03    | 4.56   | 6 33e 03               |
|----------------------------------------------------------------------------|----------------------------------------|---------------|--------|-------------------------------------------------|---------|-------------------------|------------------------|-----------------------|-----------|---------------|------------|----------------|-------|------------|--------|------------------------|
| Chamaecyparis obtusa p<br>Japanese cypress polle<br>Radweed Pollen Allerde | y i pollen allerd<br>weed pollen Amb a | b a I/Antigen | Amt a: | Ragweed Pollen Allende<br>Amb a I/Antigen Elend | Amba IC | Radweed Amt al. 3 aller | Radweed polier Ant a I | Cedar polien allerses | of Amba 1 | lergen prote: | of Arrba   | Gen Amb a 15 c | 3     | 29 G G     | 1.2 al | Ragweed poller UNC Clo |
| 22.2                                                                       | R45579<br>W4:851                       |               | . 2    |                                                 | W58729  |                         |                        |                       |           |               |            | L.             | 3     | (*)        | 7.1    | - 4                    |
| -1                                                                         |                                        |               |        |                                                 | , ,     | ٠,                      | , 4                    | 1                     | ٠,        |               | ٠,         |                | ٠,    | ٠,         |        | . 1                    |
| 514<br>514<br>397                                                          | 387                                    | 387           | 201    | עויעו                                           | S       | Œ١                      | $\sim$                 | 17                    | 294       | П             | (y         | (J)            | (y    | 358        | Ġ      | *                      |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                      | 3.13                                   | ~; ~          |        | m m                                             | (*)     | دی                      | ω.                     | ۳.                    |           | æ.            | ٠,         | ٠.             | æ,    | ω.         | ω.     | ë.                     |
| ণালাল<br>কৰ্ম<br>কেতাক                                                     | ** **                                  | ** **         |        | 141                                             |         | :41                     | 141                    | 138                   | 139       | 137           | 137        | (*)            | E     | 133        | 3      | 140                    |
| 24<br>25<br>26                                                             | 27                                     | 25<br>30      | <br>   | 33.2                                            | 34      | 2                       | 36                     | 37                    | 38        | ω<br>σ        | <b>4</b> 0 |                | 42    | <b>7</b> 7 | 4 4    | 45                     |

## PUICHMENTS

Pytide immunotherapeutic agent to treat allerand diseases.

Peptide immunotherapeutic agent to treat allerand diseases.

Peptide immunotherapeutic agent to treat allerand diseases.

Peptide immunotherapeutic agent to treat allerand and interest allerands.

Claim 5: Page 32: 58pp: Japanese.

Claim 5: Page 32: 58pp: Japanese.

Common 5: Page 32: 58pp: Japanese.

Common 6: Page 32: 58pp: Japanese.

Common 6: Page 32: 58pp: Japanese.

Common 7: Page 32: 58pp: Ja 24-MAR-1998 (first entry)
Multi-epitope peptide used as immunotherapeutic agent :)
Multi-epitope peptide; immunciherapeutic agent; alleraic disease;
T-cell epitope region; allera-m: lymphocyte; immunoglobulin E. 12-SEP-1997. 10-MR-1997. 10-MR-1996. JP-080762. (MEIP ) MELLI MILK PROD CC LIE. Dalitki K, Iwara A, Kino K, Kime A, Sone T: W2737; standard; peptide; 13, AA. W09732600-A1. RESULT 

Query Match 100.0%; Score 1026; DB 1; Length 134; Best Local Similarity 100.0%; Pred. No. 4.34e-87; Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps Query Match

0

1 MKVIVAFNQFGPNRRVFIKRVSNVIIHGRRIDIFASKNFHLQKNTIGTGRRWKNNRIWLQ 60 9 ò 61 FAKLIGFILMGRRPLWIIFSGNMNIKLKMPMYIAGYKTFDGRRAEVSYVHVNGAKFIRRV 120 g ô

DGIIAAYONPASWK 134 121 g

12:

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Dulinks K. Iwara A. K.Lo. K. Kume A. Sone II.

Dulinks K. Iwara A. K.Lo. K. Kume A. Sone II.

Peptide imminoriberapeutic agent to treat allergic diseases -
contains multi-epitope peptide occiaining T cell epitope regions.

I from different allerges.

Claim 6: Page 11: Septemble and the principe regions of the present sequence represents a multi-epitope peptide which is used as a new immunoriberapeutic acont. It comprises T cell opitope regions from 2 or more different allerges (preferably linked via arginine or lysine or more different allerges (preferably linked via arginine or lysine or more different have the T cell epitope regions; have a positivity index or allerges allerges and are not reactive with immunosity index inespending to the allerges and are not reactive with immunosity thin E (195) authordies from patients responding to the used to the allerges and are not reactive with immunosity cline deep to be used to prevent and ireat a wide variety of alterial diseases, e.g. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a multi-epitope populde which is used as a new immunocherapeutic agent. It comprises I cell epitope regions from 2 or more different allegents. It comprises I cell epitope regions from 2 dimers) where the I cell epitope regions; have a positivity index agreater than 10 as measured in a patient group responding to the different and are not reactively with immunoglobulin E responding to the allegent and are not reactive with immunoglobulin E (4E) difficultionals from the allegent and are not reactive with immunoglobulin E in used to the allegent a wide variety of allegent The agent can be used to prevent and freat a wide variety of allegent The agent can be used to prevent and freat a wide variety of alleged are reduced.
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W2739: standard; poptible 105 AA.
W2739: standard; poptible 105 AA.
W2739: Standard; poptible 100 AB.
Willimpitope poytide seed as immunotherapeutic asent *2.
Willimpitope poytide; samunotherapeutic agent; allergic disease;
Willimpitope poytide; samunotherapeutic agent; allergic disease;
Syntherial pytope region: allergen: lymphoryte; immunoalobulin E.
W697926(j.A.).
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10-MAR-1997.
10-MAR-1996.
10-MAR-1997.
10-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1) TAKLTGETTM TREPURTTESSMENTKENMPMYTAGYKTFOGRAAE 105
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16-MAR-1996; JR-080762
(MEIP.) MELJE MIEK PROCOS LED.
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4 desensitisation. Side effects, e.g. those mediated by IAE, are induced Sequence.  $80\ AA$ : New Cryptomeria pollen allerace freell epitose peptide i sed for prevention, treatment and investigation of dapanese cedar pollenosis fisiositier. Figs 1.2. 8pp. dapaneses. 875.88 is the dapanese event pollen allerace Try; I in an districtive freell epitope proprides Reviews and treatment of the prevention and treatment of try; in the prevention and treatment of try; and the fisions so for the investigation of polling size. LT 4 R7388 standard; protein: 353 AA. R75388. 12-MAR-1996 (first entry) Japanese cedar pollen allergen Cry; I. Japanese cedar: pollen allergen: Cry; I. Japanese cedar: pollen allergen: Cry; I. T-ceil epitope: peptides: prevention: treatment: cryptomeria pollicosis. Cedar: pollen: allergen: immunoglobulin E: IgE: Treeli .p:tope. antibody: politosis: therapy: immunotherapy. Cryptomeria japonica. EP-700929-A2. 73 RPLWITESGNWNIKLKMPMYIACYKIFDGRRAEVSYVHVNGA-KFIRRVGGIT 66 RPLWIIFSONMNIKLKMFMYIASYKTFDGRGAQV-YIGNGGPOVFIKRVSNVI Query Match 36.3%; Sevie 372; DB 1: Lebuth 30: Best Local Similarity 100.0%; Pred. No. 5.64e-24. Matches 51; Conservative 6: Mismatches 0: Lidels Matches Overy Match 28.6%: Score 295: DB 1. Legath 91: Best Local Similarity 73.6%: Pred. No. 6.30e-17: Matches 39: Conservative 5: Mismatches 7: Indels 1 MKVTVAFNOFGPNRRVF1KRVSNV. THGRRIDTFASKNFHLOKNTIGTGRA 91. 135 /oote- 7:cell epitope peptide\* 136. 120 /note= "I-cell epitope peptide" 736...340 /note- Trueil epitope peptide 335...346 /note= "T-cell epitope peptide" /note= "T-cell epitope peptide" /noter "T-cell epitope peptide" /note= "I-cell epitope peptide" Location/Qualitiers 61. .75 PRIS87 standard: Protein: 353 AA R81587. 24-MAY-1996 (first entry) (MEIP.) MEICI MILK PROD CO LID. WPI: 95-203834/27. 160 Cedar polles allerges B. 08-SEP-1995; 306295. 10-SEP-1994; UP-242137, 14-UUL-1995; UP-200221. 14-UUL-1995; UP-200204. 20-00T-1993: 262626. 20-00T-1993: JP-262626 Cryptomeria japonica. 09-MAY-1995. 13-MAR-1996. 107118295-A peptide pept; ded peptided peptide pep::ded peptide beptided Ġ SCOOC STANDAR BELLIEFE FEET BELLIEFE BE

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Sugi (Japanese cedar) pollen antique Cryji - is useful to: diagnosis, treatrent and prevention of sugi politiquisis. Claim 2: Page 5-7: fpp: Japanese.
The coding sequence for the Japanese cedar ("Sugi") politum alterion Cryji was isolated from a cDNA library prepared from polyn mish. All our part of the Cryji preten can be used for diagnosis, treatment and prevention of Sugi politicis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigens derived from Japanese codar pollen allergen Gry \{\ :\ \cdot contain at least two I cell epitope(s), used to treat of diagnose
24-WAR-1995 (first entry)
Japanese cedar pollen antiden Gryji.
Japanese cedar: pollen antiden: allerden: Cryji: sugi: pollinosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 RPLWIIFSGNMNIKLKMPMYIAGYKIFOGRGAGV-YIGNGGPCVFIKRVSNVI 138
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The sequence is that of the Japanese cedar pollen allergen.
Cry 1 which contains at least two T cell epitopes. Peptide antiques derived from it can be used for the treatment and diagnosis of allergies associated with Japanese cedar pollen. The peptides have enhanced therapeutic properties but reduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 RPLWIIFSGNWNIKLKMPMYIAGYKTFOGRRABVSYVHVNGA-KFIRRVOGII
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28.6%; Score 296; DB 1; Length 374;
t Local Sirilarity 73.6%; Pred. No. 6.30e-17;
ches 39; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 374
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Japanese cedar: detection: dirergy: treutment: diaquosis:
I cell epitope: sensitivity.
Cryptomeria japonica.
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15-JAN 1994
10-JUN-1992: WG-UCS581
61-SEP-1992: WG-UCS581
(IMMU-) IMMULOSIC PHARM CORE.
BORD JF, GARMAR RD, GTIFFER IJ, KHO M. POLICCK J;
WRIS 94-038066/04.
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Fred. No. 6.30e-17:
5: Mismatches 7
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/note= "signal peptide"
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/bote- "matur protide"
                                                                                                                                                                                 /label- siqual_poptide
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R45541 Standard: Protein; 374
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07-JAN-1993; CCLLIE,
07-CAN-1993; JP-001116,
(MELC.) MELCI SELKA KAISHA,
WPL; 94-Z68680/33,
N-PSDB; Q71601,
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Similarity 73.6%:
39; Conservative
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13-JUL-19 ; (first entry)
                                                                                             Cryptomeria japonica.
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for the diagnosis irrethment and prevention of allerance reactions for the diagnosis irrethment and prevention of allerance reactions.

Claim 11. Page 42: 69pp. English.

Fresh pollen and staminate cone samples were collected from a single Cryptomeria japonica (Japanese redar) tree. RNA was prepd, and used to synthesise conA. The cDNA subjected to successive rounds of PCR to yield a full leadth GTY ! I chone. GTY ! I or an antigen. I fragment of it may be used for detection, irreating and preventing an integring activative response to Japanese redar polien allerance. It is capable of modifying both the B and I cell response to a STY ; antigen.

Sequence 374 AA:
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                                                                                 New peptide(s) delived from redar police alleraens - activate alteraen specific T-colls, but not alleraen specific IgE antibodies. used for treating cedar polithosis.

Synthetic peptides Lased on portions of redar police alleraens A (R81586) and B (R81587), were tested for their ability to activate needer alleraen specific IGE antibodies. Further Specific IGE antibodies. Further antibodies at Toell epitones. These peptides, plus subsequences (R81583-79) essential for Treell recognition and homologous peptides (F81588-96) can be used as incontineration and homologous peptides (F81588-96) can pelices as incontineration agents to treat or prevent cedar pollinosis, uvoiding side-offects such as anaphylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 RELWIIFSERWIKLKMEMYTAGYKIFDGRGAQV-YIGNGGPCVFIKRVSNVI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8 RELWIIFSCHWHIKLKMPMYIACYKTFOGRRAEVSYVBVNOA-KFIRRVOGII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73-6%; Pred. No. 6.30e-17;
Matches 39; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cry ) I. Japanese cenar pollen, allergen, antident allergy. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 296: DB 1: 1
Pred. No. 6.30e-17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-04N 1993.
10-031-1993. P05661.
12-00L-1993. CS-729134.
15-036-1993. OS-730452.
(IMMO-) IMMUNGIC PHARM CORP.
SOUM US. GRITCICH IJ. POLIOCK J.
WRIL 97 645444765.
   (HAYB ) HAYASHIRARA SEIBUISU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Coalitiers
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831937 standard: Protein: 374 AA.
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                                  Tan duchi Y:
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R60164:
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73.68:
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Best Local Statlanty 73 bv.
Ens. 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #31937;
03-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      japonica.
                               Hino K Saito S.
WPI: 96-140975/15.
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W09401550-A
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                                                                            Sequence
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W PRING 194249

Wedding University to appoince (Diy J) I peptide(s) - useful for treating ullery to appoince cedar pollen alleryed or useful for treating unimmunologically cross reactive alleryed or limmunologically cross reactive alleryed or limmunologically cross reactive alleryed or limmunologically cross preform lation scheme to develop an optimised drug product for preform lation scheme to develop an optimised drug product for nearty to limmans suffering from alleryed to Japanese redain police alleryed is immunologically cross reactive with Capanese redain police alleryed is immunologically cross possess certain characteristics which render them particularly solution and uncodified populate.

Sitable for dum product formulation. Peptide finaments of cry J L sequence 334 AAs.
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                                                                                                                                                                                                                                                                                                                     Cry ) i Japanese Gedar põiker alleruen
Cry ) ii Japanese gedar polien allergen: modified: drug production:
allero; Trytpomeria Jajonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB: 055272.
Antiques derived from Japanese cedar pollen allergen Cry ( 1 -
costain at least two T cell epitope(s): used to freat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Discussive: Fig 18: 137p; English.
The sequence is that of Jun s I. a homologue of the Japanese ocdar police alleraen Cry ] I. Antigenic peptides derived from it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japanese cedar, pollen illergen: alleray, treatment diadnosis;
T cell epitope: Sansitzvity: defection.
Juniperus sabinoides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 RPLWIIFSGNMNIKLKMPRYIAGYKTFDGRGAQV-YIGNGGPCVFIKRVSNVI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  () TITE TO THE TREATMENT TO THE TO THE TREATMENT TO THE TO THE TREATMENT 
TA BELIATIES AND MAKKERY VALVETPOSERARVSYVHVIGA KETERVOSII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grery Maters 28.5%; Score 296, DB 1: Lenath 374; Nest Loca, Similarity 73.8%; Pred. No. 5.30e-17; Sirches 9; Conservation 6; Monatons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1994.
15-JAN-1992. UC0139.
UL-32F-1992. Wo-U0566.
UL-SEP-1992. US-938990.
(IRMC-) IMMULGIC PHARM CORP.
BOND A. CARMAN RD. GTILLLIN IJ, KIO M. POLICCK J.
WPI: 94-035066/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .z.
/mote= "signal peptide"
22. .367
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845871
13-JUL/1994 (first entry)
den sil
                                                                                                                                                                                                   R82490 standard: Protekn: 274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-1995; D04243.
08-ARF-1994; DS-226248.
06-DDC 1994; DS-306225.
(DMO-) IMMOUNTE PRARM CORP.
Chen X. Evous S. Frollori BM.
Shaked Z.
                                                                                                                                                                                                                                                                                   15-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               WC9401560-A.
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Disclosure: Fig 17: 137pp. 11sh. Credit of the Caparese fits sequence is that of Jun. 1. a incologue of the Caparese codar poller alleform of y j. I. Antiquence peptides decrived from it can be used for the treatment and diagnosis of allerdies asserblined
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                                                                                                                                                                        can be used for the treatment and diagnosis of allerdics associated
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14-JNN-1996; JP-153527.
14EIP) WELLY MILK PROD CO LTC.
Dairtki K. Kino K.
WPI: 98-052242/05.
7-cell epitope peptide portion of Japanese cypress pollem antiquas phollen ad Chao2 - used for diagnosis and treatment of spring tree pollen disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiques derived from Japanese cedar polite, allergen \operatorname{Gry}(y,y) contain at least two T cell epitupe(s), used to treat or diameter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-1958 (first entry)
Japanese cypress pollen antigen Chaol.
Japanese cypress pollen antigen Ticell epitope, Chaol. Chaol.
diagnosis: allergy, spring free pollen disease, pollinusis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ous varies cedar, pollen allerden, allerage treatment, diadunsis
T cell opitope, sessitivity, detection,
Juniperus virginiana.
                                                                                                                                                                                                                                                                   33 RPLWILESGNMNIKLKMEMYIAGYKTFOGSRAEVSYVHVNGAKFIRRVD311 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 370:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RPLWIIFSGNWNIKLKMPBYIASYKTEDSRRABVSYVBVVSAKFIREVOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Match 21.8%: 5.770-224; DH 1: Lenath 370 Local Similarity 55.8%: Prof. No. 2.076-10; es 29; Conservative 10; Mismatches 13, Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 KALWILFSQNMNIKLKMELYVASHKIIDSHSALVELSNGSPOLFMFRYSHVI
                                                                                                                                                                                                                                   87 KAUMIIFSONMNIKLKMPLYVAGHKIILABJADVHIGNOGPOHENKKVFHV.
                                                                                                             Length 367
                                                                                                          Score 224, DB 1: Lenath 367
Pred No. 2.07e-10;
10: Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bond OF, Garman RD, Griffith IJ, Kid M, Pullick II
WPI: 94-035066/64
N-PSDB: 055273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .21
/oote= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1: Page 14-15: 71pp: Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .T .2
WW2121 standard; protein; 354 AA
WW2121;
16-3UN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   nt 1:
R45578 standard: Protein: 470 AA
R45578:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1994.
15-JAN-1993. U00139.
10-JUL-1992. WG-U05661.
01-SEP-1992. US-938993.
(IMMC-) IMMULOGIC PHARM CGRP.
                                                                                                                Overy Match
Best Local Similarity 55.8%;
Matches 29: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with Japanese cedar pollen
                        with Japanese cedar pollen.
Sequence 367 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -JUL-1994 (first entry)
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WO9747648-Al.
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the present invention describes peptides which correspond to the T-cell epitide, sites on Japanese epptides which correspond to the T-cell epitide, sites on Japanese epptides polled antiques chaol and Chao2. The peptides can be used as a reason to the diagnosis of allegy to Japanese epptides gother, and as an actique in the treatment and prevention of symmalise pollen disease in which the pollinosis livedown with AA.
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N.PSON 19879.

N.PSON 19879.

N.PSON 19879.

N.PSON 19879.

IN PROBLEM IN THE USELI IN DEVELOPMENT OF PREVENTATIVE AND TREATMENT OF A WHICH ARE USELI IN DEVELOPMENT OF PREVENTATIVE AND TREATMENT OF A STRONG 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-N°V-1996 (first entry)
Chamarryparis obtisa pollen allerden oli (A).
Bollon alleranni Cha olli Troni epitopo; prevention; treatment;
pollinosis.
Chamarryparis obtisa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-N/V-1996 (lirst entry)
Chamanoyparis obtuse pollen allergen Cha o I cDNA (B).
Pollen allergen: Cha o I: T-cell epitope: prevention: treatment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                            73 PELMITESSMANIK: KAPAYIASYKIFUGEARVSYVHYNGAKFIRBVGSII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 RSEWLIFSKNINIKLSMPCYIAGNKTIEGRGAEVHIGNGGFCLFMRIVSHVI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denuth 354:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L0.5%, Snore 210: DB 1: Length 354, 97,7%; Fred. No. 3.61e-09.
                                                                                                                                                                                                                                                                                                                                                                                             6.8. 9.STATTESKNINIKINAPIPIAONKTINGSGAEVHIGNGGPILFARTVSHVI
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W04345;
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21-28-1944
21-28-1944 GP-335049
(MEIR) MELLI MILK FROM CO 110-
WRIT 06-768-225/37.
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21-080-1994; UP-335039;
(MSIP;) MEIJI MILK PROD CO LID.
                                                                                                                                                                                                                                                                       Justy Match
Best Lecol Similarity (77,7%)
Matches Joi Colsetvilive
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30; Canser
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30 T38519.
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24-JUN1996: JP-163287.
24-JUN1996: JP-163287.
(DAIL) PAICEL CHEM IND LITE.
(DAIL) PAICEL CHEM IND LITE.
(MELL) MELLI SERKA KAISHA HID.
HPL: 96-13563/13.
T cell epitope peptide of seri poliber antigen - useful in the litetiment of sump polibrosa.
T cell epitope peptides W444 2-88 and their derivatives react with Gialm 1 Page 1: 14pp; Jagas, Se.
T cell epitope peptides W444 2-88 and their derivatives and/or time, prepared by combining at h 2 of the above peptides and/or their derivatives is used for to revention and treatment of sem polithosis. Sequence 30 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8: Pages 11-12: 17pp: Japanese.
The present sequence is the C. obtisa pollen allerden Clain 1: the Treal epitopes of the C. obtisa pollen ferelogment of a preventive and trealing about ter C. obtisa pollen polliness.
C. obtusa pollen (2.4 kg) was degreesed with diethyl other, and filed at room temp. overnight. Chain 1 was sopd. From it unitural purified. RMA was extracted for C. obtusa pollen and mark and consider the constant of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 RSDMTIFSKNENIKENMPDYTAGNKTIDGROAEVHIGNODFODFMRIVSFVI
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match

20.5%, Frome 200, 16 in inearth 175
Best Godal Similarity 57.7%, Pred, No. 4.51e+090
Matches 30: Conservative 8: Mishalobes 14: Indols
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theell epitope peptide #1 of supinfollen antique. Theell epitope: sugi pollinosis
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Pred, No. 5,42e-09;
O: Mismatoles ();
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W44682 standard; peptide; 30 AA.
W44682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 MPLWIIFSGNMNIKIKMSMYIACYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C1-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%
Matches 25: Conservative
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J10007730-A.
                                                                                                                                                                                                                                                                                                      375 AA.
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Polease 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd.

MFsrch\_pp protein - protein database search, using Smith-Waterman algorithm Tue Dun 20 13:33:35 2000: MasPar time 4.72 Seconds 410.196 Million cell updates/sec Sabular output not generated. Run on:

>US-09-142-524A-3 [(-134) from US09142524A.pep [026] I MKUTVAFNOFGPNRRVFIKR......KFIRRVIGIIAAYGNPASWK 134 Tile: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

145:41 segs, 14437480 residues searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_CCMS 2:5B\_COMB 3:6\_CCMB 4:PCT\_CCMB 5:backtilesi Parabase:

Pred No. is the number of results pred sted by chance to have a score greater than or equal to the score of the result being printed, and is derived by avalysis of the total score distribution. Mean 28.726; Variance 129.3 3: scale 0.222 Statistics:

SUNMARIUS

|            | Pred. No.     | 2.06e-03  | 2.06e-03              |          | 2.06e-03   | 2.06e-03  | 2.06e-03  | 4.3.e-03   | 4.31e-03  | 4.31e-03   | 4.31e-03         | 4.31e-03   | 4.31e-03   | • •        | 5.18e-03   | • •        |            | 4.62e-02   | 4.52e-02   | 1.71e-01   | 1.71e-01   | i.71e-01   | 1.71e+01   | 1.71e-01   |
|------------|---------------|-----------|-----------------------|----------|------------|-----------|-----------|------------|-----------|------------|------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|            | <u>a</u>      | Applicati | - 4                   | icat     | Applicati  | Applicati | Applicati | Applicati  | Applicati | Applicati  | Applicati        | Applicati  | Applicati  | Applicati  |            | Applicati  | Applicati  | Applicati  | Applicati  | Applicatio | Applicatio | Applicatio | Applicatio | Applicatio |
|            | # .           |           | 72.                   |          | 76.        |           |           | 59.        | 59,       |            | • <del>.</del> . | 74.        | 34.        | .48        | 38.        | 78,        | 80,        | 80,        | 80.        | ω<br>ω     | œ          | 80         | œ          | α;         |
|            | Description   | Seguence  | Sequence              | Sequence | Seguence   | Seguence  | Sednesce  | Sequence   | Seguence  | Seguence   | Sequence         | Sequence   | Sednence   | Seguence   | Sednesce   | Sedneuce   | Sednence   | Sednesce   | Sednence   | Sequence   | Sequence   | Sequence   | Sequence   | Seguence   |
| NUNMAK. UN |               | 38-17     | CS-08-53C-            | 98-29    | US-08-175- | -06 - 29  | 98-29     | US-08-175- | 9-29      | US-08-290- | US-08-175-       | us-08-290- | us-08-500- | US-08-175- | US-08-290- | US-08-290- | US-08-175- | US-08-290- | US-08-250- | -08-35     | -48        | US-08-943- | - 08 - 48  | US-08-484- |
|            | <b>#</b>      | , 1       | _                     | _        | _          | _         | _         | _          | _         |            | _                | _          | <b>-</b> 1 | , 4        |            | ~          | -1         | -          | -1         | امها       | . 1        | ~          | (7         | -          |
|            | Senate DB     | 188       | 387                   | 387      | 397        | 387       | 367       | 34,        | 391       | 391        | 398              | 348        | 368        | 383        | 383        | 383        | 399        | 388        | 388        | 501        | 1079       | 1079       | 1079       | 1079       |
| نعه        | Cuerry        | 13.7      | 13.7                  | 13.7     | 13.7       | 13.7      | 13.7      | 13.4       | 13.4      | 13.4       | 13.4             | 13.4       | 13.4       | 13.3       | £ 3.3      | ۲۰         | 12.1       | 12.1       | ~;         | დ.<br>დ.   | 89.<br>89. | α.<br>α.   | 8.8        | 80<br>60   |
|            | Score         | 1.4       | , (<br><del>1</del> ; |          | . 4        | 141       |           | 100        | 137       | 137        | 137              | 137        | 137        | 136        | 136        | 361        | 124        | 124        | 1.24       | c)<br>in   | <u>ပ</u>   | O<br>o     | O.F.       | 96         |
|            | Result<br>No. | ,,        | 2                     | ندا      | 47         | ស         | 9         | 7          | 8         | 2v         | 0.5              | 11         | 12         | 13         | 1,4        | 15         | 16         | 17         | 18         | 19         | 2°C        | 21         | 22         | 23         |

| 96 8.8 1085 3 US-08-553- Sequence 5. Applicatio 1716-01. 90 8.8 1085 2 US-08-465- Sequence 5. Applicatio 1716-01. 90 8.8 1085 2 US-08-487- Sequence 5. Applicatio 1716-01. 90 8.8 1088 1 US-08-487- Sequence 5. Applicatio 1716-01. 90 8.8 1088 1 US-08-484- Sequence 5. Applicatio 1716-01. 91 91 01 01 01 01 01 01 01 01 01 01 01 01 01 | ALIGNMENTS US-28-175-069A-72 STANDARU: PRT: 387 AA. xxxxxxx Sequence 72, Application US/08175059A | equence 72, Application US/08175059A atent No. 5776761 GENERAL INFORMATION: APPLICANT: Rapper, David G. ADRESSES: LAHVES S. STREET: G. |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 4550 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                  | 7.08                                                                                              | *8888888888888888888888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

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Patent No. 56/6354
Patent No. 56/6354
GENSSALING-PRATION
ADDITIONAL NETWORKS Bruce
APPLICANT Klapper, David G.
APPLICANT Rafnal, THORMON
ADDITIONAL Reference Proteins From Requeed and Uses
NUMBER OF ENGLENCES 9
OFRESHOLDENCE ADDITIONS ADDITIONAL STREET BY
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                                                                             Query Match 14.7%; Score 141; De 1; Locath 487; Sest Lonai Similarity 43.2%; Pred. No. 2.05e-03; Satobes 19; Conservative 8; Misharotes 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Finepy disk

"OMPUTER: IBM 10 compatible

PERALING SYSTEM: PC-DOS/MS-DOS

SYFTWARE: Patentic Release #1.0. Version #1.25

OUSENT AFFICATION NUMBER: US/06/29*1449A

FILING OAKE: Adust 15, 1994
                                                                                                                                                        67 F. LWSPERINTIPSCANIKLKMPMYIACYKTERGRAEVSYVE 110
                                                                                                                                     98 FOAAGNPOLWTIFEHDWYPROXEMWWNSDKTIOGRGAKWETIN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE, May La, 1997.

APPLICATION WRHER: US 07/325.955
FILING DATE: March 17, 1989
ALTORNEY PAINT INVERMATION
NAME: Ary E. March 400 as
REGISTATION NUMBER: 36.27
FERRENDEL/DOCKE: WRHERE: IM. 0.180N
TELECOMMUNICATION INCREMENTON:
ELEFAN: (617)227-7400
ELEFAN: (617)227-7400
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1.4.7.
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APPLICATION NUMBER US 01/519.951
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LENGIH: 347 amino acids
TYPE: amino acid
TYPE: pmino acid
TOPOLEON: linori
MINIMOLE TYPE: protests
SPOCEN'E 187 AA: 41:60 MM: 736967 ON:
                                                                                                                                                                                                                       STANDARD
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amino acid
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TROUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPOURS: IBM 10 COMP
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GENERAL INFORMATION
FAPLICANT: ROGES, Fruce
APPLICANT: Rather: Thorses
APPLICANT: Rather: Thorses
APPLICANT: Rather: Thorses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk CCMPUIER: IRM PC COMPTIEN: IRM PC COMPTIEN: CCMPUIER: IRM PC COMPATIENE CCMPUIER: IRM PC COMPATIENE CORRESTING SYSTEM: PC-05/MS-FLS SUFFWEEE: Patentin Release #1.0. Version #1.25 CORRENT APPLICATION DATA: PS-05/29:1448A FILING DATE: Name: S-1994 FILING DATE: Name: 15.7/524:951 FILING DATE: Name: Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 FG. AÇMKPEMIJEBREMVIRLEKEMVVNSDKTIDGRGAKVELIN 141
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STREET: 60 State Street, 8:11e 510
CIIY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT:
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(1)
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LENGTH: J67 anino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECCLE TYPE: protein
SEQUENCE 387 AA: 41660 MW: 736967 CN:
                                                                                                                                                                                                                                                                                                                            Sequence 72. Application US/0329.4458
                                                                                                                                                                                                                                                                              Sequence 72. Application 08/0824/444A
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                                                                                                                           STANFARD
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy o
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: USA
                                                                                        US-08-175-069A-76
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98 FRAAÇINRPLWIIFERDMVIRLOKEMVVNSOKTIDGRGAKVETIN 141

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108 FAAAQNRPLWITFKNEMVININQELVVNSORTIDERGVKVE-1-INGGLTLANVKNII 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allergenic Proteins From Ragweed and Uses 93
                                                                                   Patent No. 577676.
GENERAL INFORMATION:
APPLICANT: Rogers. Bruce
APPLICANT: Rafnar: Thorung
APPLICANT: Rose, Wel-Glang
APPLICANT: Rose, Wel-Glang
TILE OF INVENTIONS: 93
CURRESPONDENCE: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 141: DB 1: Length 397: Pred. No. 2.06e-03: 12: Mismatches 22: Indels
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SOUNTRY: USA
2109 2109 318X
2219 2109 318X
2219 2109 318X
COMPUTER FEADMARE FORM:
MEDIUM TYPE: Floppy 318X
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MEDIUM TYPE: Floppy 318X
COMPUTER FORM:
MEDIUM TYPE: Floppy 318X
FILING SAFENT DECEMBER 29, 1993
APPLICATION NUMBER: US 07/525,95;
FILING DATE: MAGNATION:
MAME: Amy E. MAGNATION:
TELEPHONE: (617,227-740)
TELEPHONE: (617,227-740)
TELEPHONE: (617,227-740)
TELEPHONE: (617,227-740)
TELEPHONE: (617,227-740)
TELEPHONE: (617,227-740)
                                                                                                                                                                                                                                                                                                                                5: LAHIVE & COCKFIELD, LLP
60 State Street
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MCLECULE TYPE: protein
JENGE (97 AA: 42947 MW: 781425 CN:
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                                                        Sequence 76. Application US/08175069A
Patent No. 5776761
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Sequence 76, Application US/08175069A
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APPLICANT Klapper, David 3.
APPLICANT Rainar, Thorunn
APLICANT Kuo, Mei-chang
TITLE OF INVENTION: Allergenic
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
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west Local Similarity 37.9%:
atches 22: Conservative
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STREET: bu
TTY: Boston
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C Sequence 76, Applic

CC APPLICANT: Raf

CC APPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Rave, Wei-chang
TITLE OF INVENTION: Alie-genic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 141; DB 1; Length 397; Pred. No. 2.05e-03;
                                                                                  COMPINE SEADABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Hoppy disk
COMPUTER: 1BM PC COMPATICLE
OPERATING SYSTEM: PC DOS/WS-DOS
SOSTANE: BATENIC Release #1.6, Version #1.25
CORRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/290,446A
FILING DATE: Acquist 15, 1494
PRIOR APPLICATION DATE: Acquist 15, 1494
PRIOR APPLICATION NUMBER: US 07/229.95;
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/229.95
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/225.365
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/225.365
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/225.365
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/225.365
FILING DATE: MAY 29, 1990
APPLICATION NUMBER: US 07/225.365
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                                                                                                                                                                                                                                                                                                                  NAME: Any E. Mandragours
REGISTRATION NUMBER: 36.207
REFERENCE/DOCKE IMI-618CN
TELECOMMUNICATION INFORMATION:
TELEFONE: (617)227-740C
TELEFONE: (677)227-5941
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENTH: 397 amino doids
TYPE: amino acid
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STRET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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К.
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JENCE 397 AA: 42947 MW; 781425 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 76. Application US/08290448A
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STREET: 60 State Stree
CITY: Boscon
STATE: Massachusetts
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Best Local Similarity 37.9%:
Matches 22: Conservative
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Sequence 59, Application US/08175069A
Parent No. 977676
GENERAL INCREMATION
APPLICANT: Riapper Carid G.
APPLICANT: Riapper Carid G.
APPLICANT: Misper Carid G.
ANDRESSEE: LAHVE'S COCKFIELD, L.P
SIREEL GO State Street
CITY: Boston G. State Street
CITY: Bassethisetts
COMMISSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          query March
Hest Godal Similarity (27.9%) Pred. No. 2.06e-03;
Matches 22: Conservative 12: Mismatches 22: Indels 2: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 HAAAQMSFLWIIFKNEMVINLNQELVVNSCKTIDGRGVKVE-I-INGGLTLMNVKNII 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 FILMGRRPLWITESGNMNIKLKMPMYTAGYKTETGRRAEVSYVEVNGAKFIRRVDGII 124
SOFTWARE: Parentin Release #1.0, Version #1.25
CURREY APPLICATION DATA:
APPLICATION NUMBER: US/08/290.448A
FILING APPLICATION NUMBER: US/08/290.448A
APPLICATION NUMBER: US 07/529.951
FILING DATE: May 24, 1999
APPLICATION NUMBER: US 07/225.365
APPLICATION NUMBER: US 07/225.305
CELEPHINE: (617/227-594)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: COMPUTER: PC COMPUTED FOR SYCHEMATING SYSTEM: PC-DOS/MS-DOS SYCHEMARE: Pate:tin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39: AA
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94:0R APPLICATION DATE: US 07/529.951
APPLICATION NUMBER: US 07/529.951
FILING DATE: MAY 29, 199C
APPLICATION NUMBER: US 07/525,365
FILING DATE: MAYCH 17, 1989
ATIONENY/AGENT INFORMATION:
NAME: AMY E. MAGGRAGOUFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ir.
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02139-18
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102 FAAAQNRPLWIIFKKNMVIHLNQELVVNSLKIIDGKGVKVNIVNA-GIILMN-VKNII. 187
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 59, Application US/L 290446A
Patent NO. 567654
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Klapper, David G.
APPLICANT: Klapper, David G.
APPLICANT: Klapper, David G.
APPLICANT: Rud. Melvicand
IIILE OF INVENTION: Alloration Proteins From Radword and issue
NUMBER OF SEQUENCES: 93
UCHERSPEE: LAHVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                       Score 137: DB 1: Length Folloge red. No. 4.31e 03;
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COUNTRY DASA
ZIE: 02109-1875
CHEUTER READALE FORM:
CHEUTER READALE FORM:
CHEUTER PROJECT OF STELLE
SPERATING SYSTEM:
SYSTEM: PROJECTION NUMBER: DAYON OF STELLE
APPLICATION NUMBER: US/US/29,448A
FILING DATE: August 15, 1994
PRICATION NUMBER: US 07/259,951
APPLICATION NUMBER: US 07/259,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/25,365
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/25,365
FILING DATE: May 29, 1990
ATORNY-AGENT INFORMATION:
NAME: ANY E. MANDERRIGHS
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                              341 AA
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               1MI-018DV
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E.K.O.
                                                                                                                                    MOLECULE TYPE: protein
SECUENCE 391 AA: 42864 MW: 254545 CN.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59, Application US/ 10448A
REGISTRATION NUMBER: 6.267
REFERENCE/DOCKET NUMBER: IMITELECOMMUNICATION: INDEARTION: TELEPHONE: (617)227-74.6
INFORMATION FOR SEQ. 10 No.: 59: SEQUENCE CHARACTERISTICS:
LENGHH: 391 menico acud.
TYPE: amino acid.
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617)227-7406
TELEFAX: (617)227-5941
INFORMATION FCR SEQ ID NO: 59
                                                                                                                                                                                                                                                                                                             STANDARD
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amino acid
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Best Local Similarity 39.78
Matches 23: Conservative
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10 US-08-290-448A-59
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                      US-28-175-069A-74
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CITY: B
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                                                                                                           Gaps
                                                                                                                                                        102 FAAAQNEELWIIFKRHMVIHUNQELVVNSOKTIDGROVKVNIVNA-GLILMN-VKNII 157
                                                                                                                                                                                        67 FTLMSEMPLWITESGNWITELKMPWYSACYKTFDGRRARVSYVHVNGAKEIRKVDGII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFPLICANT: Repers, Bruce
AFPLICANT: Klapper, David G.
AFPLICANT: Rainar, Thorung
APPLICANT: Kno. Mai-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 391;
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Best Local Similarity 39.7%; Pred. No. 4.31e-63;
Matches 23; Conservative 10; Mismatches 23; Indels
                                                Score 137: DB 1: Length 391: Pred. No. 4.31e-03:
                                                                                                        10; Mismatches 23: indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: INM PC compatible
COMPUTER: INM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0. ersion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290.448A
FILING DATE: August 15, 1994
PRIOR REPLICATION NUMBER: US/07529.951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US/0725.465
FILING DATE: May 29, 1990
APPLICATION NUMBER: US/0725.465
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: August 10F MARCH 20, 1990
RECISTRATION NUMBER: MA.-018CN
FELSONMUNICATION NUMBER: MA.-018CN
FELSONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                       351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 391 AA; 42864 WW, 754045 CN:
391 AA: 42864 MW: 754045 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59, Application US/08290446A Patent No. 5698204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Application US/08290448A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617)227-7400 (617)227-594 (617)227-594 (617)227-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (617)27-594 (6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 amino acids
amino acid
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                                                  Udery Match
Best Local Similarity 39,7%;
Matches 23; Conservative
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02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5698204
GENERAL INFORMATION:
AFPLICANT: ROGETS
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CITY: Boston
STAIE: Massach
                                                                                                                                                                                                                                                                                           RESULT 9
11 US-08-290 448A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       senic Proteins from Radward and Tees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.4%; Score 137; DB 1; Length 398; Best Local Similarity 39.7%; Pred. No. 4.31e-63; Matches 23; Conservative 10; Mismatches 23; Ind.:s
                                                                                                                                                                                                                                                                                                                                  398
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PRT:
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MOLECULE TYPE: protein
HENCE 398 AA: 43664 MW: 77:006 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 74, Application US/08290448A
Patent No. 5676954
                                                                                                              Sequence 74. Application US/08:35069A
Patent No. 5776761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/.8290448A
                                                                                  Sequence 74. Application Us// %125069A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 40.207
REFERENCE/DOCKET NUMBER: IMI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Amy E. Mandradourds
REGISTRATION NUMBER: 46.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617)227-7450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                     APPLICANT: Rogers, 5:10-
APPLICANT: Klapper, bav)
APPLICANT: Rafnar, Frc:
APPLICANT: Ruo, Mei-ch
111.E OF INVENTIO: AL
CORRESPONDENCES:
CORRESPONDENCE ALCHESS.
STAND/ C
                                                                                                                                                                                                                                                     5: LAHIVE & ...
60 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTIC: LENGTH: 398 amino ac TYPE: amino acid
                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02109-1875
                                                                                                                             Patent No. 5776761
GENERAL INFORMATION:
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RESULT
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Cuery Match 13.4%; Score 137; DB 1; Length 398; sest Local Similarity 39.7%; Pred. No. 4.31e-03; Matches 23; Conservative 10; Mismatches 23; Indels 2; Gaps
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Patent No. 569824
GENERAL INFOHMATION:
GENERAL INFOHMATION:
GENERAL INFOHMATION:
REPLICANT: Riapper: David G.
APPLICANT: Rafnar, Thorum
APPLICANT: Roo. Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES:
ADDRESSEE LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                   APPLICANT: Roders, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainar, Thorum
APPLICANT: Kuo, Mai-chana
IIILE OF INVENTIVE: Allergenic Proteins From Rayweed and Uses
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                    COUNTRY: USA

AIP: 02109-1875

COMPLEX READMALE FORM:
MEDIUM IYPE: Floppy disk

COMPLES: Floppy disk

COMPLES: Repopy disk

COMPLES:
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FRIUMS DATE: August 15, 1994
FRIUMS DATE: WAY 29, 1996
APPLICATION NUMBER: US 07/529,951
FILINS DATE: WARCH: 17, 1989
ATTORNEY/AGNI INFORMATION:
NAME: AMP E. MANDIAGOULAS
REGISTRALION NUMBER: 16,207
FREERENDE/DOCKET NUMBER: IMI-9180N
FRECOMMENDICATION INFORMATION:
FRECOMMENDICATION INFORMATION:
FRECOMMENDICATION INFORMATION:
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60 State Street, saine 510
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F. F.
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UENCE 348 AA: 43664 MW: 779006 CN:
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INFORMATION FOR SEC ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
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GENERAL INFORMATION:
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Patent No. 577551
GENERAL INFORMATION:
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorum
APPLICANT: Ruo, Mei-Chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shore 137: DR 1: Length 396: Fred, No. 4.31e-03:
                                    CCAPUTER VAIGNING TO THE COMPUTER FORM:
MEDIUM TYPE: F.OPPY disk
COMPUTER: ISM FC COTHA'ILLE
OPERATING SYSTEM: PC: S/MS-DDS
SOFTWARE: PATENTIA FC -480 #1.6, Version #1 25
SOFTWARE: PATENTIA FC -480 #1.6, Version #1 25
SOFTWARE: PATENTIA DATA
APPLICATION NUMBER: U. 08/290,4448
FILING DATE: ANGUST IS. 1994
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/25.9.95;
FILING DATE: MAY 29, 1996/24.95
APPLICATION NUMBER: US 07/425.36
FILING DATE: MAY 29, 1996/24.95
ATOMORYAGENT INFORMATION:
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                       NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)277-594
INFORMATION FOR SEQ ID NOT 74,
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD
                                                                                                                                                                                                                                                                                                                                                                               398 amine acids
                                                                                                                                                                                                                                                                                                                  (617)227-7
(617)227-594
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MOLECULE TYPE: protein
JENCE 398 AA: 43664 MW.
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Best Local Similarity 39.7%;
Matches 23; Conservative
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SIATE: Massachusetts
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STAIE: Massachusetts
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                           02169-1875
               USA
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US-08-175-069A-78
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              COUNTRY:
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Patent No.
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APPLICANT: Ripper, David G.
AFPLICANT: Rapper, David G.
AFPLICANT: Roo, Met-chang
TITLE CR INVENTION: Altergenic Proteins From Rapweed and Users
OCHRESPONDENTE ATHRESS: 93
CORRESPONDENTE ATHRESS:
                                                                                                                                                                                                                                                 99 FUNAQUREUMITEERIMVIRLOBELAINNUKIIUGROAKVEIINAGEAINNVKNI 153
                                                                                                                                                                                                                                                           67 FILMGRAFILMITESGRWITKLKMPMYJAGYKTEDGRAAEVSYVHVNGAKFITRY 120
                                                                                                                                                                                                       Query Match 13.3%; Score 136: DB 1: Length 383: Best Local Studently 36.4%; Pred. No. 5.18e-03; Matches 2: Conservative 10: Mismatches 24: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.MEDIUR TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: ISH DEPOYMENTING SERTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0. Version #1.25

CONTRARE: PATENTIN RElease #1.0. Version #1.25

CONTRARE: APPLICATION DATE: 15, 1994

FILING DATE: Aquats 15, 1994

FHOR APPLICATION DATE: US 07/529,951
PRIOR APPLICATION DATA:
APPLICATION NRHER:
FILING DATE:
RATCH NO O7529,951
APPLICATION NRHER: 05 07325,365
FILING DATE:
MATCH NATCH 17, 1989
ALICHNEVASENT INFORMATION:
NAME: ATY E. MANDRAR: 35,27
REFERENCE/DOCKET UNMERH: 1M1-0180V
TELEPHONE: (517)227-7400
TELEPHONE: (517)227-7400
TELEPHONE: (517)227-7401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
A:TORING DATE: March 17, 1989
A:TORING DATE: Mandragouras
REGISTRATION NUMBER: 36,207
REFENDE/DOCKET NUMBER: IM: 0190N
TELECOMMUNICATION: TROORATION:
FELEPHONE: (617)227-7400
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50 State Street, Soite 51:
                                                                                                                                                                                                                                                                                                            PPT:
                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE 38: AA: 41852 MW: 738971 GN:
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Patent No. 5676954
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                            STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massachuse: Ls
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CITY: 808:00
STATE: Massachuse
COUNTRY: USA
ZIP: 02109-1875
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3Y: linear
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                                                                                                                                                        TYPE: ami
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APPLICANT: Rogers Bruce
APPLICANT: Ridgers, Bruce
APPLICANT: Rafnar Thorson
APPLICANT: Rafnar Thorson
APPLICANT: KTO, Melrohad
APPLICANT: NO. Melrohad
ITTLE OF INVENTION: Allergenic Profess Fich Rawmord and Uses
NUMBER OF SECUENCES: 93
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Pred, No. 5 18e-03:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
FLUNG DATE: Floppy disk
FLUNG DATE: May 29, 1990
APPLICATION NUMBER: LG CO/325,365
FLUNG DATE: March 17, 1989
ATIORREY/AGENT INFORMATION:
NAME: ANY E. Mandragouras
REGISTRATION NUMBER: 35,27
THEORY MARCH AND MARCH
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1.4
0.
                                                                                                                                                                                                                    TOPOGGOY: Linear
MOLECULE 1YPE: Protein
JENCE 383 AA: 41852 MW: 738471 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MCLECULE TYPE: protein
JENCE 383 AA: 41852 MW; 738971 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78, Application US/08290448A Patent No. 5698204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78. Application US/08290448A
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INFORMATION FOR SEC 10 No. 3
SEQUENCE CARRCIERISTICS:
LENGTH: 383 amino acid:
IYPE: amino acid:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                   Opery Match
Best Local Similarity 36.4%;
Matches 20: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS.
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STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 15
US-08-290-448A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Page 8

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   I: Gaps
                     Matches 20: Conservative 10: Mismatches 24, Indels
                                                                         Sharch completed: i.e Jun 20 14:33:43 2000 and time : A secs.
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Release 3.1A John F. Collins. Biocomputing Research Unit. 25pyright (c) 1993-1998. University of Edinburgh, U.K. Eistribution rights by Oxford Molecular Ltd.

MPsrch\_pp = protein / protein database search, using Smith-Waterman algorithm Mon Jun 19 16:21:14 2000; MasPar time 29.67 Seconds 455.076 Million cell updates/sec Rin on:

Tabular cutput not generated.

>US-09-142-524A-3 (1-134) from USC9142524A.pep 1025 | MKVIVAENQESPNRKVETKE......KFIKRVDGIIAAYQNPASKK 134 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

711208 segs, 100765575 residues Starched:

Minimum Match 0% Listing first 45 summaries Pist promestra:

is:dbase:

a-pending licit zuc6 3:060 4:07 5:086 6:081 7:082 8:083 9:084A l0:0848 11:085 12:086 13:087 14:088 15:089 16:090 17:091 18:092 19:093 20:054 21:095 22:NEWP 23:NEWD60 24:NEWD8 25:NEW09

Mean 33,909; Variance 126.583; scale 0.264 Statistics: Pred. No. is the curren of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

| Sesult |       | V10000 |        |            |            |              |            |           |
|--------|-------|--------|--------|------------|------------|--------------|------------|-----------|
| 0      | Score | March  | Length | <u> </u>   | 122        | Description  |            | Pred. No. |
| -      | 9701  | 00.    |        | 1.7        | 60         | Sequence 3,  | Applicatio | 1.618-97  |
| ~1     | 195   | Ų,     | 105    | ر.<br>د ا  | 7-6C-      | ( V          | Applicatio |           |
| m      | 372   | ÷.     | 80     | 17         | 1-60-      | Ļ            | Applicatio | 3.77      |
| ٠,     | (Q)   | :4     | C      | ω          | US-08-350- | 3            | Applicati  | 3.14e-1   |
| (£)    | 396   | 28.8   | 69     | r~         | -08-2      | 8            | Applicati  | 3.14e-1   |
| ψ      | 367   | ~      | 50     | 10         | -68-4      | 62           | Applicati  | 3.14      |
| ۲-     | 296   | ~      | 09     | <u>ှ</u>   |            | 5            | Applicati  | 3.14e-    |
| œ)     | 796   | 7      | 60     | 7          | JS-07-938- | 53           | Applicati  | 3.14e-1   |
| 6      | 596   | 28     | 90     | :          | US-08-458- | Sequence 52, | Applicati  | 7         |
| 10     | 236   | , 99   | 90     | C          | US-08-467- | 9            | Applicati  | 14e-1     |
| Ξ      | 296   | 28.    | 353    | Ξ.         | US-08-526- | Sequence 15. | Applicati  | 7         |
| 12     | 596   | (1     | 374    | 0          | US-08-467- | ď            | Applicatio | 14e-1     |
| 13     | 296   | 28.    | 374    | 10         |            | ~            | Applicatio | 14e-1     |
| ] 4    | 596   | 28.    | 374    | <b>~</b> † |            | 7            | Applicatio | 3.14e-18  |
| 15     | 296   | 28.    | 374    | œ          |            | 7            | Applicatio | 7         |
| 16     | 396   | 28.8   | 374    | 7          | US-07-938- | ?            | Applicatio | 3.14e-18  |
| 17     | 396   | .87    | 374    | ۲-         | - 08 - 2   | 7            | Applicatio | 3.14e-1   |
| 8      | 396   | 7.8    | 374    | 10         | US-08-467- | ~            | Applicatio | 3.14e-1   |
| 9      | 296   | 28     | 374    | 10         | US-38-467- | 7            | Applicatio | 3.14      |
| 50     | 967   | ά      | 1,75   | -          |            | r            | 1000       |           |

61 FAKLIGFILMGRRPLWIIFSGNMNIKLKMPMYIAGYKTFDGRRAEVSYVHVNGAKFIRRV 120

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APPLICANT: Sriffeth, 1rw, J.;
APPLICANT: Pollock, Joanna APPLICANT: Pollock, Joanna APPLICANT: Sarman, Bich APPLICANT: Sarman, Bich APPLICANT: Sarman, Bich APPLICANT: Veung, Slu-ra APPLICANT: Veung, Slu-ra APPLICANT: Veung, Slu-ra APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Exley, Mark A.;
APPLICANT: Process, Steepen P.;
IIIE OF INVENTION: Allerated Contact And Peptidos Brom. IIIE OF INVENTION: Applicant Pollocial Applicant APPLICANT: PROCESSED CONTACT APPLICATION AND APPLICANT AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Unknown Greatism post, be SEQUENCE 80 AA: 9067 MW: 30888 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKVIVAFNQFGPNRRVFLKRVSPYTTHGRRIDIFASKNFHLQKNTIGLGRR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HAVIVARNOFORNKRVETKRVSTVVIIGERIOTEASKNEHLOKKNIIGIGER 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 372: 08 37: Legath Eur
Pred. No. 3.778-26:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Parentin Pelease #1.0, Version #1.26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,225
FTLING DATE: December 6, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ž
TITLE OF INVENTION: Allergic Diseases FILE REFERENCE: Docket No. SP0-105 CORRENT APPLICATION NUMBER: US/C9/142.524 CORRENT FILING DATE: 1999-01-04 EARLIER FILING DATE: 1999-01-04 EARLIER FILING DATE: 1996-07-05 EARLIER FILING DATE: 1997-0-0-05 SOFTWARE: PATJOP97/C0740 EARLIER FILING DATE: 1997-0-05 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: December 6, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 08/25,248
FILING DATE: APRIJ 8, 1994
APPLICATION NUMBER: 07/938,990
FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/0593/00139
FILING DATE: January 15, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 62. Application USZ - 0.0225 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52, Application US/08351225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6:0 Lincoln St. CITY: Waltham STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%:
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xxxxxx
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GENERAL INFORMATION:
APPLICANT: SONG, TOSHIC
APPLICANT: Kairlki, Kazuo
APPLICANT: Kairlki, Kazuo
APPLICANT: Kairlki, Kazuo
APPLICANT: Kairlki, Kazuo
APPLICANT: Ivama, Akiko
APPLICANT: Kino, KO:Suke
IIILE OF INVENTION: Peptide-based Immunotherapeutic Agent For Treating
               HILLER HELLER HE
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(1888-1888) - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cuery March
best Local Similarity 85.7%; Pred. No. 2.24e-46:
Matches 90: Conservative 1: Mismatches 1: indexs 13: Gaps
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OENCE: 195 AA: 12303 MW: 54640 GN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FAKLIGETUMGRR------LKMPMYLAGYKTFDGRAVD 92
                                                                                                                                                                                                                                                                                                                                            105 AA
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GENERAL INFLEMATION:
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SEQ 10 NC 2
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                                                                                                                        121 DOLLARYCNEASWK 134
                                                                                                                                                                                                121 DOLLARYONPASWK 134
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PEATURE:
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ID OS
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US-09-142-524A-3.rap

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SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
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                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        xxxxx
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APPLICANT Brack, Andrew.
APPLICANT Brack, Andrew.
APPLICANT BOXES, Steven P.
IIILE OF INVENTION: Allergenic Proteins And Peptides From TILLE OF INVENTION: Japanese Gedar Pollen
VIMBER OF SEQUENCES. 201
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       6 RPLWILESONMNIKLKMPMYLACYKTEDGAGAOV-YIGNGOPGVPIKRVSNVI 57 HTT - 1 HTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immilogic Pharmaceutical Corporation, Inc.
                                                                                                                                                                                                                                                                                              Query Match 28.8%; Score 296; (3.8; Length 60; Best Local Similarity 73.6%; Pred. No. 3.14e-18; Matches 39; Conservative 5: Mismatches 7: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
DORANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/26.248A
FLING DATE: APPLI 8, 1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: ADATA:
               NAME: Dariene A Vanstone
REGISTRALION NUMBER: 35,729
REDESCHENCEDOKET NUMBER: 025.6 US (IMI-028CP2)
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617) 466-600
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERSTICS:
LENGIN: 60 amino acids
TYPE: aring acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Datlene A. Vanstone
REGISTRATION NUMBER: 35,729
REFERENCE/DOCKET NUMBER: 025.5 US (IMI-028CP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 AA
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FILING DATE: September 1, 1992
APPLICATION NUMBER: PCT/US93/30139
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.K.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/08226248A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 62. Application US/08226248A
                                                                                                                                                                                                                                               NI IYPE: internal
60 AA; 6644 MW: 19464 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Joanne:
APPLICANT: BOOKG, Cilian F.;
APPLICANT: Sarman, Richard D:
APPLICANT: Kuo, Met. Chang:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD
ALTORNEY/AGENT INFORMATION:
NAME: Darlene A. Vanston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUEL: 610 Lincoln St.
                                                                                                                                                                                                                         MALECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                           linear
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                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                  SEQUENCE
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APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Brauer. Andrew:
APPLICANT: Exiey, Mark A.:
APPLICANT: Exiey, Mark A.:
APPLICANT: Exiey, Mark A.:
APPLICANT: Dowers, Steven P.
IIILE OF INVENTION: Allengenic Proteins And Peptides From TITLE OF INVENTION: Lapancse Cedar Poilen
NUMBER OF SEQUENCES: 251
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERMITESGNMNIKEKMPMYIAGYKTEDGREAEVSYVHVNGA-KFIRKV.GIT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RPLWIIFSGNMNIKLKMPMYIAGYKTFDGRGAQV-YIGNGGPGVFIKRVSNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 296: 58.7; Length fur
Pred. No. 4.146-18;
5; Mismatches 7; Indeis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD6 (IMI-028CPD6)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: RT:
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GENERAL INFORMATION:
APPLICANT: Griffeth, Irwin J.;
APPLICANT: Pollock, Codnie:
APPLICANT: Bond, Unide:
APPLICANT: Garman, Rich (3 D)
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
UENCE 50 AA; 6644 MW: 1-164 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 62, Application US/ .67006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-600
TELEFAX: (617) 466-600
INFORMATION FOR SEO ID NO: 62:
SEQUENCE CARRACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 62:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.5%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Yeung, Sturmel H.:
APPLICANT: Brauer, Andrew;
APPLICANT: Brauer, Andrew;
APPLICANT: POWERS, STEVER P.:
TITLE OF INVENTION: Alleraenin Proteins And Peptides From TITLE OF INVENTION: Alleraenin Proteins And Peptides From VITLE OF INVENTION: Alleraenin Proteins And Peptides From VITLE OF INVENTION: 251
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                                                                                                       6 RELWIIFSGNMNIKLKMPMYIAGYKTFDGRGAQV-YIGNGGPCVFIKRVSNVI 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION 44
PRIOR APPLICATION 144
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: Coecember 6, 1994
ATORNEY/ART INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/COCKET NUMBER: 025.6 USD4 (IMI: 228CPD4)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                   Score 296, DB 10: Length 60:
Pred. No. 3.14e-18;
5: Mismatches 7; Indels
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COMFOLDER: PW 10. COMPACTION.
CPENTING SYSIEM.
PRIVARE: PRIVATE PRIVATE NO. S/MS 10.5
SOPTWARE: PRIVATE NO. OF 10.0
CORPERING NO. DATA:
APPLICATION NAMES: US/08/467.697
FILLING DATE: June 6, 1995
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      TOPOL TYPE: Incer MALSOLE TYPE: peptide INAGENT TYPE: Incernal SEQUENTE 60 AA: 6644 MW: 19464 CN:
                                                                                                                                                                                                            Sequence 62, Application US/08467697
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FRAGMENT TYPE: internal
JENCE 60 AA: 6544 MW: 19464 CN:
                                                                                                                                                                                                                                                 APPLICANT, Stiffeth, Irwin J.;
AFPLICANT, Pollock, Joanne;
APPLICANT, Bood, Julian F.;
APPLICANT, Garman, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7430
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                      STANDARD:
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                                                     Query Match
Fest Local Similarity 73.5%:
Matches 39: Conservative
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COMPUTER READABLE FORM:
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amino acid
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GENERAL INFORMATION
APPLICANT: Griffith, Irwin C.
APPLICANT: Bond Julian
TILLE OF INVENTION: Allergebic Profess And Pep'ides Flor
TILLE OF INVENTION: Allergebic Gedar Poller
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                73 RPLWIIFSGNMNIKLKMPMYIAOYKIFOGRRAEVSYVHVNGA-KFIRRVIGGT 124
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             Length fur
                                                                                        STabble
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Query Match 28.8%; Score 295; DB 15; L
Best Local Similarity 73.6%; Pred. No. 3.14e-18;
Matches 39; Conservative 5; Mismatches 7;
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28.3%; Score 296; DB 4; Le Best Local Similarity 73.5%; Pred. No. 3.14e-18; Matches 39; Conservative 5; Mismatches 7;
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STREE: Sixty State Street
CITY: Boston
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FRACMENT TYPE: internal
JENCE 60 AA: 6644 MW: 19464 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
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AMINO ACID
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MEDIUM TYPE: Floppy
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US-07-938-990A-62
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TITLE OF INVENTION: Altergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
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SIREET: 610 Lincoln St
CITY: Walthar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
DEBAING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: CS/08/468,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Darlene A. Vanstone
REGISTATION NURBER 35,729
REFERENSZIOCKET NUMBES: 025.6 US (IMI-C28CP2)
TELECOMMUNICATION INFORMATION:
                               60 AA
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PROGRAPHICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING FATE: December 6, 1994
FILING DATE: APPLICATION NUMBER: 08/256.248
FILING DATE: APPLICATION NUMBER: 07/938.990
FILING DATE: September 1, 1992
APPLICATION NUMBER: POT/US93/02139
FILING FATE: January 15, 1993
ALICHARON FORTE: January 15, 1993
                                  PRT;
                                                                                                                                                                                                                                           62. Application US/08468940 INFORMATION:
                                                                                                                                                                                                                                                                                            APPLICANT GRIEFETH, ITWE J. APPLICANT POLICCK, JOanne: APPLICANT BOND, JULIAN E. APPLICANT GARMEN, RICHARD D. APPLICANT KLO, MEL-Chang SL. APPLICANT BEALEY, AGGRES, APPLICANT EXLEY, MAIX A...
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FRAGMENI TYPE: internal
JENCE 60 AA: 6644 MW; 19464 CN:
                                                                                                                                                                                            Sequence 52, Application US/08468940
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TELEFAX: (617) 466-6040
INPORMATION FOR SEQ ID NO: 62:
SEQUENCE CHERACTERISIUS:
LENGTH: 60 aming acids
TYPE: aming acid
                             STANDARD;
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CHMUTER READABLE FURM:
MEDIUM IYPE: Floppy
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EX SEQUENCE 52. APPL

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APPLICANT BOILOCK, JOHNES,
APPLICANT BOND, Julian F.,
APPLICANT Garman, Ribard D.,
APPLICANT Kuo, Man-Chang,
APPLICANT Kuo, Man-Chang,
APPLICANT Selven F.,
APPLICANT Ex.ey, Mark A.,
APPLICANT Ex.ey, Mark A.,
APPLICANT POWERS, Steven F.
TIILE OF INVENTION Allorabile Froteins And Pertides From
TILLE OF INVENTION Allorabile
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.8%; Score 296; DB 10; Length 60; Best Local Similarity 73.6%; Pred. No. 3.14e-18; Matches 39; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jane E. Remillard
REJSSTRATION NOMERS: 94 872
REPRENCY/DOCKTI NUKBER: 925.6 USD2 (IMI-028GPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ 10 Nov. 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALCHESSEE: Immillogic Pharmaceutical Curporation, STREET: 610 Lincoln St CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENTING SYSTEM: PC: DUSKKS:UUS
SCFWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DAILS
#ILING DAIE: June 6, 1955
                           60 AA
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                           PRT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/450.225
FILLING DATE: December 5, 1994
ATTORNEY/AGENT INFORMATIC:
                                                                                                                                                                             Sequence 62, Application US/06467623 GENERAL INFORMATION:
                                                                                                                                            Sequence 52, Application US/CR467023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 50 AA: 5644 MW: 19464 CN;
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD
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MEDIUM TYPE: Floppy
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RESULT 10
Th US-08-467-023-62
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ID US-08-526-179-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Griffeth, Irwin C.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBLEM PROGRAMMER MANAGEMENT FOR THE STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 353:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                   Sequence 15. Application US/09526.79
GENERAL INFORMATION:
AFFICANT: SAITO. Saburo
AFFICANT: HINO. Katsuhiko
AFFICANT: HANISCHI Voshiluri
AFFICANT: KURIMCID. Massashi
IIII OF INVENTION: FEFILOS AND USES OF THE SAME
NUMBER OF SEQUENCES: 24
COMMESPINGENCE ACRESS: 24
COMMESPINGENCE ACRESS:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526 '7'
SILING DAIE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         usery Match 28.8%: Score 296: DB 11; i
Prest Local Similarity 77.6%: Pred. No. 3.14e-18:
Matches 39: Conservative 5: Mismatches 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
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PRICH APPLICATION DATA.
PRELIGATION NUMBER: JP 242,11571994
PRICH APPLICATION DATA: 10-28P-1994
PRICH APPLICATION DATA: 10-28P-1994
PRICH APPLICATION DATA: 10-28P-1995
PRICH APPLICATION DATA: 10-28P-1995
PRICH APPLICATION DATA: 10-28P-1995
PRICH DATE: 14-20-1995
PRICH DATE: 14-20-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: SAITO+19
TELEDOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFACK: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE INPE: poptido
ENGE 374 AA: 88502 MW: 678784 TN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'MEUTER REAGABLE FORM:
MIGGIAN TYPE: Floppy disk
CNSPUTER: IEM FO COMPATIBLE
OPERATING SYSTEM: PG-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
                          Sequence 15, Application US/08526179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEDEX: 248633
INFORMATION FOR SEQ 10 NO: 15:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 353 amino acids
acino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BROWDY, Roder I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Static
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       STREET: 419 Sevent
CITY: Washington
STATE: D.C.
TOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lisear
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APPLICANT: POLICK, Joanne,
APPLICANT: Bond, Julian F.;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard (...
APPLICANT: Yeing, Siu-rei B.;
APPLICANT: Yeing, Siu-rei B.;
APPLICANT: Exauer. Andrew:
APPLICANT: Exauer. Andrew:
APPLICANT: Exauer. Sieven: F.
APPLICANT: Exauer. Sieven: F.
APPLICANT: Exauer. Allei wen: F.
APPLICANT: Exauer. Allei wen: F.
APPLICANT: F.
APPLICANT: Sieven: F.
APPLICANT: F.
APPLICANT: Allei wen: F.
APPLICANT: Allei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 RPLWIIFSONMIKLKMPMYIAGYKIFYGBARUSYVHUNIA-KFIBRUGGI
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEC ID N 2:
SEQUENCE PARACIERISTS
LENGIR: 374 affice ac.
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COMPUTER: IBM PC COMPUTE.
COMPUTER: IBM PC COMPACT.
COPERATIN: PC DOS/MS-D/8
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/US/167.023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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374 AA: 40720 MW: 7594 P.CN:
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GENERAL INFORMATION:
APPLICANT: Grifteth, Itwin C.:
APPLICANT: POLICCK, JOSENE:
APPLICANT: Bond, Julian F.:
APPLICANT: Garran, Richard D:
APPLICANT: Kuo, Mei-Charg:
APPLICANT: Yeung, Siu-mei H.:
APPLICANT: Brauer, Andrew:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 36/350.225
FILLING DAILS DECEMBER 6, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/0846 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREFT: 610 Lincoln St
CIIY, Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD
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COMPUTER READABLE FORM:
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GENERAL INFORMATION:
APPLICANT: Griffith, Irwin 3.
APPLICANT: Pollock, Joanne 1:11LE OF INVENTION: Allergenic Proteins And Peptides From IIILE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 25
CCRRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADBRESSEE: ADB
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
IIILE OF INVENTION: Allergenic Proteins And Peptides From
IIILE OF INVENTION: Allergenic Proteins And Peptides From
IIILE OF INVENTION: Japanese Cedar Polien
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
STREET 610 Lincoln St.
CITY Walthar
STATE: MA
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46th Floor - 1 Liberty Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 374:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/US/468.34.
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION CARER: 08/350,225
APPLICATION NUMBER: 08/25,248
FILING DATE: December 6, 1994
APPLICATION NUMBER: 07/928,90
FILING DATE: September: 1992
APPLICATION NUMBER: C7/938,90
FILING DATE: January: 1993
APPLICATION NUMBER: PCT/US93/00139
FILING DATE: January: 1993
APPLICATION NUMBER: PCT/US93/00139
FILING DATE: January: 1993
APPLICATION NUMBER: 35,729
RESIGNATION NUMBER: 35,729
RESIGNATION NUMBER: 35,729
RESIGNATION NUMBER: 025.6 US (IMI-C28GP2)
TELEPHONE: (617) 466-600
INDUMER: DATE: DATE
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARD: Patentin PC-DGS/MS-DGS
CURRAND: Patentin Release #1.0, Version #1.25
CURRAND APPLICATION DATA:
APPLICATION NUMBER: US/08/468.940
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JENCE 374 AA: 40720 MW: 757477 CN:
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CHMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity 73.6%: Pred. No. 3.14e-18:
Matches 39; Conservative 5: Mismatches 7: Indels
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REPREDENCE/DOCKET NUMBER: IMPH-0401
FLEPHONE: (215) 568-3103

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ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
JENCE 374 AA: 40720 MW; 757477 GN;
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GENERAL INFORMATION:
APPLICANT: STIFETH, TYALL 3.
APPLICANT: POLICE, JOHNE
APPLICANT: HONG, JULIAN F.
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Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1997-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Jun 19 15:58:04 2000; MasPar time 11.79 Seconds 536.097 Million cell updates/sec Rin on:

Tabular output not generated.

>GS-09-142-524A-3 (2-134) from USC9142524A.pep 1026 : MKVIVAENGEGPNRRVEIKR.......KFIRRVDGIIAAYQNPASWK 134 iitle: Description: Perfect Score: Sequence:

Scoring table:

142080 seqs, 47172405 residues 9AM 150 3ap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post processing:

pir62 l:pir1 2:pir2 3:pir3 4:pir4

Database:

Mean 45.199; Variance 89.328; scale 0.484 Statistics.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total core distribution.

SUMMARIES

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JC2123 *type complete major allergen C:y j I precursor (clone pCC:-2-2) · Japanese cedar formal_name Crytcomeria japonica *common_name_Japonese cedar 14-Jul-1994 *sequence_revision 14-Jul-1994 *text_change

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Matuhasi, T.
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                                                     Sone, T.: Komiyama, N.: Shimi, . K.: Kusakabe, T.; Morikubo
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CLASSFICATION **superfamily Protate lyase LAT59

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dignoprotein: pollen

FEATURE
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#journal bischem. Biophys. Res. Commun. (1994) 199:619-625
#fitte Cloning and sequencing of CDNA coding for Gry j I.
alicipses of Japanese endar pollen.
#cross-references MUID:94183234
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Matches 39; Conservative 5; Mismatches 7; Indels
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*length 542 | #molecular-weight 58573 | #checksum 1032
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Gry 3 H protein - Ospanse cedar
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##residues 1-514 ##label NAM
##cross-references GR-D37765; NIO-4577695; PIDN-BANG702...
##cross-references GR-D37765; NIO-4577695
PID-d1007598; PID-q577696
** #length 514 #colecular-weight 56645 #cherksum
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Pred: No. 1 10e-13:
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submitted to the EMBL Data Library, October 1992
Abundancy patterns of lily pollen cDNAs: characterization of
three pollen-preferential cDNA clones.
S29612
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S21933
Pred. No. 6.01e-69: 7; Indels
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Smith, J.J.: Oison, J.R.: Klapper, E.G.
Mol. Immunol. (1988) 25:355-365
Monoclonal ant Palies to decatured ragweed poller allering Amb a 1: challerization, specificity for the decatured allerien and lization for the isolation of imminosopie peptides of Amb a 1:
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allergen Amb a 1.1 precursor - commun raywead
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B.L.: Klapper, D.G.
#journal J. Biol. Chem. (1991) 266:1229-1236
#title Cloning of AmE a I (antigen E), the major bliet ten:
short rawweed politer.
#cross-references MCID:9109325
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*length 396 *mole: :lar-weight 42709 *checksum 5506
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                                                                                   Length 434
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##residues 256-273:292->04:"W',305-306 ##label SMI
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                        *length 434 *molecular-weight 48457
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##cross-references GB:M90558: NID:q166434: F
CLASSIFICATION #superfamily pectate lyase LAT59
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##cross-references GB:M53115
NOE #FAAAA
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carbon-oxygen lyase
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Firesidues 1397 #1abel RAF FELANCAAA32666.1, PID:q:66441 inasiploation = s.perfamily pectate lyase LAI59 schwarz pollen = s.perfamily pectate lyase LAI59 schwarz = s.cert.
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B.L.: Kinpper, D.G.
#journal J. B.G. Clem. (1991) 266:1229-1236
#file Clemins of New (1 (actique E), the major allergen family of slore ranged polien.
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stournal lot, Arch. Allergy Appl. (rmsnol. (1991) 96:296-304
stitie. Sequence polymorphism of Arb a Land Amb a II, the major
allerges in Ambrosia arthemaskitolia (short ragweed).
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allergen Amb a 1.3 precifor - common ragweed
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18-Sep-1998
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18.7%: Score 141: DB 2. Lonath 397: Pest Local Stribuity 37.9%: Pred. No. 8.25e-07: Katches 22: Conservative 12: Misratches 22: Indels
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Rest Local Similarity 37.9%; Pred. No. 8.25e-67;
Matches 22: Conservative 12: Mismatches 22: Indeis
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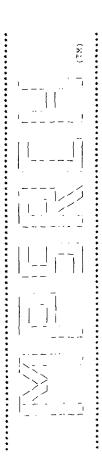
*journal Int. Arch. Allersy Appl. Immunoi. (1991) 96.296-394

*title Sequence polymorphism of Amb a Land Amb a LL. Neuranor allergens in Ambrewia artemnishipolia (short tenkened).

*Cross::eferences WCID:92234533
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29-Sep-1999
TC0856
S14206
Rounsley, S.D.: Lin, X.: Ketchum, K.A.: Grosty, M. L.:
Randon, R.C.: Sykes, S.M.: Kaul, S.: Mason, I.M.:
Rerlavade, A.R.: Addms, M.D.: Screrville, C.P.: Vul'er
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                                                                                                                                                                                                                                                                                                                        *submission submitted to the EMAL Data Library, March 1948 **
*description Arabidopsis thaliana chromosome II BAC 1208( argument
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#formal_name Ambrosia artem.siitoila #common_cance
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##CTOSS=TC:erences GB:R80562: NID:3166444; F
CLASSIFICATION #superfamily pectate lyase LAT59
KEYWORDS
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27 Nov-1991 #sequence_revision 03-Apr-1902 #text_change
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839099
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Submitted to the EMBL Data Library, September 1994
107058
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P:D:9551656
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#formal_name lycopersicon esculentum #connocicate tomato
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109 FAAAQNRPLWIIFKRNMVIHLNGEL/VNSDKTIDGRGVKVNIVNA-GLILMN-VKNII
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Polease 3.1A John F. Gollins, Biocomputing Research Unit. Pupyright (c) 1994-1995 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein i protein database search. Sing Smith-Waterman algorithm MPS:COLPP

Mon Jun 19 15:56:49 2000; MasFar time 7.87 Seconds 518.264 Million cell updates/sec facular output not generated. Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Nean 44.072; Variance 79.368; scale 0.555

# SUMMARIES

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	۲,		404	. 4	9612_CYCES	SIYLE DEVELOPMENT - SPEC	1.37e-07
	131	12.8	397	, 4	MPA2_AMBAR	POLLEN ALLERGEN AMB A	1.37e-06
	124	12.1	4	1	PES9_LYCES	PROBABLE PECTATE LYASE	1.88e-05
	in O	10.2		۲,	Y12K_SMSV4	POSSIBLE 12 KD NUCLEIC	1.59e-C2
	001	6.3	3587	٠,	TYCB_BACBR	TYROCIDINE SYNTHETASE	8.38e-02
	Ω.	9.6		•-•	RRPL_RVFV2	RNA-DIRECTED RNA POLYM	1.16e-01
	ω in	9.3		7	YHV4_YEAST	HYPOTHETICAL 123.0 KD	4.18e-01
	9		539	٦	CH61_MYCTU	60 KD CHAPERONIN 1 (PR	7.83e-01
		8.5	638	~	OIM_COXBC	60 KD INNER-MEMBRANE P	1.45e+30
	06		339	~	DPPB_ECOLI	DIPEPTIDE TRANSPORT SY	1.97e-30
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## ALIGNMENTS

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AMEDINE, 95003148.

Hiltata A., Matsumoto I., Koj'ma K., Ogawa H.;

Antigenicity of the oligosaccaride moiety of the Japanese cedar (Gryptomeria japonica) pollen illergen, Cry ji.*;

Int. Arch. Allory Immunoi. 105:198-202(1944).

I. FTM: CONTAINS FUCCSEXYLOSE-CONTAINNG N-LINKED CLIGOSACCHARIDES.

I. DISEASE: THE MOST COMMON POLLEN ALLERGEN IN JAPAN.

I. MISCELLANGCUS: THE SEQUENCE OF CRY J FORM A IS SHOWN HERE. FORM B DIFFERS IN SIX POSTITIONS.

B DIFFERS IN SIX POSTITIONS.
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FEBS Lett. 239:329-332(1988).
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SBP_CKIJA STANDARD: PRI: #74 AA.
P1862199 (Rel: 16, Created)
Ol-NOV-1995 (Rel: 32, Last sequence update)
15 DEC-1998 (Rel: 37, Last annotation update)
15 DEC-1998 (Rel: 37, Last annotation update)
SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY : ;; ("MY I: Cryptomeria japonica (Japanese celar).
Eukaryota: Viridiplantee: Streptophyta: Embryophyta: Irthoribita.
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BEDINE: 89631257.
Tantal M., Ando S., Usul M., Kuriroto M., Sakaguchi M., Inouge S.,
Matuhasi T.:
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TISSUE-POLLEN:
Nacha M., Korose M., Torianni M., Bakada S., Kolimpath M.
Swimbated (Jözlinge) on the UMDIA Ambrik Kora, dalates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Japanese cedar pollen.";
Biochem. Biophys. Res. Commun. 199:519-525(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECCENCE FFOM N.A., AND FAKTIA' SECTENCE.
IISSUE*POLLEN:
MEDLINE: 94183234.
                                                                                                                                                                                                                                                                                                                                                                                                              Taxodiaceae: Cryptomeria
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Nicotiana.
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"cDNA cloning and expression of Cry j II the second major allergen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEAL_SHYDA STANDARD) PRI, 614 AA.
MEAL_SHYDA CREATED)
01-NV-1995 (Rel. 32, Created)
01-NV-1995 (Rel. 32, Last sequence update)
01-NV-1995 (Rel. 35, Last annotation update)
POSIBLE PRIVALACTURINASE PROURSOR (EC 3.2.1.15) PG) (PECTINASE)
(MAJOR POLLEN ALLERGEN CNV J 2) (CRY 7.1).
Cryptomeria japhica (Japanese nedar).
Cryptomeria japhica (Japanese nedar).
Cubhyllophytes Spermanochytas Conferopsidas Conference.
Taxodiaccae, Cryptomeria.
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SECTION: 9342995.
Sakaguchi M., Inouye S., Taniai M., Ando S., Usui M., Matuhasi T., Tadentification of the second major allergen of Japanese cedar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 95010777.
Namba M., Kurose M., Torigoe K., Hino K., Janiguchi Y., Fikuda S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usui M.: Kurimoto M.:
"Molecular closing of the second major allerges, Gry j II, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 RPIWITESGNMNIKEKMPMYTAGYKTEDGRÖAUV-YIGNGGPOVETKRVSNVI 138
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Pred. No. 3.590-38;
5/ Mismatches 7/ indels
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FISSUE POLLEN:
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  AMB A I/AMB A II/CRY J I SUBFAMILY
                                                                                                                                                                                                                                                                        EMBL: D26544: HAN05542.1: -.
EMBL: D26545: BAA05541.1: -.
EMBL: D34594: BAA07620.1: -.
FIR: A44773: A4477.1: -.
PRAM: FF05644: Proc.lyasov.2:
PRAM: PF05644: Proc.lyasov.2: PRAM: PF0697: AMBALLERGEN.
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FEBS Lett. 353:124-128(1994).
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Post Local Similarity 73.6%;
Matches 79; Conservative
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This SWISS-PROT entry is copyright it is produced through a bonder station between the Swiss Institute of Broincing and the Profit institute of Broincing and the Profit institutions in the European Boinformatics Institutions as long as its content is in way use by non-profit institutions as long as its content is in way modified and this statement is not recoved Usage by and for manner cold entities requires a license agreement (See http://www.ish.short/snownence) or send an enail to license attach).
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EMBL: D29772: BAA6672.1. -
PROSITE: PS00502: PCLYGALACTURGNASE. 1.
PFAM: PF0295: Glycosidase. Cvi. Wull: Sinnal: Zyrogen: Exait right non-
Mydrolast: Glycosidase. Cvi. Wull: Sinnal: Zyrogen: Exait right non-
Signal.
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MEDLINE, 93043039.
Rogers H.C., Harvey A., Lonsdale D.M.;
Isolation and characterization of a tobacco gene with homology to pectate lyase which is specifically expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microsporogenesis.";
plant Mol. Biol. 201493-502(1992).
plant Mol. Biol. 2014914: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTATE TO GIVE
OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-MANN-4-ENURONDSYL GROUPS
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Eikaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta: eudicotyledous; eudicots: Spermatophyta: Magnollophyta; eudicotyledous; core eudicots: Asteridae; euasterids I; Solanales; Solanaceae;
ALIERTY 45:309-312(1990).
-:- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1.4-ALPHA-D-
-:- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1.4-ALPHA-D-
-:- SUBCELLICUAR LOCATION: SECRETED OR AMYLOPLAST (FOTENTIAL).
-:- SIMILARITY: BELOWS TO FAMILY 28 OF GLYCOSYL HYDRYLARES
(FOLYGALACTURONASES).
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FOUND (IN REF. 2)
COTON (
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Mismatches C: Indels
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> I (IN REF. 2);

+> C (IN REF. 2);

624611G3FA8C6302 (R064);
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01-FB-1995 (Rel. 31, Created)
01-FB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PECTATE LYASE PRECURSOR (EC 4.2.2.2).
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Matches 20; Conservative
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL cutstation—the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseilsb-ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1995 (Rel. 31, Created)
21-FEB-1995 (Rel. 31, Last sequence update)
21-FEB-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
17-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last annotat
                                                                                                        -! SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
                                  DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED LATE IN POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CB 1; Length 397; 3.54e-10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PECTATE LYASE,
POTENTIAL,
POTENTIAL,
POTENTIAL,
SS -> C (IN MRNA),
S -> D (IN MRNA),
S -> D (IN MRNA),
H -> N (IN MRNA),
H -> N (IN MRNA),
H -> N (IN MRNA),
W. EFOABZCESDA7643F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMSC: 217228; CAA78976.1; -.
EMBL: L1891; AAA33398.1; -.
PIR: S29612; S29612
AT THEIR NON-REDUCING ENDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44351 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: X67158: CAA47630.1: -
EMBL: X67159: CAA47631.1: -
EMBL: X61102: CAA43414.1: -
PIR: $26211: $26211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100544: pec_lyase: l.
PROC807: AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 36.7%;
ses 22; Jonservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00544:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyase: Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEL_LILLO
P40973:
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ACI_SITE
CARBCHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS.
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                                                                                                                                                                                                                                                                                                      140 FGTLR-WGVIQDRPLWIIFGKSMVIRLKQEDIINNDKTIDGRGANVG-1-AGGAGDIVGF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDDINE: 9224570.

Griffith 130 Pollock 3., Klapper E G., Fourers bills, Nailt A E.,

Sequence polymorphism of Amb a 1 and Amb a 11. the major allocateds

"Sequence polymorphism of Amb a 1 and Amb a 11. the major allocated attempts and a them allocated attempts and a the arguments."

Int. Arch. Allocaty App. Immunoi. 95:2×+54(194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of Amb a I (antigen E), the major allerden family of stort ragweed pollen.".
J. Biol. Chem. 266:1229-1236(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61-405-1992 (Rel. 23, Created)
61-405-1992 (Rel. 23, Last sequence update)
15-5EC-1998 (Rel. 37, Last sequence update)
15-5EC-1998 (Rel. 37, Last sequence update)
POLLEN ALLERGEN AMB A 11, PRECIREOR (ANTIGEN AMP A 1).
Ambrosia artemisifolia (Shor aqueed)
Embryophyta: Tracheuphyta: puphyllophyta: Tracheuphyllophyta: Spermatophyta: Magnollophyta: eudicoty: Asteridae; core eudicots; Asteridae; eudicots: Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1: IISSUE SPECIFICITY, POLLEN AND FLOWERS
-1: DISSASE, ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN,
-1: SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY ;
AMB A LYAMB A LL/CRY J I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-POLLEN;
MEDLINE: 91093235.
Rafnar T., Griffith I.J., Kio M.-C., Bond J.F., Rogers B.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR: A39099: A39099.
PIR: A53240: A53240.
PFAM: PF00544; PS00544; PS00544; PS00544; PS00807; AMBALLERGEN.
Antigen; Allergen: Signal; Multigene family: Polymorphism.
                                                                                                                                                                                                   Score 143; 58 1; Length 434,
Pred. No. 1.32e-08;
                                                                                                                                                                                                                        Pred. No. 1.32e-08;
14; Mismatches 22: Indels
                                                                                                                                                            C1F3E3CAD2HBD064 CRC64;
                                                                              PECTATE LYASE, POTENTIAL, POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                            POTENTIAL
                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asteroideae: Heliantheae: Ambrosia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M63116; -; NOT_ANNCTATED_COS.
EMBL; M80558; AAA32655.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS
                                                                                             312 312 PG
68 68 PC
97 97 PO
434 AA: 48457 MK.
                                                                                                                                                                                              Query Match
Best Local Similarity 38.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                     61 FAKLTGFTLMGRRPLWIIFSG
PFAM; PF00544; pec_lyase; 'PRINTS; PR00807; AMBALLERG
Lyase; Signal, 22
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD
                                                                                                                                                                                                                                                                                                                                                           197 VHNVI 201
                                                                                                                                                                                                                                                                                                                                                                                                    126 VDGII 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Oriffith I.U. Policek J., Klapper D.G., Rogers B.D., Nault A.K.,
"Sequence polymorphism of Amb a Land Amb a 11, the major allergens
in Ambrosia artemisticità (Short radweed).".
Int. Arch. Alleray Appl. Imminol. 94 (296-304 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                          Klapper D.G.: "Sconing of Amb a 1 (antiged E), the major allerged family of short rapped poilen.": "B.O. B.O. Dem 265:1229-1236(1991).
                                                                                       Caps
                                                                                                                                                                                                                                             Ambrosia artemisifolia (Short raqweed).
Eukaryota: Virdiplantae: Streptophyta: Enbryophyta: Tracheophyta:
euphytes: Spermatophyta: Magnollophyta: eudicutyledons:
core eudicots: Asteridac: euasterids II: Asteriales: Asteraceae:
Asteroldogo: Hollanthere: Ambrosia.
                                                                                                                                                                                                 01-A03:1992 (Rel. 24, Greated)
14-73-1992 (Rel. 23, Last sequence update)
15-EBC-1998 (Rel. 37, Last annotation update)
POLLEN ALLERGEN ARR A L.3 PRECURSOR (ANTIGEN E) (ANTIGEN ARE A 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                      ö
                                                                                                                                                                                                                                                                                                                                               driffith I.J., Kio M.-C., Bend J.F., Rogers B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBC: M62961: AAA32668.1: -.
EMBC: M62560: AAA32669.1: ALT_SEQ.
PTR: C39099: C39099; C300909.
PFRN: PFCOSA4: pec_1yase: 1.
PRINTS: PRCO807: AMBALLERGEN.
ACTION: ALLERGEN: Signal: Multiqene family: Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 1; Length 397;
Pred. No. 2.89e-38;
                                                                Lengtl. 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12: Mismatches 22: Indels
                                                                                     8: Mismatches 17: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLLEN ALLENGEN AMB A 1.3. BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C8DB41257590DD0A GRC64;
                                           GCE70DETB288841D CRC64:
                                                                                                            107 FUNAQNAPUWITIERCHVIRUDKEMVVNSDKIIDGRGAKVELIN 150
                                                                                                                        67 FILMGREPOWITESSNWHITKLENPWYLAGYKTEOGERFAEVSYME IDO
          POLLEN ALLERGEN AMB A BLOCKED.
                                                            1, DB 1; 1
2,85e-08;
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                                                                                                                                                                            6.6
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                                                                Score 141:
  PUTENT : AL
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S
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Ex
                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 397 PC
726 726 BL
48 48 L
397 AA: 42928 MW:
25 PO
26 396 PO
226 226 BL
92 92 92
396 AA: 42709 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Match
Local Similarity 37.9%;
                                                                Match
Local Similarity 43.28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Conservative
                                                                                        Conservative
                                                                                                                                                                              CHACCAGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
226
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUS-POLLEN:
MEDILINE: 91093235.
Rafnar T., Griffith
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 92234870.
Griffith I.C., Pol
                                                                                                                                                                                                                                                                                                                                                                                                                             ISSUE-POLLEN
                                                                                                                                                                     MP13_AMBAR
927761
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VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuery Match
           CHAIN
MOD_RES
VARIANT
                                              SEQUENCE
                                                                   Luery Match
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  SIGNAL
                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITICS, 9224570.

MEDITICS, 9224570.

Griffith I.J. Pollock J. Klapper D.G., Boners B.C., Nault A.K.;

Griffith I.J. Pollock J. Klapper D.G., Boners B.C., Nault A.K.;

"Sequence polymorphism of Am. #. and Amb # II. the major slietueds
"Sequence polymorphism of Am. #. and Amb # II. the major slietueds
"Int. Ambroskal artemislifolia (Short radweed)."

Int. Arch, "Archy Appl. Immennol, 96:296-504(1991).
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                                                                                                                                                                                                                                                                                                                                                            01-0EC-1992 (Rel. 24, Circated)

01-0EC-1992 (Rel. 24, Last sequente update)

15-DEC-1996 (Rel. 37, Last accounted to a pdate)

16-DEC-1996 (Rel. 37, Last accounted to a pdate)

16-DEC-1996 (Rel. 37, Last accounted to a pdate of a 
                                                   67 FILMGRRPLWIIFSGNMNIKLKMPWIJA3YKIFDGRRAEVSYVBVBVARF198VDJI
108 FAAAQNRPLWIIFKNOMVINLNQELVVNSDKTIDGRGVKVE-1-1NGSLTLMNVKNII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- TISSUE SPECIFICITY: PULLEN AND FLUWERS.
-1- DISEASE: ONE OF THE MAJOR ALLINGENS OF THE MACMEH: PULLEN
-1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY
AMB A IZAMB A TIZCRY J TSUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 FGAAQNRPLWIIFARDNVIRLDRELAINNCKTIDGRGAKVELINAGFALYNVKNI
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P. swital.
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PRESTONS AND SPECIAL
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
penarre PECTATE LYASE P56 "SCURSOR (EC 4.2.2.2).
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SIGNAL 1 25
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PKINIS: PR00807: AMBALLERGEN
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182
392 AA:
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P28744:
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P15721;
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OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-F-MANN-4-ENURONOSYL GROUPS
OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-F-MANN-4-ENURONOSYL GROUPS
AT THEIR NOW REGOIGING ENDS.
IT INSUE SPECIFICITY: EXPRESSED IN ANTHERS AND POLLEN.
IT SINLARITY: BELOANS TO THE POLYSACHARIDE LYASE FAMILY:
This SMISS-PROFEDING SOPPHIGHT: It is produced through a collaboration between the SWISS Listiute of Bidinformatics and the EMBL outstation the European Bidinformatics institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial contities requires a license agreement (See http://www.isb-sib.ch/announce/or seed as erail to license agreement (See http://www.isb-sib.ch/announce/or seed as erail to license agreement.
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                                                                                              Who R.A. Yarayuchi J., Larabell S.K., Crsin V.M., McCormick S.). Molecular and denetic characterization of two poller-expressed genes that have sequence similarity to portate lyases of the plant pathogen
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01-A07-1992 (Rel. 23, Last sequence update)
01-A07-1998 (Rel. 37, Last sequence update)
01-B0EC.1998 (Rel. 37, Last annocation update)
00-LEN ALLERGEN AMP A 1.2 PRECURSOR (ANTIGEN E) (ANTIGEN AMB A I).
00-LEN ALLERGEN AMP A 1.2 PRECURSOR (ANTIGEN E) (ANTIGEN AMB A I).
00-LEN ALLERGEN ANTIGEN ES (Streptophyta: Embryophyta: Tracheophyta: euphyllophytes; Spermatophyta: Magnollophyta: eudicots; Asteraceae:
00-LEN ASTERIO ANTIGEN ES                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1994) to the EMBL/GonBank/DDBJ databases.
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MEDLINE: 91093235.
Rafnar T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,
Klapper D.G.:
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9.30e-08;
tiches 18; Indels
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PROBABLE PECTATE LYASE P56.
POTENTIAL.
POTENTIAL.
POTENTIAL.
W. 806762505. #BC7C8 CRC64:
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Pred. No. 9.30e-
17: Mismatches
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PIR: S0383; S0838;
PPRM: PT00544; pec_lyasor.1.
PRMINS: PR00607; AMBALLERGEN.
Lyase: Multique family: Signal.
SIGNAL.
                                                                                                                                                                                                                 Plant Mol. B.ol. 14:17-28(1990)
                                                                                                                                                                                                                                                                                                   STRAIN-CV, VF36: IISSUE-ANTHER; Wing R.A.;
                                                IISSUE-ANTHER;
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Best Local Similarity 35:5%:
Matches 22: Conservative
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                     SEĞJENGE FROM N.A.
STRAIN-CV. VF36; I
MEDLINE: 91322485.
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P27760;
                                                                                                                                                                                                                                                                                                                                                                                                                      GROWTH.
                                                                                                                                                                                               Erwinia.";
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ACT_SITE
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STRAN-CV. VP16; TISSUE-PISTIL;
Budelier K.A., Smith A.G., Gasser C.S.;
Budelier K.A., Smith A.G., Gasser C.S.;
Budelier K.A., Smith A.G., Gasser C.S.;
Regulation of a sylvar transmitting tissue-specific gene in "Regulation of a sylvar transgenic tomato and tobacco.";
Mol. Gen. Genet. 224:183-192(1990).
-: FUNCTION: MAY HAVE A ROLE IN THE DEVELOPMENT OF THE TRANSMITTING TISSUE OF THE SYLLE AND/OR IN THE EVENTS RELATED TO POLLINATION SYCH AS SOME ASPECT IN THE FACILITATION OF COMPATIBLE POLLEN TUBE
                                                                                       MEDINE 9224570.

MEDINE 9224570.

MEDINE 9224570.

MEDINE 9224570.

MEDINE 9224570.

Criffith 1.3. Pollock 3., K .pper D.G., Rogers B.L., Nault A.K.

Sequence polymorphism of Am. a i and Amb a II, the major alrequent in Ambrosia artemislifolia (...ort ragweed)...

Int. Arch. Allergy Appl. Imm nol. 96:296-304(1991).

SUBMITH MONGER.

1. SUBMITH MONGER.

1. DSEASE. ONE OF THE MAJOR ALLERGENS OF THE RAGWEED PULLEN.

SIMILARITY: BELONGS TO THE PALYSACHARIDE LYASE FAMILY I.

AMB A I/AMB A II/CRV 3 I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 FAAAQNRPLWIIFKHNWVIBLNQELVVNSDKIIDGRGVKVNIVNA-GLILMN-VKNII 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloning of Amb a I (antigen E), the major allergen family of short
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Bukaryota Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solamales; Solamaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 13.4%: Score 137: DB 1: Length 199 Local Similarity 39.7%: Pred. No. 1.37e-07: hes 23: Conservative 10: Mismatches 23: Indeis
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Signal: i 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLLEN ALLERGEN AMB A 1.2.
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01-MAR-1992 (Rul. 21, Last sempence apdate)
15-301-1999 (Rul. 38, Last annotation update)
STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
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                     ragweed pollen.";
J. Biol. Chem. 266:1229-1236(1991).
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                                                                         SEQUENCE FROM N.A., AND VARIANTS
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EMRL: M80559; AAA32667.1; -:
PIR: B39099; B39039.
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382
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345
381
398 AA;
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P24396;
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SEQUENCE
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                                                                                                                                                          this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation—the European Bloinformatics Institute. There are no restrictions on its see by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isbesib.ch/angounce/or send an email to licensedisb-sib.ch).
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Griffith 1.3., Pollock J., Klapper D.G., Roders B.L., Nault A.K., Sequence polymorphism of Arb a I and Amb a II, the major allergens in Ambrosia attemisticholia (short raqweed)...

In Arch, Allergy Appl. Imminol. 96:296-304(1991)...

I. SUBGNIT: MONOMER.

II. SISUE SPECIFICITY: POLLEN AND FLOWERS.
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DISSUE SPECIFICITY: PREDOMINANTLY FOUND IN THE PISITL WHERE IT FOUND IN THE OOTER FIVE LAYERS OF THE STRANDS OF TRANSMITTING TISSUE WITHIN THE UPPER TWO THIRDS OF IHE STYLE. FOUND AT WCHLOWER LEVELS IN THE ANTHERS AND VEGETATIVE ORGANS. PREVIOUS STATES STATE: MAXIMUM LEVELS ARE FOUND DURING ANTHESIS. SIMILARITY: 54% IDENTICAL TO TOWARD PROTEINS PS9 (AC PIS72).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE: 92313060.
Rogers B.L., Morgenstern J.P., Griffith i.J., Yu X.-B.,
Counsell C.M., Brauer A.M., King T.P., Garman R.D., Kuo M.-C C.,
"Complete sequence of the allergen Amb alpha II. Recombinant
expression and reactivity with T cells from ragweed allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- TISSUE SPECIFICATY: POLLEN AND FICWERS.
-:- DISEARGE ONE OF THE MAJOR ALLENGENS OF THE RAGWEED POLLEN.
-:- SIMILARITY: RELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
AMB A 17AMB A 11/CRY J I SUBFAMILY.
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Pred. No. 1,376:07;
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404
7 402
1 41298 MM: B
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                                                                                                                                                                                                                                                                                                                             EMBL: X55193: CAA36975.1; -- PIR: S12209; S12209; POPM: PF00544; PPC_1yase; 1- PRINTS; PROCHO?: AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 54.58:
les 18: Conserver
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37
291
404 AA:
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P27762:
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SIGNAL
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the European Bioinformatics Institute of Bioinformatics and the EMBL outstallon the European Bioinformatics Institute. There are no restrictions in its use by non-profit institutions as long as its content is in us way modified and this statement is not removed. Usage by and its incorrolatentities requires a license arrespont (See http://www.istrsib.ci./announce) or send an email to license***
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-:- TISSUE SPECIFICITY: EXPRESSED IN ANTHERS AND POLLEN.
-:- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum (Idmato)
Eskaryota, Virtalplantae, Singtophyta, Embryophyta, Itanio phyta,
euphyllophytes, Spermatophyta, Mando, Iddhyta, eudichyled man
euphyllophytes, Spermatophyta, Mando, Iddhyta, eudichyled man
core eudicots, Asteridae, etasiettak It Schanates, Solanarom
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X - Y (DELOTIED NLY IN FL WER DNA)
X - F (OBTECTED ONLY IN FL WER DNA)
C CREITEACYANDICO (RCS4:
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THE FUNCTION: MIGHT BE NEEDED DURING POLICEN LEVEL, PRENT AND 1788.
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SigNal, 26 97 Filler Allergen AKF A 2.
MOD_RES 226 726 BLOCKED.
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01-APR-1990 (Rel. 14, Last sequence appare)
15-JUL-1999 (Rel. 38, Last annotation update)
PROBABLE PECTATE IYASE P69 PRECURSER (FT 4.2.2.2)
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Pred. No. 1
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PRINTS; PR02807: AMBALLERGEN.
Lyase: Multique family: Signal, 1.
SignAL.
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226 726 PL
70 70 N
138 138 K
321 321 K
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PFAM: PF00544; PCC_LYASC: :
PRINTS: PRUGB07: AMBALLENGEN.
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PIR: A46459: A46459.
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Best Local Similarity 42.3%;
Matches 22; Conservative
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MEDLINE: 91322485.
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VARIANT
SEQUENCE
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15-JUL-1999 (Rel. 38, Last sequence update)
25-JUL-1999 (Rel. 38, Last annotation update)
25-JUL-1999 (Rel. 38, Last annotation update)
25-JUL-1999 (Rel. 38, Last annotation update)
27-JUL-1999 (Rel. 38, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-EC-1998 (Rel. 37, Last annotation update)
16-EC-1998 (Rel. 37, Last annotation update)
POSSIBLE 12 NOTECT ACID-BINDING PROTEIN
SAD MIQUEL Sea 1100 VIVES (Serozype 4) (SMSV 4).
Viruses, SSPNA positive-strand viruses, no DNA stage; Caliciviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AVIQKEPLWIIFKRGMNIRLHQEMIMUSDKTIDARGVNVHITKGASITLQYIKNV 213
                                                                                                                                                                                                                                                                                                                                      68 TIMGREPLWIIFSGNMNIKLKMPMYIAGYKTFDGRRAEVSYVHVNG-A-KFIRRY 120
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                                                                                                                                                                                          Score 124: DB 1: Length 449;
Pred. No. 1.88e-05;
13; Mismatches 21: Indels
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Best Local Similarity 31.9%; Pred. No. 1.590-02;
Matches 15; Conservative 15; Mismatches 14; Indels
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                                                                              POTENTIAL.
PCTENTIAL.
17E3AA13F173B03C CRC64.
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Bacillus/Staphylococcus group; Brevibacillus.
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Rest Local Similarity 34.5%)
Matches 19: Tonservative
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CHISTOLICAL LARGE MULTENIYME CHAPLEX OF 1YCA, 1YDB AND 1YOU CHISTOLICAL LARGE MULTENIYME CHAPLEX INCLUCING AN CHERCHAIL EDUMAIN. CONSISTS OF THREE MULDLES, INCLUCING AN CHERCHAIL EDUMAIN. EACH WIDCLE INCOMPRESSINE AMBNE ACTUBING THE PERTIDE PRODOCT AND CHAPTER SUBDIVIDED INCOMING THE PERTIDE PRODOCT AND CHAPTER SUBDIVIDED INCOMING THE PERTIL OF THE PERTIL OF THE PERTIL OF THE PERTIL OF THE PARTICULAR CONTINUED. AND EPIMERIZATION (CHITWAL). AND CHISTOLICAL METHYLATION (OPTIONAL). AND CHISTOLICAL DECAPETIONS. TYROCIOINE IS A MIXTURE OF FOUR CYCLIC CRANLEUD. B. C. AND D. IN WHICH PHE, AT POSITIONS 3, 4, AND TYROCIONAL METHYLATIONS OF THESE ATTHOUGH ACTUS IN THE GROWTH MEDICAL CONCENTRATIONS OF THESE ATTHOUGH ACTUS IN THE GROWTH MEDICAL CONTINUED OF AME TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as Jong as its content is in no way modified and this statement is not removed. Usabe by and for commercial entities requires a license agreement (see http://www.isb.sib.ch/announce/or send an email to licensewish-sib.ch).
                                                                                                                          1. Bacteriol (179:6849-6855(1997).
-:- FUNCTION: ACTIVATES THE SECOND TO FRORTH AMINO ACTOS IN TYRUTHEN (IN TYROCIDINE A. PRO, PHE, AND D-PHE) AND EPIMERIZES THE LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1170 VGLVKLAENRHVLIIDMHHIISDGVSSQLILN-DFSRLYQNKALPEORIHYKDFAVWEKA 1228
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POWALN 2 (PHENYLALANINE-ACTIVATING).
POWANN 3 (D. PRENYLALANINE-ACTIVATING).
ACTI. CAPH.ER. (ACP).
                                          Modeland, Administration N.A.;
Moots E.D., Marahiel M.A.;
The tyrocidine biosynthesis operon of Racillus brevis, Camplete nucleotide sequence and biocherinal characterization of functional nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACYL CARRIER (ACP).
PH'SPHORNTETHEINE (BY SIMILARITY).
PHOSPHORNTETHEINE (BY SIMILARITY).
PHOSPHORNTETHEINE (BY SIMILARITY).
W: 322834718BB28847 CRC64;
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8.38e-02;
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Pred. No. B.38e-0
37; Mismatches
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PR.NTS; I 00154; AMPB'NDING
PROSITE: ASO0012; PROSPAPANTHEINE; 3,
PROSITE: PS00455; AMP_BINDING; 3
PROSITE: PS00455; AMP_BINDING; 3
PROSITE: PS00455; AMP_DINGING; 3
PRAM: PF00501; AMP_DINGING; 3
PFAM: PF00502; APP_DINGING; 3
PFAM: PF00560; PF-binding; 3.
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Multifunctional enzyme; Repeat.
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                STRAIN ATCC 8185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               988 TSDDAPKWALGHEVTRFALMLCBTSPKWMPL-IIRGCSMFTKKRMKMLN-YLKILDGH 1045
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                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDITIES 9202034.
MEDITIES 9202034.
Mallot A., Arabitatic C., Bouloy M., Prehaud C., Bishop D.H.L.:
Mallot A., Arabitatic C., Bouloy M., Prehaud C., Bishop D.H.L.:
"Completion of the denote sequence of Rift Valley fever philobovirus indicates that the L.HNA is negative sense and codes for a putative indicates that the L.HNA is negative sense and codes for a putative futurescriptaserrogalisase."
"Larabitatic Acids Res. 19.6433 5437(1991).
"CATALYTIC ACITIVITY: N NUCLEUSIDE TRIPHUSPHATE * N PYRCPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saps
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Rift valley fover virus (strain 28-548 Mi2) (avFV).
Viruses: ssENA negative-strand viruses: Bunyaviridae: Phlebovirus.
[1]
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PIR: S18576; S18676
Fransferase: Nicleotidyltransferase: RNA-directed RNA polymerase.
SEQUENCE: 2:49 AA: 243889 MW; 6057390507948897 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  query Match
Best Local Similarity 34.4%; Pred. No. 1.16e-01;
Matches 21; Conservative 14; Mismatches 22; Indels
                                         CIACS-1992 (RE). 23. Created)
CI-AUG-1992 (RC). 23. Last sequence update)
Ol-AUG-1992 (RE). 23. Last annotation update)
RNA-DIRECTED WNA POLYMERASE (EC 2.7.7.45) (L PROIE.N).
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Release 3.1A John F. Collins. Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh. U.K. Distribution rights by Oxford Molecular Ltd.

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>US-09-142-524A-3 (1-114) from US09142524A.pep 1026 I MKVIVAFNQFGFNRRVFIKR.......KFIRRVDGIIAAYUNPASWK 134 Description: Perfect Score: Se frence:

PAM 150 Sap 11 Scoring table:

225878 segs, 69334122 residues Minimum Match 0% Listing first 45 summaries Post processing: Searched:

Catabase:

sptiembilz lisp_archea 2/sp_blotteria 3/sp_finul 4/sp_buman 5/sp_invertebrate 5/sp_manmal 7/sp_mhc 8/sp_organelle 9/sp_finuer f0/sp_plant 11/sp_rodent 12/sp_inclassified 13/sp_vertebrate 14/sp_virus

Pred. No. 18 the number of results predicted by change to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. Mean 42,980; Variance 75,878; scale 0.556 Statistics

3.59e-21 2.54e-21 2.54e-21 3.54e-01 3.24e-02 3.28e-03 3.30e-08 3.58e-07 3.58e-07 1.77e-05 1.77e-05 3.74e-05 3.74e-05 3.75e-05 3.75e-05 3.75e-05 3.76e-05 3.76e-05 3.76e-05 3.76e-05 POLLEN MAJOR ALLERGEN
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OHTA N.,
OHTA N.,
Characterization and molecular cloning of the oil, a major allergen of Charactyparis obtusa (Japanese cypress) pollen.":
EMBL: D45404: BAA06246.1:
EMBL: D45404: BAA06246.1:
PFAR: PF0054: pec_lysse: I.
PRINTS: PR00F07: AMBALLERGEN.
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core endicots: Sosidae: eurosids II: Brassicales: Rrassicaceae:
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57.7%: Pred. No. 2.24e-21:
91.1vc 8: Mismatches 14: Indels
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42.3%: Pred. No. 5.53e-10:
ative 10: Mismatches 19: Indels
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01-JAN-1998 (TEMBLEC). 05, Last sequence update)
01-NNY-1999 (TEMBLEC). 12, Last annotation update)
PUTALIVE PECIATE LYASE (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
11011.7 PROTEIN.
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7 20088 MW; EF342606 CRC32:
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22 375 CHADI.
375 AA: 40259 MM: A0981492 CRG32:
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Matches 22: Conservative
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                                  SECUENCE FROM N.A.
                                                               TISSUE-POLLEN:
MEDLINE: 95265194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thallada (Mouser : otress).
Eukaryota, Viridoplantae) Streathphila: Empry uphyta. Clemberthytae
euphyllopbytes: Spermatophyta: Magadilophyta: eldicotyledons;
core eudlocts; Rosidae; eurosids (I) brasslaatha.
Eukaryota, Viridiplantae: Stre tophyta: Embryophyta: Tracheophyta:
euphyliophytes: Spermatophyta: Magnollophyta: eudicotyledous:
core eudicots: Rosidae: euros:is II: Brassicales: Brassicaceae:
Arabidopsis.
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STRAINTO. COLUMBIA:
STRAINTO. COLUMBIA:
STRAINTO. COLUMBIA:
STRAINTO. COLUMBIA:
SYNES S.M. LIN X. KETCHUM K.A., CROSBY M.L., BRANCON F.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.L.,
SCMERVILLE CR.Y. VENTER T. J.C.,
SUBMITTED (MAR-1993) to the EMBL/GenHank/DDBJ databases.
EMBL; ACCO2521: AACO335C.1;
MENDEL: 28505; Arath.10986:28505.
PFAM: PPROM44: pec_1yase: 1.
PRINTS; PROM907; AMBALLERGEN.
                                                                                                                                                                          STRAIN-CV. COCUMBIA: OSBORNE B.I., VYSOTSKAIA V.S., FORTUMI M., YU.G., GUI H. LIES SEBORNE B.I., VYSOTSKAIA V.S., FORTUMI M., YU.G., GUI H., FINGE K. L. HONNY A.B. C. NAMY A.B. C. NAMY A.B. C. NAMY A.B. C. NAMY B. SCN H., DAVIS B.N. EDKER J.R., FEDREK PLEL N.A., THENGAGIS A.B. SUDMILLED (AUG-1997) to the HMRL/GenBank/EDBU databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 RPLWIIFSGNMNIKLKMPMYIACYKIFDGRRAEVSYVHVNSAKFIRVNGII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4 %.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 RPLWIVEKRDMVIQLKQELIVNSFKTIRGRGANV-HIANGGELIUFVING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA:
1HEOLOGIS A.:
1HEOLOGIS A.:
1MENDITUDG (1971) TO LIME FMBI/JOHNBARK/COBJ JATADARRES
EMBLI ACCOLOFF; ARBBUCZ2.1: --
MENDEL: 25798: Arath.co88:.758
PFAM: PFOGS4: PPC_IYERSE.:
PRINTS: PROS54: ARBALLERGEN.
SEQUENCE 431 AA: 47770 MM: 808EC285 GRC32.
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Submitted (JUL/1997) to the P. L/GenHank/PURC databuses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THEOLOGIS A.,
Submitted (AUG-1997) to the ERM /GenHank/GEBS cutabases
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40.4%; Pred No. 1.26e-09;
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III Mismatches 19.
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01-A0G-1996 (TEMBLIEL 07. St seq
01-NOV-1999 (TEMBLIEL 12. St anno
PUTATIVE PEGTATE LYASS.
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Best Local Similarity 45.1%;
Matches 23: Conservative
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es 21: Conservative
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STRAIN-CV. COLUMBIA:
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                                                                                                                                                    SEQUENCE FROM N.A.
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064510;
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Arabidopsis.
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O65456
O65456;
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ID 065457
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Ekkaryota Viridiplantae: Streptophyta: Erbryophyta: fracheophyta:
euphylophytes: Sperratophyta: Magnollophyta: eudicotyledons;
core eudicots: Posidae, eurosids II; Brassicales: Brassicacee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidops.s thailata (Mouse-car cress).
Warayota Virdolplates Streptophyta: Embryophyta: Tracheophyta; eudicopytes: Spermatophyta: Magnollophyta; eudicotyledons: core eudicots: Rosidue: eurosids II: Brassicales: Brassicaceae:
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*Identification of the tobacco and Arabidopsis homologues of the polien expressed Lar59 gene of tomato.";
Plant Mol. Boli. 34 8809 814 (1997).
EMBL. U83519; AAB69759.1;
*KENDEL. 25559; Arath: U885.25559.
PRAM: PF00544; pec_lysse; 1.
PRINTS: PROC807; AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-CV. CULMBIA:
VYSOTSANA SI COLUMBIA:
VYSOTSANA SI COLUMBIA:
VXSOTSANA SI CONNAY A.B., SHIN P., DEMAR K., FENG J., KIM C., KURTZ D., PALM C.J., LI Y., SHINN P., SUN H. DAVIS K.W., ECCREPEREL N.A., THEOLOGIS A.;
SUN H., DAVIS K.W., ECCREPATION CONNAY CONNAY ACCOUNTS ACCOUNTS A.C. CONNAY A.C. CONN
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165 RPLWIIFARSMITKLQQELIIINDKTIDGRGAKI-YITGGAGLTLOFVRNV 215
                                                                         73 FPLWIIFSGNMNIKLKMPMYIAGYKIFDGRRAEVSYVHVN-G-A-KFIRRV 120
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Last segmence update)
Last annotation update)
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Last annotation update)
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Pred. No. 7.30e-08:
14; Mismatches 12;
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Pred. No. 3.27e-08;
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PFAM: PF00544: pc=lyase: 1.
SECENTS: PR0807: AMBALLERN.
SECENTE: 390 AA: 43354 MM: E0F32F84 CRC32;
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01-A03-1998 (TrEMBLIF), C7, Last seq-
01-NCV-1999 (TrEMBLIF), 12, Last and
F12F1.22 PROTEIN.
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01-3AN-1998 (TEMBLTEL, 05,
01-3AN-1996 (TEMBLTEL, 05,
01-NOV-1999 (TEMBLTEL, 12,
PUTATIVE PELIATE LYANS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 44.2%;
Matches 23; Conservative
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15; Conservative
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SEQUENCE
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AD 023665.
DI 023665.
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DE PUTATIVI
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90.70
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Estaryota, Viridiplantae: Strephophyra: Estaryota, frachemonthus emphylophyra: Strephophyra: Magnollophyra: Coudicoty) Patrix obsessibly dobbytes: Spermatophyra: Magnollophyra: Cudicoty) Patrix Core eudlocts; Rosidae: Cirosids II: Brassicales: Brassicare.
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Eukaryootay Viridiplantae: Streptophyta; Enbryophyta; Tranbeophyta
euphyilophyta; Spermatophyta: Magnollophyta; eudicotyyledons;
oore eudicots; Rosidae; eurosids II; Brassitaies; Brassicaee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394
CHILLS OF THE CONTROL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
BEVAN M., WEDLER H., WAMBUIL R., BANCROFI I., MEWES H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0018
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BEVAN M., WEDLER H., WAMBUIT H., BANCHOFT I., MEWES H.K.
SCHUELLER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022140; CAA18112.1;
MENDEL: 29068; Arath;1088;29068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU ARABIDOPSIS SEGUENCING PROJECT;
Submitted (APR-1998) to the EMSU/Genhank/DOBJ databases
EMBU: ALG22140; CAA18111.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1998) to the EMBL/GenBank/DOBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
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                                                                                                                                                                                                                                                                                                                                            01-A00-1998 (TEMBLEE), 07, Treated;
01-A00-1998 (TEMBLEE), 07, 1st sequence apdate)
01-NOV-1999 (TEMBLEE), 12, ast admotation update;
PECTATE LYASE LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         065457.
01-AUG-1998 (TERMILE). 07, Fredtel)
01-AUG-1998 (TERMILE). 07, Fredtel)
01-W-1999 (TERMILE). 07, Last sequence pdate)
01-W-1999 (TERMILE). 10, Last sequence pdate)
ETAZOLES LYASE LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 YGVIÇAKPIMITFAKDMVITLENELMVNSYKTIDGRGAKVETAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 36.4%; Pred. No. 1.62e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.18; Score 134; DB 10;
Best Local Similarity 36.4%; Pred. No. 3.58e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 AA; 43476 MW; 95399178 CHC32;
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                                                                                                                                                                                                                                                                                            354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MENDEL: 29747; Arath;1088;29747
PFAM: PF00544; pec_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00544; pec_lyase; 1.
PRINTS; PR00807; AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS: PROUBOT: AMBALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16: Conservative
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                                                                                                                                                                                                                                                                                            PRELIMINARY:
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Euwaryota: Viridiplantae, Streptophyta: Embryophyta: Tracheophyta:
euphyliophytes: Spermatophyta: Maunoliophyta: eudicotyledons:
core eudicots: Rosidae: enrosids i: Fabales: Fabaceae: Papilionoldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characherization of pollen specific matter at the sequence homology to rankeed alteracks and pectate lysses":
Plant Mol. Biol. 23:1061-1065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edkaryota) Viridiplantae, Storptophyta, Embryophyta, 710 holosoeuphyllophytas, Spermatophyta, Mudnillophyta; illiopsida, Foloso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - CARAYTIC ACTIVITY: ELMINATIVE CLEAVARE OF PECTATE DOBLING OLIGOSACCHARIDES WITH 4-DELXY-ALPHA-D-GLUC-4-ENURAN SYL DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%; Score 130; DB 10; Length, 450; Best Local Similarity 37.3%; Pred. No. 1.72e-26; Matches 22; Conservative 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lennary 4 en
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WU Y., GID X., DERICKSON L.;
WU Y., GID X., OT X., DERICKSON L.;
WU Y., GID X., OT X., DERICKSON L.;
WU Y., GID X., DERICKSON L.;
EMBL; U11472: AAA86241.1,
MENDEL: 9442: Medsa;1068:904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CINOY-1995 (IndMeLre), 01. Dreated)
C1-NOV-1996 (IndMeLre), 01. Last sequence update)
C1-NOV-1999 (InfMeLre), 12. Last accordation update)
POLLIN SPECIFIC PECTATE LYASE BOMOLGOUE (EC.4.2.2.2)
Zea Tays (Maize).
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01-NW-1949 (TEMBLEG. 1). Last sequence goate;
01-NW-1999 (TEMBLEG. 12, Last amountion update)
PECIATE LASE HOMOLOG.
Medicago sativa (Alfalfa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coery Match
Best Local Similarity 47.1%: Fied. No. 1.17e-14.
Matches 16: Conservative ': Mismatches 14.
Pred. No. 5.32e-07-
6: Mismatches 10
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                                                                                                                                                                                                                                                                                                                                          156 RPLWIVEARDMVIELRQELIVNHNRILLGRINGV 189
                                                                                                                                                                                          54 PLWIIFQRDMTIQLKEELIMNSFKIIDGRGASV 86
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MENDEL: 11.55; Zeama 17.059.1:165.
PRAM: PF00544; pec. Judes.
PRINTS: PR00607: AMBALLEBGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 438 AA: 49138 WW:
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PRINTS: PR00807; AMBALLERGEN.
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Best Local Similarity 51.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINASY
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040319;
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Q4 3862
Q4 3862;
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Gaps
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EMBL: U63550: AA871208-1: 1.
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euphyllophytes: Spermatcphyta: Magnoliop! ta: eudicotyledons:
core eidicots: Rosidae: eirosids I: Rosalos: Rosaceae: Fragaria.
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Bukaryota Viridiplantae Szeptophyta: Embryophyta: Tracheophyta:
Bukaryota Viridiplantae epopyta: Naunollophyta; eudicotyledons:
core_eudicots: Rosidae: eurosids II: Brassicales: Brassicaceae.
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MEDLINE: 97422463.
MEDLINE: 97422463.
MEDLINE: 97422463.
MILLIANDERS R., MCCORMICK S.;
FULLINE STATES R., MCCORMICK S.;
FOR THE CONTRIBUTION OF THE LODGECT AND AND AND STATES AGE OF COMMUTE. THE PERMIT WAS AND AND STATES AN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CHANDLER: #8592.
MEDLINE: #48592.
MEDINA ESE SAR N. CARDENAS U., MOYAND E., CABALLERO J.L., MUNUE-SLANDE OF LANDERS J.L.,
1.dels
                                                                                                                     105 YSVIÇAKPUMITFAKDMVITLANELMVNSYKTIDGE AKVEIAY 148
                                                                                                                                                                                                                                    67 FILMGREPLWITESGNENIKLKMPMYLAGYKTEDG: -RAEVSY 108
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51-CAN-1998 (TERMILE), 05. Last sequence ipdate)
C1-N.V-1999 (TERMILE), 12. Last annotation update)
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JUNA-1998 (TREMBLEEL 35, Last sequence appare)
JL-KCV-1999 (TEMBLEEL 12, Lost adoptation appare)
PUTATIVE PECIALS LYASE (FRAGMENE).
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226 AA: 25103 MW; 5F1C8DD2 CRC32:
M. smatches
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PPAM: PF06544; pec_lyase: 1
Ivaga
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      Conservative
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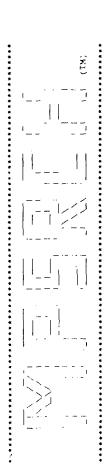
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160 FOAVQROPEWIIFQRSMVITLTGELMVSSDKTIDGRGANVQ-IR-DGAGITMGFVNNVI 216
                                   67 FILMGRRUGHIESGNMNIKLKMPMYIAGYKTFEGBRAEVSYVHVNGAKFIRR-VOGII 124
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Bukaryota: Viridiplunder: Streptophyta: Embryophyta: Tracheophyta:
euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons:
core eudicots: Asteridae: euasterids I: Solanales: Solanaceae;
Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Morse-ear cress).
Eukaryota, Vitidopiantse: Streptophyta, Enbryophyta, Tracheophyta, euphytiophytes, Spermatophyta, Magnoliphyta, eudicolyjedons, obre eudicols, Rosidae, eurosids II. Brassicales, Brassicaceae,
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SEQUENCE FROM N.A.
MEDLINE: 97422403.
MEDLINE: 97422403.
KULIKACSKAS R., MCCORMICK S.;
"Identification of the tobacco and Arabidopsis homoloques of the Tobacco and Databour, and McCordine of the Tobacco and Arabidopsis homoloques of the Public Mol. 36.9999914 (1997).
EMBL: 033622, AAR69762.1; -.
MENDEU: 25562. Arath:1088:25562.
PPM: FF00544: pec_lyuse: 1.
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"Identification of the tobacco and Arabidopsis homologues of the
pollen-expressed LAT59 gene of tomato.";
Plant Mol. Bol. 34, 8859-814(1997).
EMBL; U85546; AAB69758.1;
"MENDEL: 25645: Nicta:1088:25645.
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                                                                                                                                                                                                                                          01-JaN-1998 (TrEMBLTEL 05, Created)
01-JAN-1998 (TREMBLTEL 05, Last sequence update)
01-NNV-1999 (TREMBLTEL 12, Last annotation update)
PUTATIVE PECIALE LYASE (FRAGMENT).
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01-JAN-1998 (frEMBLiel, 05, Last sequence update)
01-AW-1999 (frEMBLiel, 12, Last annotation update)
01-MW-1999 (frEMBLiel, 12, Last annotation update)
NTS9.
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Best Lord Similarity 42.4%; Pred. No. 2.55e-06;
Matches 14: Conservative 10; Mismatches 9;
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227 : 227
227 AA: 25336 MW: C09AB147 CRC32;
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274 AA; 30790 MW; D2CBC820 CRC32;
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Db 154 YAVIQKEPLWIIFERSMITHLHOELIMUSDKIIDARGANVHIAKGAGITLLYIKNY 209 (1919) | 114 | 114 | 117 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 1
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Search completed: Mon Jun 19 15:57:47 2000 Job time : 29 secs.



Release (LIA John F. Collins, Biocomputing Research Unit. Copyrigh: (c) 1993-1998 University of Edinburgh, C.K. Cistribution rights by Gxiord Molecular Ltd.

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Much 30,632; Variance 132,267; Scale 0,232 Statistics

Pred. No. is the number of results predicted by chance to have a score greater this or equal to the score of the result being printed, and is do not by analysis of the folial score distribution.

### SHIMMARIES

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Posuit No.	927.08		Sucry March Length Ds	O	Description	Pred. No.
7	9807			W27271	Multi-epitope reptide	
77	49.8	۲۰ ۲۰ ۵۰	ر د د	0.E.C.M	Multi-epitopo poptide	6.58e-42
٠٠.	37.2	6.36		W27369	Multi-epitope peptide	
4	808	213	02	W44682	I-ce. epitope peptide	
S	158	15.4	20 1	R45549	Cry ; I pollen allerde	
9	158	15.4		382498	Crv j I Japanese Cedar	1.13e-34
Ļ	142	3 3.38	3.0	R45579	Cry j I pollen allerde	
80	1 38	13.5	1.7	R8:581	Cedar polien allergen	5.24e-03
6	137	¥.	1.8	W80346	Sug: allergen protein	

Note: Post processor removed 36 summaries from list due to search parameters chosen

## ALIGNMENTS

M27371 standurd, peptide: 134 AA. W27371 standurd, peptide: 134 AA. W27371. 24-MAR 1998 (first entry) Multi-repitor, peptide: in-uncothers matti-repitory peptide: in-uncothers 1-cell epitory region: allergent	poptide: 134 AA.	24-MAR 1998 (first entry) Multi-replice, poptide used as immunotherapeutic agent #3. Multi-replice, poptide: immotherapeutic agent: alleyic disease; T-cell epitopy region: allergen: lymphocyte; immunoglobulin E.
LT 1 W27371 W27371 24-MAR Multi- Multi- T-cell	Standard;	1998 (fix epitope pep epitope pep epitope re
	RESCLT 1 10 W27371 AC W27371	24-MAR Multi- Multi- T-cell

SO	Synthetic.
Z.	W09732650-A1.
PD	12-SEP-1997.
Ω.	10-MAR-1997; JC0740.
er.	10-MAR-1995; UP-080702;
ď.	(MEIP ) MEIUL MILK PROD CO 110.
i,	Dairiki K. Iwama A, Kino K. Kune A. Sone I.
DR	WPZ: 97-470495/43.
ΡŢ	Peptide immuno:therapeutic agent to treat alleraid diseases :
ΡŢ	contains multi-epitope peptide containing I cell epitope regions
ΡŢ	from different allergens
PS	Claim 6; Page 32; 58pp; Japanese.
S	The present sequence represents a nulti-opitope peptide which is used as
ပ္ပ	a new immunotherapeutic agent. It comprises I cell epitupe reduces from 2
S	or more different allergens (preferably linked via arquinge or lysine
ö	dimers), where the I ceil epitope regions: have a positivity index
8	greater than 100 as measured in a patient group responding to the
DO O	allergen: have at least 70% reactivity with lymphocytes from pathenns
Ö	responding to the allergen; and are not reactive with immunoulobulin E
ပ္ပ	(IgE) antibodies from patients responsive to the alleraem The agent can
ပ္ပ	be used to prevent and treat a wide variety of allergic diseases, e.g. Ly
ပ္ပ	desensitisation. Side effects, e.g. those mediated by IOE, are reduned.
SO	Sequence 134 AA;
O	
an z	Pred. No. 4.34e-87;
2.	Matches 134: Conservative U. Mismatches U. Indexs Condition
DP	1 MKVIVAFNQFGDNRRVEIKRVSNVIIHGRRIDIFASKNFHLQKNTIGIGRPWKNNFIMLO 50
0	NEVERON PROPERTY   P
5	
QQ	61 FAKLTGETLMGREPLWIIFSGNMNIKLKMPMYTAGYKTENGRRAEVSYVHVNGAKFTRFV 120
	-
Ġ	61 FAKLIGETLMGRRPLWIJES THNNIKLKMPMYJAGYKTFLOHRAEVSYVEVNJAKFIBRY 120
â	12] DGIIAAYQNPASWK 134

>-

105 AA; Synthetic. W097326C0-A1.

54.7%: score 561; DB 1; Length 105;

Query Match

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A CMEN 1990 TO 1802.

A CMEN MEDIA WITH BEND OF LID.

A CMEN MEDIA WITH A KING K. KUTC A. Some I.

BOBITIST K. TATTA A KING K. KUTC A. Some I.

WEDER TO 42045/A.

WEDER TO 1804 TO A MINISTRATION AGENCY. TO SELECTION OF THE CONTRIBUTION TO SELECTION OF THE CONTRIBUTION OF THE CONTRIBUTI
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                                                                                    I MKVIVAFNIJFGENKRVEIKHVSNVIIHGRRIDJEASKNEHLQKNTIGIGARÆKNNRIMLG 60
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Claim 1: Page 1: (4pp: Japanese,
Tobil epitops peptides W44592-88 and their derivatives react with
                                 Sars
                                                                                                                                                                                                                                                                                                                                                                                                                                                24-KRP-1948 (1918) POLITY)
MAILL OPATOR (1918) STANDARD AS DEFINITION ASSENTED AS SERVICE AGENCY AS TOUGHT OF THE PROPERTY OF 
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                                                                                                                                                                                                                 6] PAKUTGUTUM BERTTOTT TO THE TEMPRITACYKIFDGERVE 92
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C1-MAY-1998 (11st entry)
Troch, uplope populde #1 of sigl pollen autiden.
Synthetic pollen antique sigl pollen antique sigl pollen
best Lodd. Similarity 85.7%; Pred. No. 6.58e-42;
Matches 90: Tunservative It Mismatches It
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Local Similarity 10:10** Pred. No. 5:64e-24;
les 51; *** Sarvatire* 0: *** Xismatches* 6
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24-0DN-1996. DE-18287
24-0DN-1996. DE-18287
(DAIL) DAICED CHEM INC LID.
(MEIL) MEDIL SELKA KAISHA LTD.
WPIL H-13353,/33
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                                                                                                                                                                                                                                                                                                                                                                                                       W27:00 stander: profide. Ful AA
W27:69:
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Jioboffco.A.
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12-SEP-1990
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derivatives is used for the prevention and treatment of some fullinears Sequence. 30\ \mathrm{AAz}
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The sequence is that of an isolated poptide of the datanese redained leadernee of the feptide of 1:20 can be used for the treatment and diagnosis of allerates assertated with Japanese redai polien. It has enhanced therapeutic proportions but induced side effects compared to naturally occurring alleraness Sequence. 20 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified Cryptomeria japonica (Cry ) I peptide(s) - useful for treating allergy to japanese cedar pollen allergen or faminations reactive allergens. Discussionally constructed (Gpp: English Novel peptides of cry ) I have been modified as a part of a preformalization scheme to develop an optimised drug product for therapeutic treatment of humans suffering from allergy to Japanese codar pollen allergen or an allergen which is immunologically cross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cry j i Japanese Ceda: pólico allergen peptide fragment (GJI-8).
Cry j I: Japanese ceda: pollen allerach: modificá: drug production: allery: Crytpomeria japonica.
Crytpomeria japonica.
W09527786-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigens derived from Japanese ceda: pullen allergen 'Ty contain at least two T cell epitope(s), used to treat of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dr Indeas
                                                                                   Match 20.3%: Score 208: DB 3: Length 40: Local Similarity 100:08: 1724. No. 5.42e-09: sea 25: Conservative or Mismatches 6, 100:03
                                                                                                                                                                                                                                                                                                                                                                                                             13-3UL-1934 (first entry)
cry j i poilen aliergen peptide CII's
Capanese cedar; detection; allergy: freatment; diagnosis.
T cell epitope, sensitivity
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00.0%: Frv. No. 1.138-04;
Wattye O: Mismatches C: Index
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                                                                                                                                                                                                                             79 RPLWIIFSGNMNIKLKMPMYIAGYK 97
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R62498:
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R45549 standard; Protein; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1992: WO-JU5661.
01-SEP-1992: US-978990.
(IMMU-) IMMULGIC PHARM COMF
BOOM JF. Garman RD. GYIIIITH
WPI: 94-035066/04.
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08-APR-1994; US-226248.
06-DEC-1994; US-350225.
(IMMC-) IMMULOGIC PHARM CORP.
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es 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptomeria japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1994.
15-JAN-1993: CC0139.
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                                                                                      Query Match
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reactive with Japanese cedar pollen allergen. Such modified peptides possiss certain characteristics which render ther particularly such ministers. Repride fragments of Crg.) It modified and namodified, are diversing 984591884525. This peptide fragment contemporate to are over 11990 of the dilergen ratine.
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                                                                                                                                                                                                  Sans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R81551 standard: Peptide: 17 AA. 881581.
24-MAY:1996 (first entry)
24-MAY:1996 allergen peptide 9 (T-cell eptiope)
Cedar Cryptomeria Japonica; polien: allergen: immuncalobulin E: Tedar Cryptomeria Japonica; polien: allergen: immuncalobulin E: Tedil epitope: antibody: politicsis: therapy: immuncherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allerny class 137 pp. English.

The average of the Japanese cedar.

The average of the Japanese cedar.

Police allerner fry 11. The peptide, CCT-41, can be used for the Teacher of the Teachese cedar.

Police allerner and diameters of allerians associated with Japanese cedar.

Police it has enhanced fortage of the periods but reduced side effects engineed to nationally occurring allergous.
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Cry J I polken blacken peptide CJT-41
Japanese cedar: detection: alleray: treatment: diadrosis:
Cryptus epitope, sensitivity.
Cryptusfia [aponica.
                                                                                                                                                        TS-4%; Score 15%; DW 1. Leogth 20; dest Lonar Similarity 100:1%; Fred. No. 2 13e-14. Santches 20: Insertains to Mismatches 0: Indels
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Rond JF. Garmon RC. Briffith IS. Kno M. ..
WPI: 94-0357(5/54)
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Hino K. Saito S. Taniquohi Y:
                                                                                                                                                                                                                                                                                                                                                    R45579 standard, Protein, 30 AA
                                                                                                                                                                                                                                       I TESSNALLKEAMFMYTAGYK 20
                                                                                                                                                                                                                                                           79 (FSGNSN1813MEWY1A 17 97
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08-SEP-1995.
10-SEP-1994. 09-242137.
14-CHL-1995. UP-200221.
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15-CAN-1993, 000139,
10-700-1992, W-P0566,
01-88, 1992, RS-93899;
                                                                                                     protein.
Seguence 23 AA:
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EP-78(929-A2.
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30 84
      1185 REFE
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A linked T cell epitope peptide cosed for the freather of such politics.

Such pollinosis

Ciaim 7: Page 18: 21pp; Uapa cse.

M60339-58 represent epitope. For T cells, derived from the such alection proteins Cryl (M80339-44, Ne 550-54 and W80355-59) and Cryl. (M90345-45 and W80354-55). The peptides are useful too the treather. of such pollinosis, an allergi reartion of the body to polling.
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Claim 4; Page 28: 36pp; Eng. 1...
Synthetic peptides based on positions of cedar pollen accessors A f815.65; and 5 (861587) were cested for their ability, positionary cedar allergenespectation feed for their ability, positional antibodies. Begindes 188.6 ** 8815.6 ** were dominional accessors. These peptides, plus subsequences (Reiffles) resolutions for freeling cognition, and homologous peptides (Reiffles) resolution and homologous peptides (Reiffles) resolutional politicosis, avoid any identification of prevent or prevent orbits. Sequence 17 AA:
                                                                                                                                                                                                                                                                                                                                                                                                         WeC346 standard; peptide: 18 AA.
WeC346.
H1-JAN-1999 (first entry.
Sudi alleraen protein Cry52 derived epitope to: 1 cells
Sudi epitope: Sudi alleraen proteins Cry34 (1992 - testen).
Sugi-politinosis: allerate reaction; politen.
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31 No. 5.240-08:
Mismarches of Objects
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22-DEC-1997: 353448.
24-DEC-1990. DF-34144.
4-MAYS) HAYASHIRAKA SEIBUTSU KASAKU.
(SANY.) SANKKO CO LE
WPI: 98-577037/49.
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Job time : 15 secs.
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Best Local Similarity 34(1%)
Marches 16: Conservative
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Best Local Similarity 100.0%;
Matches 17, Conservative
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                                                                                                                                                                                                                                                                                            1 NRIWLOFAKLTGFTLMS 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 | 111 | 1111 | 56 RIWLOFAKLIGETLMGR 72
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$6696666668
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Polease (1A Juli F. Collins, Blod puthor Research Unit. Payrlabt (v) 1994-1998 Chloursity of Edinbursh, U.K. Distriction rights by Oxford Molecular Ltd.

profess profess database search. Saind Smith-Waterman algorithm Mi sechipi 100 104

Lateral and continue and and and and contraction of the contraction of

-038-03-142-5248-3 -026-03-11-07-03691425248-pep -026-03-11-07-03691425248-03-03-134-03611AAYUNPASWK 134 Color priod. Porfect Score: Scrience:

PAM 150 Searing table:

145341 Seqs. 14437480 residues Sourched:

Minimus Matter 0% listing first 45 summarres Maxicum 18 seg length 194 F -t-provessine:

#FISSOR*)
1:SALT MS 2:58_COMB 3:6_COMB 4:POT_COMB 5:backfl.es1

larabase.

Prof. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by manysis of the total some distribution. Mosto 19,725; Variance 129,313; scale 0,222 Statistics

Pauli No. Score Maich Genath OB ID Description Pred. No.

Result

No matches found.

Search completed: Tue Jun 20 13:38:57 2000 Jub time : 6 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit. (Oppright (C) 1993-1998 University of Edinburgh, J.K. Distribution rights by Oxford Molecular Ltd.

protein - protein database search, using Smith-Waterman algorithm MFsrch_pp

Min Jin 19 16:02:39 2000: MasPar Line 30:42 Seconds 443:817 Million cell updates/sec Run on:

not generated. labular output >US-09-142-524A-3 (1-14) Ifom USC9142524A.pep 1026 I MKVTVAFNU-GPNPRVFIKR.......KFT3RVDGIIAAYQNPASWK

totte: Skaription: Prifect Score: Scluence:

PAM 150 Cap 11 scoring table:

721208 seqs, 100765575 residues Syarched

P. SI - processing.

Minimum Match 0% Listing first 45 surmaries Miximum DB seq length 134

arpending lipcr 2:06 3:060 4:07 5:080 6:081 7:082 8:083 9:084A lipcr 2:085 12:085 13:087 14:088 15:089 16:090 17:091 18:092 19:093 20:094 21:095 22:NEWP 23:NEWD60 24:NEWD8 25:NEWG9

Mean 43,909; Variance 128,683; Scale 0.264

Pred No. is the righer of results predicted by charse to have a score greater that or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

NO.	Secre	Match	Match Length	e,	ai ai	Description	uo.		Pred. No.
-1	1026	100.0	134		US-09-142-	Sequence 3,		Applicatio	1.6.e-97
7	552	54.7	105	1,	US-09-142-	Seguence	-	Applicatio	2.24e-46
۳.	47.2	36.3	08	Ü	US-09-142-	Sequence	1, Ap	Applicatio	3.77e-26
47	967	28.8	09	ဏ	US-08-350-	Sequence	62, 4	Applicati	3.14e-18
S	367	28.8	63	r-	US-08-226-	Seguence	62, 4	Applicati	3.14e-18
9	296	28.8		10	US-08-467-	Sedmence		Applicati	3.14e-18
۲.	396	28.8	09	10	US-08-467-	Seguence		Applicati	3.14e-18
00	367	28.8		77	US-07-938-	Sequence		Applicati	3.14e-18
G)	296	28.8		0.7	US-08-468-	Sednence	62, 4	Applicati	3.14e-18
0.7	296	26.8	50	7.0	US-08-467-	Sequence		Applicati	3.14e-18
11	172	8.97		ထ	03-08-320-	Sednence	187,	Applicat	7.10e-06
12	172	8.3.	128		US-08-468-	Sequence	6.1	Applicat	7.10e-06
13	172	16.8		0.1	US-08-467-	Sednesice	187,	Applicat	7.10e-06
7.4	172	α 			115-08-467-	Sedilence	, מ ר	200, 1004	7 100-76

from list due to search parameters chosen. Note: Post-processor removed 31 summaries

ALIGNMENTS

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Sequence 3, Application US/09142524
GENEAL INFORMATION:
APPLICANT: Sone, 18.00
APPLICANT: Sone, 18.00
APPLICANT: Sone, 18.00
APPLICANT: Walk Mazuc
CURRENT FILING DATE: 1995 1.04
EARLIER APPLICATION NUMBER: PCT/J997/30746
EARLIER PLLING DATE: 1996-03-10
NUMBER OF SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NO 3
LEMETH: 334
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GENERAL INFORMATION:
APPLICANT: Sone, Toshio
APPLICANT: Kure, Athiori
APPLICANT: Kure, Athiori
APPLICANT: Karixi, Kazuo
APPLICANT: Karixi, Kazuo
APPLICANT: Karixi, Kazuo
APPLICANT: Kino, Kohsuke
IITLE OF INVENTION: Peptide-based immunotherapeutic Agent For Treating
FILE REFERENCE: Docket No. 8F0-103
CURRENT APPLICATION NUMBER: US/09/142,524
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SEQUENCE 134 AA: 15646 Mk: 90017 ON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1026; DB 17; Length 14: Best Local Similarity 100.0%; Pred. No. 1.61e-97; Matches 134; Conservative 0: Mismatches 0; Indels :
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                                                                                                                                                                                                     Sequence 3. Application US/09:42524
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ORGANISM: Unknown
FEATURE:
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                        US-09-142-524-3
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APPLICANT KOME AKIDOT

TITEL OF INVENTION PROPRICE HISTORY

TITEL OF INVENTION PROPRICE HISTORY

CURRENT APPLICATION NUMBER 8/2/2/12 5/4

EARLIER REFERENCE CONTON NUMBER 8/2/2/2

EARLIER FILING DALE 1997-02-1C

EARLIER FILING DALE 1997-02-1C

EARLIER FILING DALE 1997-02-1C

SOUTHARE PLANG DALE 1997-02-1C

NOMBER OF SEU ID NOS. 5

SOUTHARE PLANG DALE 1997-02-1C
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Fest Local Shmithity 69,7%: Pred. No. 2,24e-46:
Fatches 90: Purseivative 1: Miscatches 1: Indels 13: Gaps
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                                                                                                                                                                                          CHREW INFORMATION CONTRIBUTION OF GRACIMATISMS poptide SECTIONS (15% AA) 1240 AWS 54040 ON.
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| HTT | HTT | HTT | HTT | HTT | HTT | HTT | HTT |
| MKVIVAFNGESPARREVETREVSNVIIHGREIDIFASKAFHLGKATIGTGRE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 36.3%; Score 372; DB 17; Length 90; Lotal Similarity 100.0%; Pred. No. 3.778-26; No. 3.778-26; les 51; Conservative 0; Mismatches 0; Indels
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EARLIER APPLICATION NUMBER: 8/EU/702
EARLIER FILING AND 1996-03-10
EARLIER FILING AND 1996-03-10
EARLIER FILING AND NUMBER: PIT/SP97/00740
EARLIER FILING AND NOS 5
SCHIMMAE: PALENTIN VC: 2.0
SCHIMMAE: PALENTIN VC: 2.0
SEQ IN NC 2
CENTR | 10%
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General information:
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                                                                                                                                                             ORIANISM: Unkrown
FEATURE:
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GENERAL INCORMATION:
APPLICANT STITEON TEATLOOD
APPLICANT SCHOOK JOANNE
APPLICANT BOND, JAINA F.
APPLICANT BOND, JAINA F.
APPLICANT BOND TO STORE TO A APPLICANT BOND TO STORE TO A APPLICANT FOR STORE H.
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PATCHILLE
OPERATING SYSTEM: PATCHILLE
OPERATING SYSTEM: PATCHILLE
CORRENT APPLICATION DAIN
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AND DAI
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STREET: 610 Lincoln St.
CITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AA: 6644 MW: 19464 CN:
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TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: +2:
    STANDARU
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LENGTH: 60 amino acids
TYPE: amino acid
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FRAGMENT TYPE: interna
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1D US-U8-226-248A-62
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US UB-350-225-62
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Sequence 62, Application US/08467006
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AFFLICANT POLICE, Johnson Police, Michael D. AFFLICANT Word Starter, B.:
AFFLICANT POWER AND EX. A. AND POLICE POLICE OF INVENTION: Albergenic Proteins And Poptides From TITLE OF INVENTION: Albergenic Proteins And Poptides From TITLE CF INVENTION: Albergenic Johnson Police Constructions and Applicant Applied Construction Constructio
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APPLICATION NUMBER: PCT/US02/00139
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REGISTHATION UNMERS. 35,729
REGISTHALFLOOCKIT KNASK: 025,5 US (IKI-0240P)
TELECOMMONICATION INFORMATION:
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28.8%: Score 296; DS 7; Let
Aest Local Similarity 73.6%: Pred. No. 3.14e-18;
Aatches 39; Conservative 5; Mismatches 7;
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MOLECULE TYPE: peptide
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TELEFAX: (517) 456-600
TNICRMATION FOR SEQ 10 NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 aman
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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APPLICANT: Yeung, Sturmet H.:
APPLICANT: Brauer, Andrew:
APPLICANT: Exely, Mark A.:
APPLICANT: Powers, Steven F.
APPLICANT: Page 1.  

TITLE OF INVENTION: Albander Terting Policy
NUMBER OF SEQUENCES: 26:
ADPRESSEE: ADPRESSES:
ADPRESSEE: ADMILICATION (Harmacoutical Corporation (Hr.)
STREET: 610 Lincoln of
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Pred. No. 3.14e-18:
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GENERAL INFORMATION:
APPLICANT: GILIffeth, Irwin J.;
APPLICANT: Pollock, Joanne,
Sequence 62, Application 75/18457066
SENERAL INFORMATION:
APPLICANT: Giffich, win 7:
APPLICANT: Pollock, 1 drie:
APPLICANT: Bond, 0110, Ft.
APPLICANT: Garman, Richard E.
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FRAGMENT TYPE: internal
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Local Similarity 73.6%:
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TITLE VE INVENTION: Allergenic Proteins And Puptides From
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COMPUTER READABLE FORM:
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APPLICANT Grifferth Irwin ().
APPLICANT Grifferth Irwin ().
APPLICANT Boilock, Joanne.
APPLICANT Bond, Julian F.,
APPLICANT Garman, Richard ()
APPLICANT Garman, Richard ()
APPLICANT Kun, Mei Dhang,
APPLICANT Frunc. Stumme: H.,
APPLICANT Frunc. Stumme: H.,
APPLICANT Stummer, Madrew.
APPLICANT Powers, Steven P.
ITILE OF INVENTION: Allergenic Proteins And Peptides From IIILE OF INVENTION: Algebres Cedar Polien
NUMBER OF SECURENCES: 25,1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Impulogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match
Rest Local Similarity 73.6%, Fred. No. 5.146-185
Matches 39: Conservative 1. Kismatches 7. Locus
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 161 02900 (IM1+128)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 222-7409
TELEPHONE: (617) 227-594;
INFORMATION FOR SEU ID NO: 64
SEÇUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 62, Application US/08456946 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FPAGMENT TYPE: internal
JENCE 60 AA: 6644 MW; 19464 (N.
Sixty State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 60 amino acids
TYPE: AMINO ACID
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                Boston
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COUNTRY: USA
ZIP: 02154
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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   Gaps
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APPLICANT: Griffeth, Irwin J.;
APPLICANT: Bollock, Joanne;
APPLICANT: Bond, Unitan F.;
APPLICANT: Garman, Richard D.;
APPLICANT: Garman, Richard D.;
APPLICANT: Weng, Siu-mei H.;
APPLICANT: Fanger, Andrew;
APPLICANT: Brauer, Andrew;
APPLICANT: Brauer, Andrew;
APPLICANT: Brauer, Sieven P.
IILE OF INVENTION: Allergenic Proteins And Peptides From IIILE OF INVENTION: Allergenic Proteins And Peptides From IIILE OF INVENTION: Allergenic Proteins And Peptides From MYMBER OF SOUTHOUS: 261
CORRESPONDENCE ADDRESS:
ADDRESSE: Limmulogic Pharmaceutical Corporation, Inc. STARE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (17) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) | (1) |
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                                                                                                                                                                                                                                                                FILING DATE:

CLASSIFICATION NOMBER: CS/CO/455/940

FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: C8/350,225

FILING DATE: December 6, 1994
APPLICATION NUMBER: 08/256,246
FILING DATE: APPLIE: 08/256,246
FILING DATE: SEPTEMBER: 08/256,246
FILING DATE: SEPTEMBER: 08/39,39
FILING DATE: SAPLED 1 1993
APPLICATION NUMBER: 07/93,99
FILING DATE: January 15, 1993
APPLICATION NUMBER: 07/0593/90139
FILING DATE: January 15, 1993
APPLICATION NUMBER: 07/0593/90139
FILING DATE: January 15, 1993
APPLICATION NUMBER: 02/05/93/90139
FILING DATE: January 15, 1993
APPLICATION NUMBER: 35, 729
APPLICATION NUMBER: 02/05/93/90139
FILING DATE: January 15, 1993
APPLICATION NUMBER: 02/05/93/93/90139
FILING DATE: January 15, 1994
APPLICATION NUMBER: 02/05/93/93/90139
FILING DATE: January 15, 1994
APPLICATION NUMBER: 02/05/93/90139
FILING DATE: January 15, 1994
APPLICATION NUMBER: 02/05/93/90139
APPLICAT
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                                                      COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PF COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: Patentin Release *1.0. Version #1.25
CCREENT APPLICATION DATA:
APPLICATION DATA:
VS/C8/468,940
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Local Similarity 73.6%; Pred. No. 3.14e-18;
es 39; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RPINITESONMNIKLKMPMYIAGYKIFDGRGAUV-YIGNGGP-
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60 AA: 6644 MW: 19464 CN:
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MOLECULE TYPE: peptide
FRACMENT TYPE: intercal
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Gaps
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APPLICANT Bollock, Joanne;
APPLICANT Bond, Julian F.;
APPLICANT Bond, Julian F.;
APPLICANT Garmat, Richard J.
APPLICANT Kuo, Mei-Chang;
APPLICANT Yeung, Stu-mei H.;
APPLICANT Brader, Andrew;
APPLICANT Exley, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT Exley, Mark A.;
APPLICANT STOWNENS Albergenic Proteins And Peptides From TITLE OF INVENTION: Japanese Cedar Pollen NUMBER OF SEQUENCES, 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 RF WILESGNMAIKLKMPMYIAGYKTFDGRRAEUSYUGUNGA-KFIRRUNGII 124
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE PATENTIN PC-DSSADS.
SOFTWARE: Patentin PC-DSSADS.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/46/1.23
RILING DATE: Durie 6, 1995
FILING DATE: Durie 6, 1995
FILING DATE: Docember 6, 1994
ATTON REYAGEN: INFORMATION:
RAME: Jane E. Remillard
REGISSRATION NUMBER: 38, 672
REGISSRATION NUMBER: 32.6 USD2 (IMI-C26CPD2);
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACIPRISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc. STREET: 610 Lincoln St. CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RPIMIIFSGNMNIKLKMPMYIAGYKTFDGRGAQV-YIGNGGPCVFIKAVSNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 28.8%; Score 296; DB 10; Length 60; Local Similarity 73.6%; Pred. No. 3.14e-18; hes 39; Conservative 5; Mismatches 7; Indeis
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 187. Application US/U8191225
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGNENT TYPE: internal
CENCE 60 AA: 6644 MW: 19464 CN:
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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MOLECOLE TYPE: peptide
FRAGMENT TYPE: Internal
JENCE 128 AA; 14445 MW: 84272 GN:
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MEDIUM TYPE: Floppy
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Best Local Similarity 95 24.
The ZC: Conservative
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ID US-08-467-023-187
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ANDRESSENTENCE JAMBRICGGC PARAMACEUTICAL COFFCRATION, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0:
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STREET: 610 Lincoln St
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uery Match
est Local Similarity 95.2%: Pred. No. 7.10e-06:
atches 20: Conservative I: Mismatches C: Indols
                                                                                           PRIOR SAFET AT A SAFET AT A SAFET A SA
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SOFTWARE, Fatentic Release #1.0, Version #1.25 CHPENT APPLICATION DATA: APPLICATION NUMBER: US/08/350.225 FILING IATE: December 6, 1994 (LASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W-USCOLE TYPE: peptide
FRAGMENT TYPE: Internal
TENTE 128 AA: 1445 MW: 84272 CN:
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CANT. GEITLOCH. ITWO: :
CANT. POLICCK. JUGARION:
CANT. Bond. Julian F.;
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEPY O
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US-08-458-940-187
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APPLICANT STITLE IN THE STATE APPLICANT FOLLOW.

APPLICANT FOLLOW. JOANNER

APPLICANT FOLLOW. JOANNER

APPLICANT KUO, Mel Chard.

APPLICANT KUO, Mel Chard.

APPLICANT FRUO, SLUTHER H. JAPPLICANT BROWN.

APPLICANT SAVEY, MARX A.:

APPLICANT BROWN.

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STREET: 610 Lincoln St
CITY: Waltham
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APPLICATION NUMBER: US/8/456,940
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/56,246
FILING DATE: December 6, 1944
APPLICATION NUMBER: US/26,246
FILING DATE: AFFIL 8, 1944
APPLICATION NUMBER: US/26,246
FILING DATE: AFFIL 8, 1944
APPLICATION NUMBER: PCI/1993/PCI/1000
APPLICATION NUMBER: PCI/1993/PCI/1000
APPLICATION NUMBER: PCI/1993/PCI/1000
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FILICATION NUMBER: US/1994
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GENERAL INFORMATION
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REGISTRATION NUMBER: 38.872
RECOMPUNICATION NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMPUNICATION NUMBER: 027-7400
TELECOMPUNICATION: 1617) 227-7400
TELECOMPUNICATION: 1677-75941
INP. MAAILEN N. (617) 227-75941
INP. MAAILEN N. (617) 227-75941
INP. MAAILEN N. (617) 227-7400
SEQUENCE CHARACTERISTICS: 187: 1785 anino acids TYPE: 1786 acid acid acid acid acid acid populate populate PRASMENT TYPE: 10 po
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APPLICATION DATA.
FILING SATE: June 6, 1995
CLASSIFCATION: 424
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          08/08/457.023
APPLICATION NUMBER: US/08/467.027
FILING UNTE: 5.00 6, 1995
CLASSIFICATION: 424
PHIOR APPLICATION DAIN:
APPLICATION NUMBER: 08/350.225
APPLICATION NUMBER: 08/350.225
ATION BATE INFORMATION:
NAME: 5ane E. Remillard
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DGS
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PHIDR APPLICATION DAFA:
ADDELICATION NUMBER: 08/350.225
FILING DATE: December 6, 1994
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CC NTORNEY AGENT INFORMATION:
CC NAME: Dade E Westilaid
CC REFERENCE/DOORST NUMBER: 88.672
CC TELECOMMUNICATION INFO: 1710.
CC TELEC
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Release A.1A John F. Collins. Biocomputing Research Jult. Cupyridh: (c) 1993-1998 University of Edinburgh U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Materman algorithm Mon Jun 19 14:01:35 2000: MasFar time 11:24 Seconds 552.380 Million cell updates/sec MFsrch_pp R...: On:

>05-09-142-5244-3 101-134) from USG9142524A.pep 1026 1 MKVIVAENUEGENRRVEIKR......KFIRRVOGIIAAYQNPASWK 134 Tabular output not generated. Description: Perfect Score:

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PAM 150 Gap 11 Souring table:

142080 segs, 47172406 residues

Scarched:

Minimum Match 08 Listing first 45 summaries Maximum DR seq length 134 Fost-processing:

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Pred. No. is the further of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by unalysis of the total score distribution. Mean 43,199; Variance 89, 18; scale 0.484 Statistics

## SUMMARIES

Fred. No.	9.82e-02 1.36e-00 5.45e+00
South County No. Score Match Longth OR ID Description Fred. No.	hypothetical mucleic hypothetical protein hypothetical protein
10	548562 F75052 I40656
m :	21212
Score Match Length 38 ID	110 2 111 2 131 2
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Note: Post-processor removed 42 summaries from list due to search parameters chosen.

## ALIGNMENTS

RESULT I	048562 *type complete
371	hypothetical nucleic acid-binding protein - San Miguel sea
PRIBANISM	#formal_name San Miguel sea lion virus
CATE	17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
ANTESSIONS	27-Mat : 99-8 D48562
REFERENCE	A48562
*authors	Neill, C.D.
#journal	Virus Res. (1992) 24:211-222
#title	Nucleotide sequence of the capsid protein gene of two
	serotypes of Sap Miguel sea lion virus: identification of

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Suban, M.: Chen, S.Y.; Inompson, B.A.; Hoover, T.A.; Hill. A.; Williams, J.C., (1994), 176:5233-5243
Cloning and characterization of an autonomous replication sequence from Coxiella burnetti.
                                                                                                                                                                                                                                                                                                                sequence extracted trom NCBI backbone (NCBIF 11977) #length 110 | #molecular-weight 12566 | #checksur 27
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##Cross-references GB:AJ248287: GB:AJC96836: NID-9545H-57.
##Cross-references PIGN:CAP59351: PID-e1516213. FID-0545H-28
##Experimental_source stinin Orsay
conserved and non-conserved amino acid sequencys callcivirus capsid proteins.
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##molecute_type DNA
##resides 1-131 ##label RES
##cruss-references EMBLU10529: NID:q511451: PID:q511461
SURMARY ##ength 13: #molecular-Weight 15592 #checksum 3153
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Query Match Rest Local Similarity 25.0%; Pred. No. 5.45e-00: Matches 18: "Asservative 21: Mishatches 30: Indels 3: Gaps 3:

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Rolease 7.1A John F. Collins, Biocorputing Posearch Unit. Jopyricht (c) 1993-1998 University of Edinburgh. U.K. Distribution rights by Oxford Molecular Ltd

profeso - proteso database search, using Smith-Waterman algorithm MasPar time 7.92 Seconds 515.241 Million cell updates/sec Mod Jun 19 16 00:24 2000: labular output not generated. Run On:

(.-134) from US09142524A.pep 1.26 1.KVIVAFNOFSPNRRVFIKR......KFIFFVDGIIAAYQNPASWK 134 DCS-09-142-524A-3 Description. Perfect Score: Sequence:

1988 250 Jup 11 Scoring table:

8:857 segs, 30454973 residues Minimum Match 0% Listing thrst 45 Fust-processing. Seirched:

Listing first 45 surmaries Maximum DH seg length 134

Swiss-profit Database:

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Variance 79.368; scale 0.555 Mean 44.072: Statistics:

SUMMARIES

110 1 Y12K_SMSV4 POSSIBLE 12 KD NUCUEIC 1.59e-02 Description Score Matty Length DB 1D 105 10 2 Result

Note: Post processor removed 44 summaries from list due to search parameters chosen.

PAGERS, 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) POSSIBLE 12 KD NUCLEIC ACID-BINDING PROTEIN. San Miduel sea lion vius (serotype 4; (SMSV 4). Viruses, SSENA positive-strand viruses, no DNA staye: Caliciviridae: 110 AA STANDARD: LI : Y12K_SMSV4 RESULT CORECTOR SOCIAL SERVICES

SEQUENCE FROM N.A. SEQUENCE 92413750. Neill Jul.: "Nucleotide sequence of the capsid protein gene of two serotypes of

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Search completed: Mon Jun 19 16:00:34 2000 Job time: 10 secs.

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Release 7.1A John F. Collins, Riocomputing Research Unit. Copyriat (c) 1953-1998. University of Edinburgh, U.K. Listribution rights by Oxford Molecular Ltd.

proter reprotein database search, using Smith-Waterman algorithm

Mon dan 19 16:00:52 2000; MasFar tare 18:49 Seconds 502.347 Million cell updates/sec and one

Tabular output not generated.

-05-09-142-524A-3 (1-174) from USSS142524A.pup 1026 UMKUTVAR NGFORNRAVEIKR......KPIRRVDGIIAAYQNPASWK Description: Perfect Score: Sequence:

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3	01-330-1397	(TremBLrel, 04,	Created)		
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Search completed: Mon Jun 19 .6:01:18 2000 Job time : 26 sets.

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KETCHON K.A. DODSON B.O. TOKE DI-F. WHITE O. NEISON K.E.,

KETCHON K.A. DODSON B.O. GWINN M., HICKEY E. K., FETERS N. J. T.

RESISCHANN R.D. OCANENHING D. LEE. N. HICKEY E. N., J. D.

RICHARDSON E.L., KERLAVASE A.R., GRANAM DE., KYPFITIS N. J.

RICHARDSON E.L., KERLAVASE A.R., GRANAM DE., KYPFITIS N. J.

RICHARDSON E.L., FOUGHERTY F. A., MCKENNEY K. DOLGEK A., GILL S.

AR KINNESS E.F., DOUGHERTY F. A., MCKENNEY K. BADGER J. H., GUILL S.

AN ELERRON R., GOCANNE J.D., WEIDMAN J.F., MCHONALD L. GILLERAN K.T.

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